

```

TTCAGGAATT GATTGTAAGT TCTGTTATCA ACTAAAGCCG ACAGCGGTTG      50
CTGATATGCT CTAGAACAAC ATTGCTAAGG CTCACGGTGG TTACTCCGTG      100
TTCAGTGGTG TCGGTGAGCG TACCCGTGAG GGTAACGATT TGTACCATGA      150
AATGCAAGAG ACCCGTGTCA TTCAACTCGA CGGAGAGTCC AAGGTCGCTC      200
5  TTGTCTTCGG TCAAATGAAC GAGCCCCCTG GTGCCCCGTGC CCGTGTTGCC      250
CTTACCGGTT TGACCATTGC TGAATACTTC CGTGACGAGG AAGGCCAAGA      300
CGGTAGGCTT CATGCTTCTA TCGCTAGGGG CGTGTGATAC AGGAGGCTAA      350
TCGCTTTTCT AGTGCTTCTC TTTATTGACA ACATTTTCCG TTTCAC TCAA      400
GCTGGTTCTG AAGTGTCTGC CTTGCTCGGT CGTATTCCTT CCGCTGTCGG      450
10 TTACCAACCT ACTCTCGCCG TCGACATGGG TGTATGCAG GAACGTATCA      500
CCACCACCAC CAAGGGATCC ATTACTTCAG TGCA                        534

```

15 2) INFORMATION FOR SEQ ID NO: 480

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 494 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Cryptococcus albidus
(B) STRAIN: ATCC 66030

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

```

30 CGTCTTGATT CAAGAATTGA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
ACTCGGTCTT CACCGGTGTC GGTGAGCGAA CTCGAGAGGG TAACGATCTG      100
TACCACGAAG TGAGTTGCGC CGTCCGAGTG TTTCCCGGGG AATCGCAAGA      150
CTGATGTTGT CCCTTCTTCT CAGATGAGGG AAACCGGTGT CATCAACCTC      200
35 GAGGGTGACT CCAAGGTCGC CTTGGTCTTC GGTCAGATGA ACGAGCCCCC      250
TGGAGCCCCA GCCCGAGTCG CCTTGACCGG TTTGACCATT GCCGAATACT      300
TCCGAGACGA GGAGGGTCAG GATGTCTTGT TGTTTCATTGA CAACATTTTC      350
CGATTACCC AAGCCGGTTC CGAAGTGTCC GCCTTGTTGG GTCGTATCCC      400
CTCCGCCGTC GGTTACCAGC CCACTCTGTC CACCGACATG GGTACCATGC      450
40 AGGAGCGAAT TACCACCACC AAGAAGGGTT CCATCACTTC CGTC          494

```

45 2) INFORMATION FOR SEQ ID NO: 481

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 415 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

55 (A) ORGANISM: Fusarium oxysporum
(B) STRAIN: WSA-212

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481

```

60 TTCAGGAGCT TATCAACAAC ATCGCCAAGG CCCACGGTGG TTACTCCGTC      50

```

```

TTC ACTGGT G TCGGTGAGCG AACTCGTGAG GGTAACGATC TGTACCACGA 100
AATGCAGGAG ACTTCCGTCA TTCAGCTTGA TGGCGAGTCC AAGGTCGCCC 150
TGGTCTTCGG TCAGATGAAC GAGCCCCCTG GAGCTCGTGC CCGTGTCGCC 200
CTTACCGGTC TTAGTGATG TGAATACTTC AGAGATGAGG AGGGTCAGGA 250
5 CGTGCTGCTC TTCATTGACA ACATTTTCCG ATTCACTCAG GCCGGTTCCG 300
AGGTGCTGTC CTTTCTCGGT CGTATCCCCT CTGCCGTCGG TTACCAGCCC 350
ACCCTCGCCG TCGACATGGG TGGTATGCAA GAGCGTATTA CCACCACCAC 400
CAAGGGTTCC ATTAC 415

```

10

2) INFORMATION FOR SEQ ID NO: 482

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 1281 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Geotrichum spp.
    (B) STRAIN: Lev-4

```

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

```

AGGACAACCT CCCCGCTATT CTTAACGCTC TTGAGCTTAA GAGAGATAAC 50
GGTGAGAAGC TCGTTCTCGA GGTTGCCAG CATCTGGGTG AGAACAAGTGT 100
30 CCGTACTATT GCTATGGACG GTACTGAGGG TCTCGTCCGT GGTCAGCCCCG 150
TTGTTGACAC CCGTGCCCCC ATTACCATT CCGTTGGTCG TGGTACTCTT 200
GGTAGAATTA TCAACGTCAT TGGTGAGCCC ATCGATGAGC GTGGACCCAT 250
TGAGGCTACC AAGTACCTCC CCATCCACAC CGAGCCCCC ACCTTCGCTG 300
AGCAGTCTAC CTCCGCTGAG GTTCTTGAGA CTGGTATCAA GGTGTGTCGAT 350
35 CTCCTTGCCC CTTACGCCCC TGGTGGTAAG ATTGGTCTCT TCGGTGGTGC 400
CGGTGTCGGT AAGACCGTTT TCATTCAGGA GCTGATTAA AACATTGCCA 450
AGGCCCATGG TGGTTTCTCC GTTTTCACCG GTGTCGGTGA GAGAACCCGT 500
GAGGGTAACG ATTTGTACCG TGAGATGAAG GAGACCGGTG TCATCAACCT 550
CGAGGGTGAG TCTAAGGTCG CTCTCGTTTT CGGTCAGATG AACGAGCCCC 600
40 CTGGAGCCCG TGCCCGTGTT GCTCTTACTG GTCTTACCAT TGCTGAGTAC 650
TTCCGTGATG AGGAGGGTCA GGATGTGTTG CTCTTCGTTG ACAACATTTT 700
CCGTTTCTACT CAGGCCGGTT CCGAGGTGTC TGCCCTTTTG GGTGCTATTC 750
CCTCCGCTGT CCGTTACCAG CCCACCCTTG CCACTGATAT GGGTGCCCTG 800
CAAGAGCGTA TTACCACCAC CCAGAAGGGT TCCGTCACTT CCGTCCAGGC 850
45 CGTCTACGTC CCTGCCGATG ATTTGACCGA TCCTGCCCCC GCTACCACCT 900
TCGCCCATTG GGATGCCACC ACCGTCTTGT CGCGTTCCAT TTCTGAGTTG 950
GGTATCTACC CCGCTGTCGA TCCCCTTGAT TCCAAGTCTC GTCTTTTGGA 1000
TATCACCGTC GTTGCCAGG AGCACTACGA TGTTGCTACC CAGGTCCAGC 1050
AGACCCTCCA GTCCTACAAG TCTCTTCAGG ATATCATTCG CATTTTGGGT 1100
50 ATGGATGAGT TGTCTGAGGC TGATAAGCTT ACTGTCGAGC GTGCCCCTAA 1150
GATCCAGAGA TTCTTTTCCC AGCCCTTCAC TGTCGCTGAG GTTTTCACTG 1200
GTATCGAGGG CCGTCTCGTT CCTTTGAAGG AACTGTTCG CTCTTTCAAG 1250
GAGATCCTTG AGGGCAAGTA CGACCACCTC C 1281

```

55

2) INFORMATION FOR SEQ ID NO: 483

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 586 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G185A5

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 483

	ATTCAAGAAT	TGATCGTACG	TTCCTCCGCC	CCACACACGA	TCAATGGAGA	50
	AAGAAACAAA	TTTTTTGGGA	GTGGTCAATT	TTTCTAATAA	TTCGAATAGA	100
15	ACAACATTGC	CAAAGCCCAC	GGTGGTTACT	CCGTGTTTAC	TGGTGTCCGC	150
	GAGCGGACCC	GTGAAGGAAA	TGACTTGTA	CACGAAATGC	AGGAAACCCG	200
	TGTTATCCAG	CTCGATGGAG	AGTCCAAGGT	CGCCCTCGTT	TTCGGTCAGA	250
	TGAACGAGCC	TCCCGGAGCC	CGTGCCCGTG	TTGCCCTCAC	TGGTCTGACC	300
	GTTGCCGAGT	ACTTCCGTGA	CGAGGAAGGC	CAAGACGGTA	TGTATAAGTA	350
20	TACACCGTAG	CAAATCAACA	CAGAGCTTCA	CTCACGCTCG	GATTTAGTGC	400
	TTCTCTTCAT	CGACAACATT	TTCCGCTTCA	CTCAGGCCGG	TTCCGAAGTG	450
	TCTGCCCTGC	TCGGCCGTAT	TCCCTCCGCC	GTCGGTTACC	AACCCACCCT	500
	CGCCGTGGAC	ATGGGTGGTA	TGCAGGAACG	TATCACC ACT	ACCACCAAGG	550
25	GCTCCATCAC	CTCTGTGCAR	GCCGTCTACG	TCCCCG		586

2)INFORMATION FOR SEQ ID NO: 484

30 (i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

40

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 484

	GCGTGGCCAG	AAGGTCATTG	ACACTGGTGC	TCCCATCACC	ATCCCCGTCG	50
45	GTGGTGCCAC	ACTGGGTCGT	ATTCTGAACG	TCACGGGTGA	CCCTATTGAC	100
	GAGCGTGGCC	CCGTTAAGAC	TGACGTTTTT	CGCCCCATTC	ACCGTGACCC	150
	CCCTGCCTTT	GTCGAGCAGT	CGACTGATGC	CGAGATTCTC	GAGACTGGTA	200
	TCAAAGTCGT	TGACCTGATT	GCCCCTTACG	CCCGTGGTGG	TAAGATTGGT	250
	CTGTTTCGGTG	GTGCCGGTGT	CGGTAAGACC	GTGCTTATCC	AGGAGCTCAT	300
50	CAACAACATC	GCCAAGGCC	ACGGTGGTTT	CTCCGTGTTC	ACTGGTGTCTG	350
	GTGAGCGTAC	TCGTGAGGGT	AACGATTTGT	ACCACGAGAT	GATTGAAACC	400
	GGTGTCATTA	ACCTCGAGGG	TGACTCGAAG	GTGGCTCTGG	TGTTTCGGTCA	450
	GATGAACGAG	CCCCCGGGTG	CCCGTGCGCG	TGTCGCTCTT	ACTGGTCTGA	500
	CTGTGGCCGA	GTAATTCCGT	GACGACGAGG	GCCAGGATGT	GCTGCTGTTC	550
55	ATTGACAACA	TTTTCCGTTT	CACCCAGGCC	GGTTCGGAGA	CTTCGGCTCT	600
	GCTGGGTCGT	ATCCCTTCGT	CGGTCGGTTA	CCAGCCCACT	TTGTTCGACCG	650
	ATATGGGTGC	CATGCAGGAG	CGTATCACCA	CCACCAAGAA	GGGTTCGATT	700
	ACGTCGGTGC	AGGCCGTCTA	CGTGCCCGCC	GATGATGTCA	CTGACCCTGC	750
	CCCTGCCACT	ACCTTCGCCC	ACCTTGACGC	TACCACTGTG	CTTGACCGTT	800
60	CGATCGCTGA	GCTGGGTATC	TACCCCGCTG	TTGACCCGTT	GAACCTCGAAC	850

```

TCGCGTATGC TTGACCCCGC TATTGTGGGT CAGGAGCACT ACGACGTGGC 900
CTCTGGCGTG CAGAAGCTGC TCCAGGACTA CAAGTCGCTT CAAGATATCA 950
TTGCCATTCT GGGTATGGAT GAGCTTTCTG AGGAGGACAA GCTCACTGTC 1000
GAGCGTGCCC GTAAGATGCA GCGTTTCATG TCGCAGCCTT TCGCTGTCGC 1050
5 CCAGGTCTTT ACTGGTATCG AAGGTCGTCT TGTGGCCCTG AAGGACACGA 1100
TCAAGGCCTG CAAGGAGATC CTGTCGGGCA AGCACGACAA CCTCC 1145

```

10 2) INFORMATION FOR SEQ ID NO: 485

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 1261 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Malassezia pachydermatis
    (B) STRAIN: ATCC 42756

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

```

25 TCCCGCCATC TTCAACGCC TGGAGGTCCA GGACATGAAG AACGGTGGCC 50
   GCCTTGTTCT GGAGGTTGCC CAGCACCTTG GTGAGAACAC TGTTCTGTTGC 100
   ATTGCTATGG ACGGTACCGA GGGTCTTGTC CGTGGTCAGA AGGTCCTTGA 150
   CACTGGTGCC CCGATCACTA TCCCTGTCGG TAACGGTACC TTGGGCCGYA 200
30 TCCTGAACGT CACTGGTGAG CCTGTGGATG AGCGTGGTCC GGTAAAGACT 250
   GACGTCTACC GTCCAATCCA CCGTGAGCCC CCGGCGTTCTG TTGAGCAGTC 300
   GACTGATGCT GAGATTCTTG AGACTGGTAT CAAGGTGGTC GACCTGCTCG 350
   CCCCATACGC TCGTGGTGGT AAGATTGGTC TWTTCGGTGG TGCYGGTGTY 400
   GGTAAGACCG TGCTGATTCA GGAGCTTATC AACAACATTG CCAAGGCCCA 450
35 CCGTGGTTTC TCGGTGTTCA CTGGTGTCGG TGAGCGTACT CGTGAGGGTA 500
   ACGATCTGTA CCATGAAATG ATTGAGACTG GTGTCATCAA CGTTGACGGT 550
   GACTCGAAGG TCGCTCTCGT GTTCGGTCAG ATGAACGAGC CCCCAGGTGC 600
   CCGTGCCCGT GTCGCCCTGA CYGGTCTGAC CATCGCCGAG TACTTCCGTG 650
   ACGACGAGGG TCAGGATGTG CTGCTCTTCA TTGACAACAT TTTCCGTTTC 700
40 ACTCAGGCTG GTTCGGAGAC TTCGGCTCTG CTGGGTCGTA TCCCGTCGGC 750
   TGTCGGTTAC CAGCCACGCC TTGCCACGGA TATGGGTGCC ATGCAGGARC 800
   GTATYACCAC CACCAAGAAG GGTTCGATTA CCTCGGTGCA GGCYGTTTAC 850
   GTTCCGGCCG ACGATGTGAC TGACCCTGCC CCGGCCACGA CCTTCGCCCA 900
   CTTGGACGCC ACCACGGTGT TGGACCGTTC GATTGCTGAG CTGGGTATCT 950
45 ACCCGGCCGT CGACCCGCTG AACTCGAAGT CGCGTATGCT TGACCCGTCA 1000
   ATTGTCGGTG TGGAGCACTA CAACGTTGCT TCGGGTGTCC AGAAGCTTCT 1050
   YCAGGACTAC AAGTCGCTCC AAGATATCAT TGCCATTCTG GGTATGGATG 1100
   AGTTGTGCGA GGAGGACAAG CTCACTGTCTG AGCGTGCCCG TAAGATGCAG 1150
   CGTTTCCTGT CGCAGCCTTT CGCTGTGGCC CAGGTCTTCA CTGGTATCGA 1200
50 GGGTCGTCTT GTGTCGCTCA AGGACACCAT CAACGCCTGC AAGGAGATTC 1250
   TGTCCGGTAA G 1261

```

55 2) INFORMATION FOR SEQ ID NO: 486

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 1282 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double

```


(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*

(B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486

10 AGGAGGGCAA CTTGCCAGCT ATCTTCAACG CTTTGACGTT GAAGAACGGC 50
 GACCAGAAGT TGGTCTTGGA GGTGGCCAG CACTTGGGTG AGAACACCGT 100
 CAGAACCATT GCCATGGACG GTACCGAGGG TTTGGTCAGA GGCGCCTCTG 150
 TCACCGACAC YGGTGCCCTT ATCTCCGTGC CTGTCGGCCG TGAGACCTTG 200
 15 GGTTCGTATTA TCAATGTTGT TGGTGAGCCA ATCGACGAGA GAGGCCCAAT 250
 CAACACCAAG AAGAGAAACC CTATTCACAC CGACCCACCT TCGTTTGTCC 300
 AGCAATCCAC TTCCGCCGAG GTCTTGGAGA CTGGTATCAA GGTGTGCGAC 350
 TTGTTGGCCC CTTACGCCAG AGGTGGTAAG ATTGGTTTGT TCGGTGGTGC 400
 CGGTGTTCGGT AAGACCGTGT TCATCCAGGA GTTGATTAAC AACATTGCCA 450
 20 AGGCCACCGG TGGTTTCTCC GTTTTCACCG GTGTCGGTGA GAGAACCAGA 500
 GAGGGTAACG ATTTGTACCG TGAAATGCAG GAGACTGGTG TCATCAACTT 550
 CGAGGGTGAC TCCAAGGTCG CCTTGGTTTT CGGTCAGATG AACGAGCCTC 600
 CAGGAGCTAG AGCYAGAGTT GCCTTGACCG GTTTGACCAT CGCCGAGTAC 650
 TTCAGAGACG AGGAGGGTCA GGATGTGTTG TTGTTCTGTCG ACAACATTTT 700
 25 CAGATTCACC CAAGCCGGTT CTGAGGTGTC TGCCTTGTTG GGTCGTATTC 750
 CATCCGCTGT CGGATACCAG CCAACCTTGG CCACCGATAT GGGTGCCTTG 800
 CAGGAGAGAA TTACCACCAC CAAGAAGGGT TCCGTCACCT CCGTCCAGGC 850
 CGGTACTCGT CCAGCCGATG ACTTGACTGA CCCTGCGCCA GCCACCACTT 900
 TCGCCCCTT GGACGCCACC ACTGTGTTGT CCAGAGGTAT CTCTGAGTTG 950
 30 GGTATCTACC CCGCTGTCTGA CCCCTTGGAC TCCAACCTCA GATTGTTGGA 1000
 CGCCACCGTT GTTGGCCAGG AGCACTACGA CGTCGCCACC AACGTCCAGC 1050
 AAACCTTACA AGCTTACAAG TCCTTGCAGG ATATCATTGC CATTTTGGGT 1100
 ATGGATGAGT TGTCCGAGAC CCGACAAGTT GACCCGTCGA GAGAGCCAGA 1150
 AAGATCCAGA AGTTCTTGTC CCAGCCATTT GCCGTCGCCG AGGTTTTCAC 1200
 35 CCGTATTGAG GGTAGATTGG TTAGATTGGA GGACACCGTT AGATCCTTTA 1250
 AGGAGGTTTT GGAAGGTAAG TACGACCACT TG 1282

40 2) INFORMATION FOR SEQ ID NO: 487

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*

(B) STRAIN: WSA-214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487

55 TGTCTTTATC CAGGAGTTGA TTGTACGTCT TTACCTTTCT GCCTGACTGT 50
 TTACGACAAC TAACGAAAGC GTAGAACAAC ATTGCCAAGG CTCACGGTGG 100
 TTA CTCTGTC TTA CTGTTG TCGGTGAACG TACTCGTGAG GGTAACGATT 150
 TGTACCACGA AATGCAGGAA ACTGGTGTCA TTCAGCTCGA GGGTGAATCC 200
 60 AAGGTCGCCC TCGTGTTCGG TCAGATGAAC GAGCCCCCG GTGCCCGTGC 250

	CCGTGTCGCT	CTTACTGGTT	TGACCATTGC	CGAGTACTTC	CGTGACGAGG	300
	AAGGTCAGGA	CGTGCTTCTC	TTCATTGACA	ACATTTTCCG	TTTCACTCAG	350
	GCCGGTTCTG	AGGTGCTCTG	CCTTCTGGGT	CGTATCCCCT	CTGCCGTCGG	400
	TTACCAGCCC	ACCCTTGCCG	TCGACATGGG	TATCATGCAG	GAGCGTATTA	450
5	CCACCACCAC	CAAGGGTTCC	ATCACCTCCG	TC		482

2) INFORMATION FOR SEQ ID NO: 488

10

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1290 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
15	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20	(A)	ORGANISM: <i>Pichia anomala</i>
	(B)	STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

25	TCGAACAAGG	TAACTTACCA	GCTATCTTGA	ATGCTTTAGA	AATCAAAACC	50
	CCAAGTGGTA	CTCCATTAGT	TTTAGAAGTT	GCTCAACATT	TAGGTGAAAA	100
	CACTGTCAGA	ACTATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTCGTGGTG	150
	AACAAGTTAC	TGATACTGGT	TCTCCAATCA	CTGTCCCAGT	TGGTCGTGAA	200
	ACTTTAGGTC	GTATTATCAA	CGTTGTTGGT	GAACCAATTG	ATGAACGTGG	250
30	TCCAATTAAC	ACCAAAACAAA	GAAACCCAAT	TCACGCTGAA	CCACCTTCAT	300
	TCAGTGAACA	ATCAACTGCT	GCTGAAGTTT	TAGAAACTGG	TATCAAAGTT	350
	GTYGATTTAT	TAGCTCCATA	CGCTAGAGGT	GGTAAAATTG	GTTTATTCGG	400
	TGGTGCCGGT	TGCTGTAAAA	CTGTCTTTAT	CCAAGAATTG	ATTAACAACA	450
	TTGCTAAAGC	TCATGGTGGT	TTCTCAGTTT	TCACCGGTGT	TGGTGAAAGA	500
35	ACCAGAGAAG	GTAACGATTT	ATACCGTGAA	ATGAAAGAAA	CTGGTGTTAT	550
	TAACTTGGA	GGTGATTCTA	AGGTCGCTTT	AGTTTTCGGT	CAAATGAATG	600
	AACCACCAGG	TGCTAGAGCT	CGTGTGCTT	TAACTGGTTT	GACCATTGCT	650
	GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCGTTGATAA	700
	CATTTTCAGA	TTCAACCAAG	CCGGTTCAGA	AGTTTCTGCC	TTATTAGGTC	750
40	GTATTCCATC	TGCTGTCCGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	800
	TTGTTACAAG	AACGTATTAC	CACCACACAA	AAAGGTTTCA	TTACTTCTGT	850
	CCAAGCTGTT	TATGTCCCAG	CTGATGATTT	AACAGATCCT	GCTCCAGCTA	900
	CCACTTTCGC	CCATTTGGAT	GCTACTACTG	TCTTGTCTCG	TGGTATTTCA	950
	GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCAAGATT	1000
45	ATTAGATGCT	TCAGTTGTTG	GTCAAGAACA	TTATGATGTT	GCTACCAACG	1050
	TTCAACAAAC	TTTACAAGCT	TACAAATCTT	TACAAGATAT	TATTGCTATT	1100
	TTAGGTATGG	ATGAATTGTC	TGAACAAGAT	AAATTGACTG	TCGAAAGAGC	1150
	AAGAAAAATC	CAAAGATTCT	TATCTCAACC	ATTTGCTGTT	GCCGAAGTTT	1200
	TCACTGGTAT	YCCAGGTAGA	TTGGTTAGAT	TAAAAGACAC	TATCAAATCA	1250
50	TTCAAAGATG	TTTTGGAAGG	TAAATATGAT	CACTTACCAG		1290

2) INFORMATION FOR SEQ ID NO: 489

55

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1291 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
60	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

```

10 CCAATTCGAA CAAGGTAAC TACCAGCTAT CTTGAATGCT TTAGAAATCA 50
   AAACCCCAAG TGGTACTCCA TTAGTTTTAG AAGTTGCTCA ACATTTAGGT 100
   GAAACACTG TCAGAACTAT TGCTATGGAT GGTACTGAAG GTTTAGTCCG 150
   TGGTGAACAA GTTACTGATA CTGGTTCTCC AATCACTGTC CCAGTTGGTC 200
   GTGAAACTTT AGGTCGTATT ATCAACGTTG TTGGTGAACC AATTGATGAA 250
15 CGTGGTCCAA TTAACACCAA ACAAAGAAAC CCAATTCACG CTGAACCACC 300
   TTCATTCACT GAACAATCAA CTGCTGCTGA AGTTTTAGAA ACTGGAATCA 350
   AAGTTGTTGA TTTATTAGCT CCATACGCTA GAGGTGGTAA AATTGGTTTA 400
   TTCGGTGGTG CCGGTGTCGG TAAACTGTC TTTATCCAAG AATTGATTAA 450
   CAACATTGCT AAAGCTCATG GTGGTTTCTC AGTTTTACC GGTGTTGGTG 500
20 AAAGAACCAG AGAAGGTAAC GATTTATACC GTGAAATGAA AGAACTGGT 550
   GTTATTAAC TGGAAAGGTGA TTCTAAGGTC GCTTTAGTTT TCGGTCAAAT 600
   GAATGAACCA CCAGGTGCTA GAGCTCGTGT TGCTTTAACT GGTTCGACCA 650
   TTGCTGAATA CTTCAGAGAT GAAGAAGGTC AAGATGTCTT GTTATTCGTT 700
   GATAACATTT TCAGATTCAC CCAAGCCGGT TCAGAAGTTT CTGCCTTATT 750
25 AGGTCGTATT CCATCTGCTG TCGGTATCA ACCAACTTTA GCAACTGATA 800
   TGGGTTTGTT ACAAGAACGT ATTACCACCA CACAAAAGG TTCAGTTACT 850
   TCTGTCCAAG CTGTTTATGT CCCAGCTGAT GATTTAACAG ATCCTGCTCC 900
   AGCTACCACT TTCGCCCATT TGGATGCTAC TACTGTCTTG TCTCGTGGTA 950
   TTTCAGAATT AGGTATTTAC CCAGCTGTCG ATCCATTAGA TTCTAAATCA 1000
30 AGATTATTAG ATGCTTCAGT TGTTGGTCAA GAACATTATG ATGTTGCTAC 1050
   CAACGTTCAA CAAACTTTAC AAGCTTACAA ATCTTTACAA GATATTATTG 1100
   CTATTTTAGG TATGGATGAA TTGTCTGAAC AAGATAAATT GACTGTGCGA 1150
   AGAGCAAGAA AAATCCAAAG ATTCTTATCT CAACCATTTG CTGTTGCCGA 1200
   AGTTTTCACT GGTATCCCAG GTAGATTGGT TAGATTAAAA GACACTATCA 1250
35 AATCATTCOA AGATGTTTTG GAAGGTAAAT ATGATCACTT A 1291

```

2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 508 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Rhodotorula minuta*
 (B) STRAIN: ATCC 10658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

```

55 CGTATTGATT CGTGAGTGGC CGTTCCTTA CAGCAAGCTT ATAAAGGAGC 50
   GAAAAAGATC TGACATTCCG CTTATGTGCT ATACAGAGGA ACTCATCAAC 100
   AACGTCGCCA AGGCTCATGG TGGTTACTCT GTCTTCACCG GTGTCGGAGA 150
   GCGAACACGT GAAGGTAACG ATCTCTACCA CGAAATGATT GAAACCGGTG 200
   TCATTCACT CAAGAACGAC AAGTCCAAGG CCGCTCTGGT CTTGCGACAG 250
60 ATGAACGAGC CCCCCGAGC TCGTGCCCGT GTCGCTCTGA CCGGTCTCAC 300

```

CATCGCCGAG TACTTCCGTG ACGTCGAAGG ACAGGATGTG CTACTCTTCA 350
 TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCAGAGGT ATCTGCCCTG 400
 CTCGGACGTA TCCCATCTGC TGTCGGATAC CAGCCCACAC TCTCAACCGA 450
 TATGGGTGGT ATGCAAGAGC GAATCACAAC CACCAAGAAG GGTTCGATTA 500
 5 CCTCCGTC 508

2) INFORMATION FOR SEQ ID NO: 491

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhodotorula mucilaginosa*
 (B) STRAIN: ATCC 66034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

25 TGTCTCATT CAGGAGCTCA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
 ACTCGGTCTT CACCGGTGTC GGCGAGCGTA CCCGTGAGGG TAACGGTGAG 100
 TCTCCCCCTT CAAACTTTTG GCCGGCTAGT TGGCGCAGCG CAAACTGACG 150
 CGCGCGCCCT GTCCAGACTT GTACCACGAG ATGATCGAGA CTGGTGTCAT 200
 CCAGCTCGAG AACGACAACT CGAAGTGCGC TCTCGTGTTT GGCCAGATGA 250
 30 ACGAGCCCCC TGGTGCCCGT GCCCGTGTCG CTCTCACTGG GTTCGTCCTT 300
 TCTCTCTCTC GAGCGTCCTG GCTTGATACG GAACGCTGAC ACGTCACGCA 350
 GTCTCACTAT TGCTGAGTAC TTCCGTGACG AGGAGGGCCA GGACGTGCTC 400
 CTCTTCATCG ACAACATCTT CCGTTTCACC CAGGGTGAGC CGCCTCCGCG 450
 GGCATTCTCC CGTTTCTTTC GCGCTGACGT CTGTCCCGTA TAGCCGGTTC 500
 35 GGAGGTGTCT GCCCTTCTCG GACGTATCCC GTCCGCTGTC GGATACCAGC 550
 CGACTCTCTC GACCGACATG GGTCAGATGC AGGAGCGTAT CACGTAAGTT 600
 TGGCCGCAGC TCCGTCCGCG GCGCCCTTTG TGTCTGACCG TGTTCACCG 650
 CTCAGCACCA CCAAGAAGGG CTCGATCACC TGTGTC 686

2) INFORMATION FOR SEQ ID NO: 492

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

TGTCTTGATT CAGGAGCTCA TCAACAACGT CGCCAAGGCC CACGGTGGTT 50
 ACTCCGTTTT CACCGGTGTC GGTGAGCGTA CCCGTGAGGG TAACGGTGAG 100
 60 CAACTTTTCG CCGACCTGGC CATTCGGAA CGTGCGGACT GACGAGGACC 150

	ACCTCGAACA	GATCTCTACC	ACGAGATGAT	CGAGACCGGT	GTCATTTCAGC	200
	TCGACAACGA	CAAGTCGAAG	ACTGCTCTCG	TCTTCGGCCA	GATGAACGAG	250
	CCCCCTGGCG	CCCGTGCCCC	TGTCGCTCTT	ACTGGTCTCA	CCATCGCGGA	300
	GTACTTCCGT	GACGACGAGG	GCCAGGACGT	GCTTCTCTTC	ATCGACAACA	350
5	TCTTCCGTTT	CACCCAGGGT	ACGTTCGATC	CCGCCCCGTCC	AACACGAATG	400
	TCGTGGTGAC	TGACAACCTG	TTGCGCGTGC	AGCCGGTTTCG	GAGGTGTCTG	450
	CCCTTCTCGG	TCGTATCCCC	TCCGCTGTCTG	GATACCAGCC	CACTCTCTCG	500
	ACCGACATGG	GTGGCATGCA	GGAGCGTATC	ACGTACGCCC	TCTTCTGCTT	550
	TCTCTCGTTT	CGCTCTGCAT	CGTTCACGCA	TGTTTCGCCCC	ACAGCACCAC	600
10	CAAGAAGGGT	TCGATCACCT	GTGTC			625

2) INFORMATION FOR SEQ ID NO: 493

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: WSA-148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

30	TCTCGTCCGT	GGTGCTAAGG	CCACTGACAC	TGGTTCCCCC	ATTACCATCC	50
	CCGTGCGCCC	CGGTACCCCTC	GGTCGCATCA	TGAACGTCAC	CGGTGACCCG	100
	ATCGACGAGC	GCGGTCCCCT	CAAGACCGAC	AAGTTCCGTC	CCATCCACGC	150
	TGAGGCTCCC	GAGTTCGTTG	ACCAGTCGAC	CACCGCTGAG	GTTCTCGTGA	200
35	CTGGTATCAA	GGTCGTCGAT	CTGCTTGCTC	CCTACGCCCC	TGGTGGTAAG	250
	ATTGGTCTGT	TTGGCGGTGC	CGGTGTTGGC	AAGACCGTGT	TCATCCAGGA	300
	GCTCATCAAC	AACATCGCCA	AGGCCCACGG	TGGTTACTCC	GTCTTCACCG	350
	GTGTCGCGCA	GCGTACCCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	400
	GAGACCTCTG	TCATTACAGT	TGACGGTGAC	TCCAAGGTCG	CCCTGGTGTT	450
40	CGGTGAGATG	AACGAGCCCC	CTGGTGCTCG	TGCCCCGTGC	GCCTTGACCG	500
	GTTTGACTGT	CGCTGAGTAC	TTCGCTGACG	AGGAGGGCCA	GGATGGTATG	550
	TTTTGAATTA	TTTCCTTGTC	GTACAGTTCC	AAATCGAAGA	ATTACTAACT	600
	TGTCAGTGCT	TCTCTTCATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	650
	TCTGAGGTGT	CTGCCCTTCT	GGGTCGTATT	CCCTCCGCTG	TCGGTTACCA	700
45	GCCCCACGCTC	GCCGTGGACA	TGGGTCTGAT	GCAGGAGCGT	ATTACCACCA	750
	CCCGCAAGGG	CTCAATTACC	TCCGTCCAGG	CCGTCTACGT	GCCCCGCTGAC	800
	GATCTGACGG	ATCCCGCCCC	CGCCACCACC	TTCGCCCCATC	TGGACGCCAC	850
	CACTGTGCTG	TCCCCGAGGT	TCTCTGAGCT	GGGTATCTAC	CCCGCTGTCTG	900
	ACCCCCCTCGA	CTCCAAGTCG	CGTATGCTGG	ACCCCCGTAT	TGTCGGTGAC	950
50	GACCACTACG	AGACCGCCAC	TCGCGTCCAG	CAGATCCTCC	AAGAGTACAA	1000
	GTCGCTGCAG	GACATCATCG	CCATTCTGGG	TATGGACGAG	CTGTCTGAGG	1050
	CCGACAAGCT	TACAGTCGAG	CGTGCTCGTA	AGATCCAGCG	TTTCCTGAGC	1100
	CAGCCGTTCA	CGGTGCGGCA	GGTCTTCACT	GGTATCGAAG	GCCAGCTGGT	1150
	CGATCTGAAG	GACACTATCG	CTTCGTTCAA	GGCTATCCTG	AGCGGTGAGG	1200
55	GTGACAGCCT	T				1211

2) INFORMATION FOR SEQ ID NO: 494

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

```

15  TCTTGTTAGA GGCACCCAG TCAAGGACAC TGGTGCTCCA ATTACCATTC      50
    CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA      100
    ATTGATGAGC GTGGACCAAGT CAAGGCTGAC AAGTTCAGAC CTATTCACGC      150
    TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA      200
    CCGGTATTAA GGTTGTCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG      250
20  ATTGGTCTTT TCGGTGGTGC CGGTGTCGGT AAGACTGTGT TCATTCAGGA      300
    GCTTATTAAC AACATTGCTA AGGCCACCG TGGTACTCT GTCTTCACTG      350
    GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG      400
    GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTTGTT      450
    CGGTGAGATG AACGAGCCTC CAGGAGCCCC TGCCCCGTGT GCCTTGACCG      500
25  GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCTTG      550
    TTGTTTCATTG ACAACATTTT CCGATTCACC CAGGCCGGTT CTGAGGTCTC      600
    TGCCTTGTTG GGTCGTATCC CATCTGCCGT CGGTACCAA CCAACCTTGG      650
    CTACTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAGGGT      700
    TCCGTCACCT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA      750
30  TCCTGCCCCA GCTACCACCT TCGCCCATTT GGACGCCACC ACCGAATTGT      800
    CCCGATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTCTGA CCCTCTTGGT      850
    TCCAAGTCCC GTCTTTTGGA TGCCTCCGTC GTCGGCCAAG AGCACTACGA      900
    CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCTTACAAG TCTCTCCAGG      950
    ATATCATTCG CATTTTGGGT ATGGACGAAT TGTCTGAGGC TGATAAGCTC      1000
35  ACTGTCGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTAC      1050
    CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG      1100
    ACACCATCCG ATCCTTCAAG GAGATCCTTG ACG                        1133
  
```

2) INFORMATION FOR SEQ ID NO: 495

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

```

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG      50
GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTTCG      100
AGTATTAATT GTTTTATAG AACAACTTG CCAAGGCTCA CGGTGGTTAC      150
60  TCTGTCTTCA CTGGTGTGCG AGAGCGTACC CGTGAAGGAA ACGATCTCTA      200
  
```

CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG 250
 TCGCCCTGGT CTTCCGCCAG ATGAACGAGC CCCCAGGTGC CCGTGCCCGT 300
 GTTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG 350
 TCAAGACGGT GAGTTTCTTA TGGATAAAAA AAAATTTTTT TTTTTTTTTT 400
 5 TTTTTTTCAA GAAATTCATG TTCTAACAAA GTGTATTCTA GTGCTTCTCT 450
 TCATCGACAA CATTTTCCGT TTTACTCAGG CTGGTTCCGA AGTGTCTGCC 500
 CTGCTTGGTC GTATCCCATC TGCCGTCGGT TACCAACCCA CTCTTGCCGT 550
 CGACATGGGT GGTATGCAGG AACGTATTAC CACCACCAAG AAGGGATCCA 600
 TTACCTCC 608
 10

2) INFORMATION FOR SEQ ID NO: 496

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Wangiella dermatitidis*
 25 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

GTTTATTCAA GAATCATTG TGGGTGGCAT TCTCATAATG TTTCGGCCAC 50
 30 AATTACTGAT TGAAAATAGA ACAACATTGC AAAGGCTCAT GTGGTTACT 100
 CCGTGTTTAC TGGTGTGGC GAGCGAACTC GTGAGGGTAA CGACTTGATC 150
 CACGAAATGC AGGAGACCTC TGTCATTAG CTGATGGCG AGTCCAAGGT 200
 CGCGCTGGTG TTTGGTCAA TGAACGAACC TCCTGGTGCT CGTGCTCGTG 250
 TTGCTCTGAC TGGGTAAGTT GTTCCTTCGC TTCTTGCGCG TATCCACATC 300
 35 CCCATCTTGA GAATACGCTC GCCACCATGT CATGTGATGT TGGGCTGGTT 350
 CTGGTTTTTG GGAGGCCCTC AAGTTCAATT TTTGGATGAC AGCACCAGCT 400
 TTACAAGATT ATGCTAACTT AATGGAGTCT TACGGTGGCT GAGTTCTTCA 450
 GGGATGAGGA GGGACAGGAT GGTAAGTTTG ATAACAATCT CGTCGGTGTC 500
 AATATCGACG GCGTACTCTT CGCATCAAAA AACCAAAGAG GTGGTTTGGT 550
 40 GTGAGAAGTG CGCCGGAAT AATGGCAACC ACGTGACAAT GACCACGTGT 600
 GGGGCTCCCG TGCTAACACG TGACAGTCTT GCTCTTCATC GACAACATTT 650
 TCCGATTCAC TCAASCCGGT TCTGARGTGT CTGCCTTGCT TGGTCGTATT 700
 CCATCTGCCG TCGGTTACCA ACCCACACTC GCCGTCGACA TGGGTCTCAT 750
 GCAGGAACGT ATCACCACCA CCCGGAAGGG ATCCATCACA TCTG 794
 45

2) INFORMATION FOR SEQ ID NO: 497

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1148 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 55
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yarrowia lipolytica*
 60 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

```

5   TCTTGTCCTGA GGCACCGCCG TCGCTGACAC CGGTGCTCCC ATCACTATCC      50
    CCGTCGGCCG AGGTACCCTT GGTCGAATCA TCAACGTCTG TGGTGAGCCC      100
    ATTGACGAGC GAGGACCCAT CGAGGCTTCC AAGTACCTCC CCATCCACGC      150
    TGACCCCCCT ACCTTCGCTG AGCAGTCTAC CTCCGCTGAG GTTCTCGAGA      200
    CCGGTATTAA GGTCGTCGAC CTCCTCGCCC CTTACGCCCC AGGTGGTAAG      250
    ATTGGTCTCT TCGGTGGTGC CGGTGTCGGT AAGACTGTCT TCATCCAGGA      300
10  GCTGATTAAAC AACATTGCCA AGGCCCATGG TGGTTTCTCC GTTTTCTGCG      350
    GTGTCGGTGA GCGAACCCGA GAGGGTAACG ATCTTTACCG AGAGATGAAG      400
    GAGACTGGTG TCATCAACCT CGAGGGTGAG TCTAAGGTCA CCCTCGTCTT      450
    CGGTGAGATG AACGAGCCTC CCGGAGCCCC TGCCCCGAGTC GCCCTTACTG      500
    GTCTGACCAT TGCCGAGTAC TTCCGAGACG AGGAGGGTCA GGATGTGTTG      550
15  CTCTTCGTTG ACAACATTTT CCGATTCAAC CAGGCCGGTT CCGAGGTGTC      600
    CGCTCTGCTT GGTCGAATTC CCTCCGCTGT CGGTTACCAG CCCACTCTGG      650
    CCACCGATAT GGGTGCCCTC CAGGAGCGAA TTACCACCAC CCAGAAGGGT      700
    TCCGTCACTT CCGTCCAGGC CGTCTACGTG CCTGCCGATG ATTTGACCGA      750
    TCCTGCTCCC GCCACCACCT TCGCCCATCT TGACGCCACC ACCGTCCTGT      800
20  CCCGAGGTAT TTCCGAGCTG GGTATCTACC CCGCTGTCGA TCCCCTTGAT      850
    TCCAAGTCTC GACTTCTGGA TATCGATGTT GTCGGAAGG AGCACTACGA      900
    TGTTGCTTCC AACGTCCAGC AGACCTCCA GGCTTACAAG TCTCTCCAGG      950
    ATATCATTGC CATTCTTGGT ATGGATGAGC TGTCCGAGCA GGACAAGCTG     1000
    ACCGTCGAGC GAGCTCGAAA GATCCAGCGA TTCCTGTCTC AGCCCTTCAC     1050
25  CGTCGCCGAG GTTTTCAACG GTATTGAGGG ACGACTTGTC TCTCTCAAGG     1100
    AACTGTCCG ATCCTTCAAG GAGATCCTTG ACGGTAAGCA CGATGCTC     1148

```

30 2) INFORMATION FOR SEQ ID NO: 498

(i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 966 bases
    (B) TYPE: Nucleic acid
35  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Aspergillus fumigatus
    (B) STRAIN: WSA-172

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

```

45  GCGCTATTGT CGTTGTTGCT GCCTCCGACG GTCAGATGTA GGTGGAACAT      50
    CTTGGGAAAT ACGTCGTAAA ACACGTCGCT TACGTTTTTCG CGAATAGGCC      100
    CCAGACTCGT GAGCATTTGC TGCTCGCCCC CCAGGTTGGT GTCCAGAAGA      150
    TCGTTGTCTT CGTCAACAAA ATCGATGCTA TTGATGATCC GGAGATGCTG      200
50  GAACTGGTCG AACTCGAGAT GCGTGAGCTG CTGAACAGCT ACGGTTTCGA      250
    GGGTGAAGAG ACTCCGATCA TTTTCGGTTC CGCTCTCTGT GCTCTCGAAG      300
    GACGCCGTGA CGACATCGGT AAAGACAGAA TTGAGCAGCT TATGAACGCT      350
    GTCGACACCT GGATCCCCAC TCCTCAGCGT GACCTCGACA AACCTTTCTT      400
    GATGTCTGTC GAGGAAGTGT TCTCTATCGC CGGCCGTGGT ACCGTGGCTT      450
55  CTGGTCGTGT CGAGCGTGGT ATCTTGAAGA AGGACTCTGA GGTGAGATT      500
    GTTGGAGGCT CCTTCGAACC CAAGAAGACC AAAGTCACCG ACATTGAAAC      550
    CTTCAAGAAG AGCTGTGATG AATCGCGTGC TGGTGACAAC TCTGGTCTCC      600
    TCCTGCGTGG TATCCGACGT GAAGACGTCA AGCGTGGTAT GGTCAATTGCT      650
    GTTCCCGGCA GCACCAAGGC TCACGACAAG TTCCTCGTCT CCATGTACGT      700
60  CCTGACCGAG GCGGAGGGTG GTCGTCGTAC TGGCTTCGGT GCCAACTACC      750

```


GTCCCAAGT CTTTCATCCGT ACTGCAGGTA AGTTCCCGCA CACCGTGTCC 800
 AGATCTTCCG AGAGATTAGC GATATATGCT AATGATTCAT CAGACGAGGC 850
 TGCTGACCTC AGCTTCCCTG ACGGCGACCA ATCTCGCAGA GTTATGCCTG 900
 GTGACAACGT CGAGATGATC CTGAAGACCC ACCACCCTGT TGCTGCTGAG 950
 5 GCTGGTCAAC GCTTCA 966

2) INFORMATION FOR SEQ ID NO: 499

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

25 TGGTGCTATT ATTGTTGTTG CTGCTTCTGA TGGTCAAATG CCCCAAACCC 50
 GTGAGCACTT GCTTCTTGCT CGTCAAGTTG GTGTTAAGCA CATTGTTGTT 100
 TTCGTTAACA AGATTGATAC TATTGATGAT CCTGAAATGT TGGAACCTGT 150
 CGAAATGGAA ATGAGAGAAC TTCTTTCTTC TTACGGTTTT GATGGCGATA 200
 ACACCCCTGT CATTATGGGT TCTGCTCTCT GTGCTCTTGA AGGTCGTGAA 250
 30 CCAGAAATG GTGAACAAAG AATCAACCAA CTCCTTGATG CTATCGATGA 300
 ATACATTCCT ACCCCAGTTC GTGATATGGA CCAACCTTTC TTGATGCCAC 350
 TTGAAGGTGT TTTCTCTATT CCAGGTCGTG GTACTGTTGC CACTGGACGT 400
 GTCTATCGTG GTACTTTGAA GAGAGGTGAA GAAGTTGAAG TTGTTGGCTA 450
 CAATGATGCT CCAATCAAGA CCACCGTTAC TGGTATTGAA ATGTTCAAGA 500
 35 AGGAACCTGA TCAAGCTCAA GCTGGTGACA ACGCTGGTAT TCTTTTGAGA 550
 GGTGTTAAGC GTGAAGACCT TAAGCGTGGT ATGGTTGTTG CTAAACCAGG 600
 TACCGTTAAG CCACACACCA AGTTCCTTGC CTCCATCTAT GTTTTGACTA 650
 AGGAAGAAGG TGGCAGACAC TCTGGCTTTG GTCTTAACCTA CAGACCTCAA 700
 CTTTTCCTTG GTTCTGCTGA TGTTACCCT GTCTTGACCT TCCCAGAGGG 750
 40 TGTTGACCAA AGCACTCAAG TCATGCCAGG TGACAACACT GAAATGGTTT 800
 GCGAACTTGT TCACCCAGTT GCTGTGGAAC AAGGCCAACG TTTCAA 846

2) INFORMATION FOR SEQ ID NO: 500

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

	GGTGCCATTA	TTGTTGTTGC	TGCCTCTGAT	GGACAGATGC	CCCAGACCCG	50
	TGAGCATCTT	TTGCTTGCCC	GCCAAGTCGG	TATGCAAAAG	GTCGTTGTGT	100
	TTGTTAACAA	GATTGATACC	ATTGATGACC	CTGAAATGCT	TGATCTTGTC	150
	GAGATGGAGA	TGCGTGAAC	GTTGAATGAA	TATGACTTCG	ATGGAGATAA	200
5	CTCTCCTGTC	ATTATGGGCT	CTGCTCTTGC	TGCTCTTGAG	GACAAGAACC	250
	CCGAGATTGG	TAAGGACCGT	ATCATGCAGC	TCTTGGACGC	TGTTGATGAA	300
	TGGATCCCTA	CCCCCGAGCG	TGACCTTGAC	AAGCCTTTCA	TGATGCCTAT	350
	TGAGGCCTCT	TTCTCCATTT	CTGGTCGTGG	TACTGTTGCC	ACTGGCCGTG	400
	TCGAGCGTGG	TATTCTCAAG	AAGGGTGAGG	AAGTCGAGAT	CGTTGGTTTC	450
10	AACAAGCAGC	CCCTGAAATC	TGTTGTTACT	GGTATTGAAA	TGTTCAAGAA	500
	GGAAC TTGAT	CAGGCCCAGG	GCGGTGATAA	TGCTGGTATC	TTGCTTCGTG	550
	GTATTCGTCG	TGAGGACTTG	CAGCGTGGTA	TGGTTTTGGC	CAAGCCTGGA	600
	ACTGTTAAGG	CTCACACCAA	GTTCC TTTCC	TCCATCTACG	TTCTCTCCAA	650
	GGAAGAGGGC	GGCCGTCAC	CTCCTTTCCG	TATGAACTAT	CGTCCCCAGA	700
15	TGTTGCTTTT	TGCACGTGAT	CTCACCGTTA	CTCTTACTTT	CCCTGAGGGT	750
	GTTGAACAGC	ACACTCAGGT	CTTCCCTGGT	GAGAACACCG	AGATGGTTGG	800
	CGAGCTCGTT	CACCCTACTG	CTATTGAGGT	TGGTCAACGC	TTCAAC	846

20

2) INFORMATION FOR SEQ ID NO: 501

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 944 bases
25	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Coccidioides immitis</i>
	(B)	STRAIN: Silveira

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

	AGTTGTCGTC	GTTGCTGCTT	CAGACGGTCA	AATGTATGCA	ACCGAGAGCA	50
	CTCCCGGATC	TTGGTTTAAA	TGGCACTAAT	ATAAGACAGG	CCTCAAACCTC	100
	GAGAGCATTT	ACTTCTCGCC	CGTCAGATCG	GTATCCAAAA	AATCGTCGTC	150
40	TTCGTGAACA	AGGTTGATGC	CATCGAGGAC	AAAGAGATGT	TGGAGCTTGT	200
	TGAATTGGAG	ATGCGTGAAC	TCCTAACCAG	CTACGGTTTC	GAGGGTGAAG	250
	AAACTCCCAT	CATTTT TGGC	TCTGCTCTCT	GTGCCCTCGA	AGGAAGACAA	300
	CCCGAGATCG	GTGTTACCAA	GATTGATGAG	CTCTTGACAG	CCGTCGACAC	350
	CTGGATTCCC	ACTCCTCAGC	GTGAGACTGA	CAAGCCCTTC	TTGATGTCCA	400
45	TTGAGGAAGT	GTTCTCTATT	TCCGGACGAG	GAACCGTTGT	CTCCGGCCGT	450
	GTGGAGCGTG	GTATCCTCAA	GAAGGACTCC	GAAGTTGAAA	TTGTCGGCGG	500
	TTCGCCCGAG	CCAATCAAAA	CCAAGGTTAC	CGATATCGAA	ACCTTTAAGA	550
	AGTCTTGCGA	CGAGTCTCGC	GCTGGTGATA	ACTCCGGCTT	GCTCCTACGA	600
	GGCGTTAAGC	GTGAAGATAT	TAGCCGTGGC	ATGGTCGTCG	CTGTACCAGG	650
50	AAGTGTC AAG	GCCCATACTG	AATTCTTAGT	TTGCTTTTAC	GTCCTCACCG	700
	AAGCTGAGGG	TGGGCGCAAA	TCTGGATTCA	GCAGCAAGTA	CCGCCCACAG	750
	ATGTTTCATTC	GCACTGCCCG	TATGTAATAC	TGTGATAATT	TCGTTGACAT	800
	GGTACTGATT	GAATTCTATA	GACGAAGCGG	CTCAGCTCAG	CTGGCCCGGA	850
	GAAGATCAAG	ACAAGATGGC	TATGCCAGGA	GACAATATCG	AAATGATTTG	900
55	CACCACCTTG	CACCCAGTTG	CCGCCGAGGC	TGGCCAGCGA	TTCA	944

60

2) INFORMATION FOR SEQ ID NO: 502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
 (B) STRAIN: WSA-212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

```

15  GCTATCATCG TCGTTGCTGC CTCCGATGGA CAGATGCCCC AGACCCGTGA      50
    ACACTTGCTC CTCGCTCGTC AGGTTCGGTGT CCAGCGAATT GTCGTCTTCG      100
    TCAACAAGGT CGATGCCATT GATGACCCCG AGATGCTTGA GCTCGTCGAG      150
    ATGGAGATGC GCGAGCTTCT TAACACCTAC GGCTTCGAAG GCGACGACAC      200
    TCCCGTCATC ATGGGCTCTG CTCTTATGTC TCTCCAGAAC CAGCGCCCCG      250
20  AGATTGGCAC CGAGAAGATC GATGAGCTCC TTGCTGCCGT CGACGAGTGG      300
    ATCCCAACCC CCGAGCGTGA CCTTGACAAG CCCTTCCTTA TGTCCGTCGA      350
    GGATGTCTTC TCCATTGCCG GCCGTGGTAC CGTCGTGTCT GGCCGTGTGG      400
    AGCGTGGTAT TCTGAAGCGT GATCAGGAGA TCGAGCTTGT CGGAAAGGGG      450
    CAGGAGGTTA TCAAGACCAA GGTTACCGAC ATTGAGACCT TCAAGAAGTC      500
25  TTGTGAGCAG TCCCAGGCTG GTGACAACCT TGGTCTCCTC ATCCGAGGTG      550
    TTCGCCGTGA GGATGTCCGC CGTGGTATGG TTGTCTGCGC TCCTGGCACC      600
    GTCAAGTCTC ATACCCAGTT TCTCGCTTCC CTCTACGTCC TCACCAAGGA      650
    GGAGGGTGCG CGACACACCG GTTTCAGGA GCACTACCGA CCCCAGCTCT      700
    ATCTCCGAAC TGCAGATGAG TCCATTGACC TGACTTTCCC CGAGGGTACT      750
30  GAGGATGCCT CCAGTAAGAT GGTTCATGCCT GGTGACAACA CCGAGATGGT      800
    TGTCACCATG GGTCAACCCA ATGCCATCGA GGTGGTTCAG CGATTCAAC      849
  
```

35 2) INFORMATION FOR SEQ ID NO: 503

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

```

50  TGGTGCTATT GTCGTTGTTG CTGCTGCTGA CGGCCAAATG TAAGACGCCG      50
    CGAGGGACTG CTGAGGGTTT TATGCTTTT AGGCCCCCTT GTTTCTGAGA      100
    GCATGATGAT ACTAATATTC GGAAACGTAT CTATTAGGCC TCAAACACGT      150
    GAGCATTTGC TCCTTGCCCC ACAGGTCGGT GTCCAAAAGA TCGTCGTTTT      200
55  CGTGAACAAA GTCGACGCCC TTGAGGACAA GGAGATGTTG GAGCTTGTCG      250
    AGTTAGAAAT GAGAGAGCTC TTAAACACCT ACGGCTTCGA GGGTGAAGAG      300
    ACACCCATCA TCTTTGGTTC TGCCCTTTGC GCCATGGAAG GCCGTGAGCC      350
    TGAGTTGGGA GAAAAGAAAA TTGATGAATT GCTGGAGGCT GTTGATACTT      400
    GGATCCCCAC ACCACAACGT GATACCGAAA AACCTTTCTT GATGTCCGTT      450
60  GAGGAAGTAT TCTCTATCTC CGGCCGTGGA ACCGTTGCCT CCGTTCGTGT      500
  
```

```

5    TGAGCGCGGT GTCCTCAAGA AGGATTCAGA AGTCGAGCTA ATTGGGGGCG 550
      GCTCCACCCC CATCAGGACG AAGGTAAGTG ATATCGAAAC TTTCAAGAAA 600
      TCCTGTGACG AGTCTAGAGC TGGGGACAAC TCCGGTCTTT TATTGCGTGG 650
      TATCAAGCGT GAAGATATCC GCCGTGGTAT GGTAGTTGCC GTTCCTGGCA 700
      GCGTCAAGGC CCACGACAAG TTCTTGGTGT CGATGTATGT CCTGACCGAA 750
      GCTGAGGGTG GTCGCCGAAC CGGATTCGGC CAGAACTATC GTCCTCAAAT 800
      GTTCATCCGC ACAGCTGGTA TGTCAAAATG GGACCCCTTT TCATAATCCT 850
      TTCTTTTTTT CTTTTTCCTC TCTATCTCTC TTTCTGTTTC CTTTCAACTC 900
      GCCTGATTCA CGAAATTAAC TAACCCGTTT GATTATAGAC GAAGCCGCCC 950
10   ATCTCAGCTT CCCTAGTGGA GCAGATGAAA GCAAACTCGT TATGCCTGGT 1000
      GACAACGTCG AGATGATCCT CCAGACACAC CGCCCCGTGG CTGCTGAGGC 1050
      CGGCCAGCGA TTCA 1064

```

15

2) INFORMATION FOR SEQ ID NO: 504

(i) SEQUENCE CHARACTERISTICS:

```

20   (A) LENGTH: 982 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Paracoccidioides brasiliensis
      (B) STRAIN: ATCC 32071

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

```

      TGGTGCTATC GTCGTTGTTG CTGCCTCTGA CGGCCAAATG TAGGGATTTT 50
      GCAAGACTGG TGAAAAAATC TAAAGAAAAT AGAAAAGATT GTGCTGATGT 100
      TTGGTATCAG GCCCCAAACA CGCGAGCATC TGCTTCTTGC CAGACAAGTC 150
35   GGTGTTTCAGA AAATCGTTGT TTTCGTCAAC AAGGTCGATG CTGTAGAGGA 200
      TAAGGAGATG TTGGAGCTTG TCGAATTGGA GATGAGAGAG CTCTTGACCA 250
      CCTATGGGTT CGAGGGTGAG AAGACACCTA TCATCTTTGG TTCTGCGCTC 300
      TGTGCTATGG AGGGCCGTCA GCCCGAGTTG GGAGAGCAGA AAATTGATGA 350
      ATTACTCGAG GCTGTGGATA CTTGGATCCC TACGCCACAG CGTGATACTG 400
40   ACAAGCCCTT CCTGATGTCC ATTGAGGAGG TGTCTCTAT CTCTGGACGA 450
      GGAACCGTTG CCTCCGGCCG CGTTGAGCGT GGTATCCTCA AGAAGGACTC 500
      CGAAGTTGAA ATTATTGGCG GCGGTGTTCC CACAATCCTG ACCAAGGTGA 550
      CTGATATCGA AACCTTCAAG AAGTCTTGCG ACGAGTCCAG AGCCGGGGAC 600
      AACTCCGGCC TCTTGTTGCG CGGTGTCAA GGTGAGGATA TCCGCCGTGG 650
45   TATGGTCGTT GCAGTTCCCG GAAGCGTCAA AGCACATGAC AGATTCTTGG 700
      TGTGATGTA CGTTCTGACC GAGGCTGAGG GTGGTCGCCG CACTGGCTTC 750
      GGTGAGAACT ATCGTCTCA AATGTTTCAT CGCACAGCTG GTACGTTTCAT 800
      TCTTTCACTA TATTCCTATA TGCATAGCCC GATCCTCCCA TTAATAATT 850
      GACACAGACG AGGCTGCTGA ACTCAGCTGG CCTGATGGAG ACGACGAAGC 900
50   CAAAATGGTC ATGCCCGGTG ACAATGTTGA AATGGTCCTG AAGTCACACC 950
      GCCCGGGGCC GCTGAGGCTG GACAGCGATT CA 982

```

55 2) INFORMATION FOR SEQ ID NO: 505

(i) SEQUENCE CHARACTERISTICS:

```

60   (A) LENGTH: 931 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double

```

(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

5 (vi)ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 58950

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 505

10 CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
 AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
 CACTTGCTCC TCGCCCGTCA GGTCCGGTGT CAAAAGATCG TCGTCTTCGT 150
 CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
 15 TGGAAATGCG TGAACCTCTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
 CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
 GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA 350
 TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG 400
 GAAGTTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
 20 GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATAACCAGA 500
 AGAACCCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
 TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
 CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
 CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
 25 GAAGGTGGTC GTCGTACTGG ATTCGGCGCC AACTACCGTC CTCAAGCTTT 750
 CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
 GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CCGTGACGAT 850
 CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
 ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

2) INFORMATION FOR SEQ ID NO: 506

35 (i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*

(B) STRAIN: ATCC 18205

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 506

50 TGGTGCTATT ATTGTTGTTG CTGCTTCTGA TGGTCAAATG CCTCAAACCA 50
 GAGAACATTT RTTATTGGCT AGACAAGTTG GTGTTCAACA CATTGTTGTC 100
 TTTGTTAACA AAGTTGATAC TATTGATGAC CCAGAAATGT TGGAATTAGT 150
 TGAAATGGAA ATGAGAGAAT TGTTAAGTAC TTATGGTTTT GATGGTGATA 200
 ACGTCCCACT TGTTATGGGT TCTGCTTTAT GTGCCTTGGA AGGTCGTGAA 250
 GAAGAAATTG GTGTCAAAGC TATTGATAAA TTATTAGCTG CTGTTGATGA 300
 55 ATATATCCCA ACCCCACAAA GAGATTTAGA AAAACCATTC TTGATGGGTG 350
 TTGAAGATGT CTTYTCAATC TCAGGTAGAG GTACCGTTGT TACTGGTCGT 400
 GTTGAACGTG GTAACCTGAA GAAAGGTGAT GAAGTTGAAA TTGTTGGTTT 450
 AAACAAAACCT CCATTGAAAA CTACTGTYAC NGGTATTGAA ATGTTCAAAA 500
 AAGAATTGGA CCAAGCTATG GCTGGTGATA ACTGTGGTAT CTTATTACGT 550
 60 GGTATCAAAA GAGATGACAT YAAAAGAGGT ATGGTTATTG CTAAAACCGG 600

	TACCATCTCW	GCTCACACTA	AATTCTTAGC	CTCAATGTAT	ATTTTGACTA	650
	AAGAAGAAGG	TGGTCGTCAC	TCAGGTTTTG	GTGAACATTA	CAGACCTCAA	700
	TTATTCATCA	GAAGTGGTGA	TGTTACCGTT	GTTTTAACCT	TYCCAGAAGG	750
	TGGTGATTCA	TCTCAACAAA	TCTTACCAGG	TGACAATGTC	GAAATGGTTT	800
5	GTGAATTGGT	TCACCCAAC	GCTTTAGAAG	CTGGTCAAAG	ATTCAA	846

2) INFORMATION FOR SEQ ID NO: 507

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 964 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

25	GGAGCTGTTG	TCGTTGTCGC	AGCTTCTGAC	GGTCAAATGT	AATTGAATGC	50
	CCGCCCAGAC	GGATGAAAGG	ATTTGACGTT	TCTAACATCA	GTCTAGGCCT	100
	CAGACCAGAG	AACATTTGCT	CCTTGCCCGC	CAGGTCGGTG	TCCAGAAGCT	150
	GGTCGTTTTT	GTTAACAAGG	TCGATGCCGT	TGAGGACCCA	GAGATGTTGG	200
	AGCTTGTCGA	ACTTGAAATG	CGTGAACCTC	TCAGCCACTA	CAGTTTTGAG	250
30	GGTGAGGAGA	CCCCATCAT	TTTTGGCTCT	GCTCTCTGTG	CCCTCGAGTC	300
	CCGTCGACCT	GAGCTTGGTG	TCGAGAAGAT	TGACGAGCTA	TTGAACGCCG	350
	TCGACACCTG	GATCCCCACC	CCCGAGCGCG	CCACTGATAA	GCCTTTCCTC	400
	ATGTCCATTG	AGGAAGTGTT	CTCTATCTCT	GGTCGTGGTA	CCGTCGTCTC	450
	CGGTCGTGTT	GAGCGTGGTA	TCCTCAAGAA	GGATTCCGAC	GTCGAAATTG	500
35	TTGGTGCGTC	TACCACCCCT	ATCAAGACCA	AGGTCACAGA	TATCGAAACC	550
	TTCAAGAAGT	CCTGCGATGA	ATCTCGAGCT	GGTGACAAC	CTGGTCTCCT	600
	TCTCCGAGGT	ATCAAGCGTG	AGGACTTGAA	GCGTGGAATG	GTTGTTGCTG	650
	CCCCCGGATC	CACCAAGGCT	CACACCGACT	TCATGGTCTC	CCTCTACGTC	700
	CTGACTGAGG	CTGAGGGTGG	TCGTTCCAAC	GGCTTCACCC	ACAAGTACCG	750
40	CCCTCAAATG	TTCATCCGTA	CTGCTGGTAT	GTAACCAAAG	TTCCCGCTAT	800
	TTACTAAGTA	GATCATTGCT	AACTTGATAT	CCCTTCCGTA	GACGAAGCCG	850
	CATCTTTCAG	CTGGCCTGGA	GAAGACCAAG	ACAAGAAGGC	TATGCCTGGT	900
	GACAACGTCG	AGATGATTG	CAAAACCCTC	CACCCCATTG	CTGCCGAGGC	950
	TGGCCAACGA	TTCA				964

2) INFORMATION FOR SEQ ID NO: 508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

	GGTGCTATCA	TTGTCGTTGC	TGCTGGAGAC	GGTTCCAAGC	CCCAGACCCG	50
5	AGAGCATCTG	CTGCTTGCTC	GACAGGTCGG	TGTCCAGAAC	CTGGTTGTGT	100
	TTGTTAACAA	GGTTGATCAG	ATTGATGATA	AGGAGATTCT	TGAGCTCGTT	150
	GACATGGAGA	TGCGAGATCT	GCTGACCCAG	TACGGTTTTG	ATGGTGACAA	200
	CACCCCCGTT	GTCATGGGCT	CTGCTCTGTG	CGCTCTTGAG	GGCAAGCAGA	250
	AGGATATTGG	AGAGGACGCC	ATCATGGCCC	TTATGGATGC	CGTTGATGAG	300
10	CACATCCCTA	CCCCTAACCG	TGACCTTGAG	AAGCCCTTCC	TGATGCCCCG	350
	TGAGGACGTT	TTCTCCATCT	CTGGCCGAGG	AACTGTTGTT	ACTGGCCGAG	400
	TCGAGCGAGG	AAACCTGAAG	AAGGGTGAGG	AAATCGAGAT	TGTTGGCTAC	450
	AACAACAAGC	CCATCAAGGC	TGTTGTACC	GGTATTGAGA	TGTTCAAGAA	500
	GGAGCTCGAG	TCCGCCATGG	CCGGTGACAA	CGCCGGTATC	CTGCTCCGAG	550
15	GTATCAAGCG	AGACGAGATC	AAGCGAGGTA	TGGTCATGTG	CAAGCCTGGC	600
	ACCGTCAACG	CCCACAGCAA	GTTCCTTGCT	TCTCTTTACA	TCATCCCCAC	650
	CGAGGAGGGT	GGTCGAACCA	GCTCTTTCGG	CGCCAACACT	CGACCCAGAG	700
	TGTTTCATCCG	AACTTCTTCC	GTCACCGCCA	CTCTCACCTT	CCCCGAGGGT	750
	ACCGACGAGT	CCCAGACCGT	CAACCCCGGT	GACAACACTG	AGATGGTTCT	800
20	CGAGCTTGTT	CACCCTACCG	CCATTGAGGT	CAACCAGCGA	TTCA	844

2) INFORMATION FOR SEQ ID NO: 509

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1067 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Babesia bigemina*
- (B) STRAIN: Suarez-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

40	CTTGGACAAG	CTGAAGAGCG	AGCGTGAGCG	TGGTATCACC	ATTGACATTA	50
	CCCTGTGGAA	GTTCGAAACT	GGCAAGTACT	ACTACACCGT	CATTGACGCC	100
	CCCGGTCACC	GTGACTTCAT	TAAGAACATG	ATTACGGGTA	CCTCCCAGGC	150
	CGATGTTGCT	ATGCTTGTCG	TGCCCCGCCG	GGCTGGTGGT	TTCGAAGCTG	200
	CCTTCTCTAA	GGAAGGTCAG	ACCCGTGAGC	ACGCTCTTTT	GGCCTTCACC	250
45	CTTGGTGTC	AGCAGATCAT	TTGCGCCATC	AACAAGATGG	ACAAGTGCGA	300
	CTACAAGGAG	GACCGTTACA	GCGAAATCCA	GAAGGAAGTT	CAGGGTTACC	350
	TGAAGAAGGT	CGGTTACAAC	ATCGAGAAGG	TGCCTTTCGT	CGCCATCTCC	400
	GGTTTCATGG	GTGACAACAT	GGTTGAGCGC	TCCACCAACA	TGCCGTGGTA	450
	CAAGGGCAAG	ACCTTGGTCG	AGGCCCTCGA	CATGATGGAG	CCCCGAAGA	500
50	GGCCCGTCGA	CAAGCCCCTG	CGTCTTCCCC	TCCAGGGTGT	GTACAAGATC	550
	GGTGGTATCG	GTACCGTCCC	TGTCGGTTCG	GTGGAGACTG	GTCAGCTCAA	600
	GGCCGGTATG	GTCTCACCT	TCGCCCCCAA	CCCGATCACT	ACTGAGTGCA	650
	AATCCGTCGA	AATGCACCAC	GAAGTTATCG	ATGTTGCCAG	CCCTGGTGAC	700
	AACGTTGGTT	TCAACGTGAA	GAACGTGTCC	ACCTCTGACA	TCCGCACTGG	750
55	TCACGTGCTG	TCTGACTCCA	AGAACGACCC	CGCCAAGGCC	GCCGTGTCCT	800
	TCACCGCCCA	GGTCACTATC	TTGAACCAAC	CTGGTACCAT	CAAGGCCGGT	850
	TACTCCCCTG	TGGTTGACTG	CCACACTGCC	CACATCTCGT	GCAAATTCGA	900
	CGAGATCACC	AGCCGTATGG	ACAAGCGTAC	CGGTAAGGCC	CTTGAGGAGA	950
	ACCCCAAGAC	CATCAAGAAC	GGCGACGCCG	CTATGGTTCG	CCTGAAGCCG	1000
60	TGCAAGCCCA	TGGTCGTCGA	GGCCTTCACT	GAATACGCTC	CCCTTGGTCG	1050

TTTCGCCGTG CGTGACG

1067

5 2) INFORMATION FOR SEQ ID NO: 510

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

20 GTGAACGTGA ACGTGGTATT ACTATTGATA TTACCTTATG GAAGTTCGAG 50
 ACCACCAAGT ACTACTACAC CGTCATTGAT GCCCCTGGTC ACCGTGACTT 100
 CATCAAGAAC ATGATTACGG GTACTTCTCA AGCCGATGTT GCTATGCTTG 150
 25 TTGTACCAGC TGAGGCTGGT GGTTCGAGG CCGCTTTCTC CAAGGAAGGA 200
 CAGACCCGTG AGCACGCTCT TTTGGCTTTC ACCCTTGGTG TCAAACAGAT 250
 CATCTGTGCC ATTAACAAGA TGGACAAGTG CGACTACAAG GAGGACCGTT 300
 ACAGTGAAAT CCAGAAGGAA GTCCAGGGTT ACCTCAAGAA GGTCGGTTAC 350
 AATATTGAGA AGGTGCCCTT CGTTGCCATC TCCGGTTTCA TGGGAGACAA 400
 CATGGTTGAG CGTTCCACCA ACATGCCCTG GTATAAGGGA AAGACATTGG 450
 30 TCGAGGCCCT TGATCAGATG GAACCCCAA AGAGGCCCGT TGACAAGCCA 500
 CTTCTCTTTC CCCTCCAGGG TGTCTACAAG ATCGGTGGTA TCGGTACCGT 550
 CCCCCTCGGT CGTGTGAAA CTGGTATGTT GAAGGCTGGT ATGATTCTAA 600
 CCTTTGCTCC TAACCCAATC ACCACTGAAT GCAAATCCGT TGAAATGCAC 650
 CACGAAACCG TTGAGGTTGC TTACCCCGGT GACAACGTCG GTTTCAACGT 700
 35 AAAGAACGTT TCTACTTCTG ACATTGCGAG TGGTCACGTT GCCTCTGATT 750
 CTAAGAACGA CCCTGCCAAG GCTGCTGTTT CCTTCACTGC CCAGGTCATT 800
 GTGCTCAACC ACCCTGGTAC CATTAAAGCC GGTACTGCCC CCGTCGTCGA 850
 TTGCCACACC GCTCACATTT CATGTAAATT CGAAGAGATC ACCAGCCGTA 900
 TGGACAAGCG TACCGGTAAA TCTCTTGAGG AAAACCCCAA GACCATCAAG 950
 40 AACGGTGACG CTGCCATGGT TGTGCTCAAG CCAATGAAGC CCATGGTTGT 1000
 CGAATCCTTC ACTGAGTATG CTCCTCTTGG TCGTTTCGCT GTTCGTGAC 1049

45 2) INFORMATION FOR SEQ ID NO: 511

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*
 (B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

	TGGACAAGCT	GAAGGCGGAG	CGCGAGCGCG	GTATCACGAT	CGATATTGCC	50
	CTGTGGAAGT	TCGAGTCGCC	CAAGTCCGTG	TTCACGATCA	TCGATGCCCC	100
	CGGCCACCGC	GACTTTCATCA	AGAACATGAT	CACCGGCACC	TCCCAGGCCG	150
5	ATGCCGCCAT	TCTGATGATT	GACTCGACCC	AGGGTGGCTT	CGAGGCTGGC	200
	ATCTCCAAGG	ACGGCCAGAC	CCGCGAGCAC	GCCCTGCTTG	CCTTCACGCT	250
	GGGCGTGAAG	CAGATGGTTG	TGTGCTGCAA	CAAGATGGAC	GACAAGACGG	300
	TGCAGTACGC	CCAGGCCCCG	TACGAGGAGA	TCAGCAAGGA	GGTCGGCGCG	350
	TACCTGAAGC	GCGTGGGCTA	CAACCCGGAG	AAGGTGCGCT	TCATCCCGAT	400
	CTCGGGCTGG	CAGGGCGACA	ACATGATCGA	GAAGTCCGAC	AACATGTCGT	450
10	GGTACAAGGG	TCCCACGCTG	CTGGAGGCGC	TCGACCTGCT	GGAGGCCCCC	500
	GTGCGTCCGG	TGGACAAGCC	GCTGCGCCTG	CCCCTGCAGG	ACGTGTACAA	550
	GATCGGCGGT	ATCGGCACTG	TGCCCCGTGG	CCGTGTGGAG	ACCGGCGTGA	600
	TGAAGCCGGG	TCGAGTTGTG	TGTGTCGCGC	CTGCCAACGT	GACGACCGAG	650
	GTGAAGTCGA	TCGAGATCGA	CCACGAGCAG	CTGGCTGAGG	CCGTGCCCCG	700
15	CGACAACGTG	GGCTTCAACG	TGAAGAACGT	GTCCGTGAAG	GATATCCGCC	750
	GTGGTAACGT	GTGCGGCAAC	ACGAAGAGCG	ACCCCCGAA	GGAGGCGGCC	800
	GACTTCACTG	CCCAGGTGAT	CGTGCTGAAC	CACCCCGGCC	AGATCAGCAA	850
	CGGCTACGCG	CCGGTGCTGG	ACTGCCACAC	GAGCCACATC	GCGTGCAAGT	900
	TCGCGGACAT	CGAGTCCAAG	ATCGACCGCC	GCTCTGGCAA	GGAGCTGGAG	950
20	AAGAGCCCGA	AGGCCATCAA	GTCCGGCGAT	GCGGCCATCG	TGAAGATGAT	1000
	CCCGCAGAAG	CCGATGTGCG	TGGAGGTGTT	CAACGACTAC	CCGCCGCTGG	1050
	GCCGCTTCGC	TGTCCGCGAT				1070

25

2) INFORMATION FOR SEQ ID NO: 512

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Entamoeba histolytica*
 (B) STRAIN: HM1-IMMS

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

	GCTGAAAGAG	AAAGAGGAAT	TACTATTGAT	ATTTTCATTAT	GGAAATTTCGA	50
	AACATCTAAA	TACTACTTCA	CTATTATTGA	TGCCCCAGGT	CAYAGAGATT	100
	TCATTAAGAA	CATGATTACT	GGAACTTCAC	AAGCTGATGT	TGCCATCCTT	150
45	ATTGTTGCTG	CTGGTACTGG	WGAATTTGAA	GCTGGTATTT	CAAAGAATGG	200
	ACAAACCAGA	GAACAYATTC	TTCTTTTCATA	CACTCTTGGA	GTAAACAAA	250
	TGATTGTTGG	WGTTAACAAG	ATGGATGCTA	TTCAATATAA	ACAAGAAAGA	300
	TATGAAGAAA	TTAAGAAAGA	AATTAGTGCA	TTCTTAAGA	AGACWGGATA	350
	TAATCCAGAC	AAGATTCCAT	TTGTCCCAAT	TTCAGGATTC	CAAGGAGATA	400
50	ATATGATTGA	ACCATCAACC	AACATGCCAT	GGTACAAAGG	ACCAACATTA	450
	ATTGGAGCAC	TTGATTTCAGT	CACACCACCA	GAAAGACCAG	TTGATAAACC	500
	ACTTAGACTT	CCACTTCAAG	ATGTTTAYAA	GATTTTCAGGT	ATTGGAACCTG	550
	TACCATGTGG	AAGAGTTGAA	ACTGGAGTTC	TTAGACCAGG	AACTATTGTT	600
	CAATTTGCAC	CATCAGGAGT	TTCATCTGAA	TGTAAATCAG	TTGAAATGCA	650
55	TCACACAGCA	CTTGCTCAAG	CTATTCCAGG	TGATAATGTT	GGATTCAATG	700
	TTAGAAAYTT	AACAGTTAAA	GATATTAAGA	GAGGAAATGT	AGCATCAGAT	750
	GCTAAGAATC	AACCAGCTGT	TGGATGTGAA	GATTTCACTG	CTCAAGTCAT	800
	TGTCATGAAC	CATCCAGGAC	AAATTAGAAA	GGGATATACA	CCAGTTCTTG	850
	ATTGCCATAC	ATCACACATT	GCATGTAAAT	TCGAAGAATT	ATTAAGCAAG	900
60	ATTGATAGAA	GAACAGGTAA	ATCCATGGAA	GGAGGAGAAC	CAGAATATAT	950

TAAGAATGGA GATTCAGCAC TTGTTAAGAT TGTTCCTCAACT AAACCACTTT 1000
 GTGTTGAAGA ATTTGCTAAA TTCCCACCAT TGGGAAGATT TGCTGTTAGA 1050
 GA 1052

5

2) INFORMATION FOR SEQ ID NO: 513

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1082 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Giardia lamblia*
 (B) STRAIN: Faubert-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

25 GACGAGCGCG AGCGCGGGAT CACGATCAAC ATCGCGCTCT GGAAGTTCGA 50
 GACGAAGAAG TACATCGTCA CGATCATCGA CGCCCCGGGC CACCGCGACT 100
 TCATCAAGAA CATGATCACG GGGACGTCCC AGGCCGACGT CGCGATCCTC 150
 GTCGTGCGCG CGGGCCAGGG CGAGTTCGAG GCCGGGATCT CGAAGGACGG 200
 CCAGACGCGC GAGCACGCGA CCCTTGCGAA CACGCTCGGG ATCAAGACGA 250
 TGATCATCTG CGTCAACAAG ATGGACGACG GCCAGGTCAA GTACTCGAAG 300
 GAGCGTACG ACGAGATCAA GGGCGAGATG ATGAAGCAGC TCAAGAACAT 350
 30 CGGCTGGAAG AAGGCCGAGG AGTTCGACTA CATCCCGACG TCCGGCTGGA 400
 CCGGGGACAA CATCATGGAG AAGTCCGACA AGATGCCCTG GTACGAGGGC 450
 CCGTGCCTGA TCGACGCGAT CGACGGGGCTC AAGGCCCGCA AGCGCCCGAC 500
 CGACAAGCCC CTCCGCCTCC CGATCCAGGA CGTCTACAAG ATCTCGGGCG 550
 TCGGGACCGT CCCC GCGGGC CGCGTCGAGA CGGGCGAGCT CGCGCCCGGG 600
 35 ATGAAGGTCG TCTTCGCCCC GACGTCCAG GTCTCGGAGG TCAAGTCCGT 650
 CGAGATGCAC CACGAGGAGC TCAAGAAGGC CGGGCCCGGG GACAACGTCG 700
 GCTTCAACGT CCGCGGGCTC GCCGTCAAGG ACCTCAAGAA GGGCTACGTC 750
 GTCGGGGACG TGACGAACGA CCCGCCGTC GGCTGCAAGA GCTTCACCGC 800
 CCAGGTCATC GTCATGAACC ACCCGAAGAA GATCCAGCCC GGCTACACGC 850
 40 CCGTCATCGA CTGCCACACC GCGCACATCG CGTGCCAGTT CCAGCTCTTC 900
 CTCCAGAAGC TCGACAAGCG CACGCTCAAG CCCGAGATGG AGAACCCGCC 950
 CGACGCAGGC CGCGGCGATT GCATCATCGT CAAGATGGTC CCCCAGAAGC 1000
 CCCTGTGCTG CGAGACGTTT AACGACTACG CGCCCCCTCGG CCGCTTCGCC 1050
 45 GTCCGCGACA TGCGCCAAAC CGTTGCCGTC GG 1082

2) INFORMATION FOR SEQ ID NO: 514

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

	ACGCGTGGGT	GCTCGACAAG	CTGAAGGCGG	AGCGCGAGCG	CGGCATCACG	50
5	ATCGACATTG	CGCTGTGGAA	GTTCGAGTCG	CCCAAGTCCG	TGTTCACGAT	100
	CATCGATGCG	CCCGGCCACC	GCGACTTCAT	CAAGAACATG	ATCACGGGCA	150
	CGTCGCAGGC	GGACGCCGCC	ATCCTGATGA	TCGACTCGAC	GCATGGTGGC	200
	TTCGAGGCTG	GCATCTCGAA	GGACGGCCAG	ACCCGCGAGC	ACGCGCTGCT	250
	TGCCTTCACT	CTTGCGGTGA	AGCAGATGGT	GGTGTGCTGC	AACAAGATGG	300
10	ACGACAAGAC	GGTGACGTAC	GCGCAGTCGC	GCTACGATGA	GATCAGCAAG	350
	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAACCCGG	AGAAGGTGCG	400
	CTTCATCCCG	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	GAGAAGTCGG	450
	ACAACATGCC	GTGGTACAAG	GGTCCCACGC	TGCTGGACGC	GCTCGACATG	500
	CTGGAGCCGC	CGGTGCGCCC	GGTGGACAAG	CCGCTGCGCC	TGCCCCTGCA	550
15	GGACGTGTAC	AAGATCGGGC	GTATCGGGAC	GGTGCCCGTG	GGGCGCGTGG	600
	AGACCGGCAT	CATGAAGCCG	GGCGACGTGG	TGACGTTTCG	GCCCGCCAAC	650
	GTGACGACTG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	AGCTGGCGGA	700
	GGCGCAGCCC	GGCGACAACG	TCGGCTTCAA	CGTGAAGAAC	GTGTCGGTGA	750
	AGGACATCCG	CCGTGGTAAC	GTGTGCGGCA	ACTCGAAGAA	CGACCCGCCG	800
20	AAGGAGGCGG	CCGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	ACCACCCCGG	850
	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	ACGAGCCACA	900
	TTGCGTGCCG	CTTCGCGGAA	ATCGAGTCCA	AGATCGACCG	CCGCTCCGGC	950
	AAGGATCTGG	AGAAGAACC	CAAGGCGATC	AAGTCTGGCG	ATGCCGCGAT	1000
	CGTGAAGATG	GTGCCGCGAG	AGCCGATGTG	CGTGGAGGTG	TTCAACGACT	1050
25	ACGCGCCGCT	GGGCCGCTTT	GCCGTGCGCG	ACATGCGCCA	AACCGTTG	1098

2) INFORMATION FOR SEQ ID NO: 515

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

45	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTACGCA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
50	TTGCCTTCAC	TCTTGCGGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCG	CGCTACGAGG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
55	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTG	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGCGCACAA	GTCGGCTTCA	ACGTGAAGAA	CGTGTCCGTG	750
60	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800

```

GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA     1000
5 TCGTGAAGAT GGTGCCGCGAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC     1100
CGTC                                     1104

```

10

2) INFORMATION FOR SEQ ID NO: 516

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 1106 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Leishmania tropica
    (B) STRAIN: ATCC 30815

```

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

```

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA      100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
30 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
TTGCCTTCAC KCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
GACGACAAGA CGGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
35 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG      450
GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCCTGC      550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGTGCCCGT GGGGCGCGTG      600
GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA      650
40 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG      750
AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
45 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA     1000
TCGTGAAGAT GGTGCCGCGAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC     1100
CGTCGG                                     1106
50

```

2) INFORMATION FOR SEQ ID NO: 517

55

(i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 1099 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

```

10  TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
    GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA      100
    TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
    ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
    CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
    TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
15  GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
    GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
    GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC      450
    GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
    GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC      550
20  AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG      600
    GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTC CGCCCGCCAA      650
    CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
    AGGCGCAGCC CGCGGACAAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG      750
    AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
25  GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
    GCCAGATCAG CAACGGCTAC GCGCCGCTGC TGGACTGCCA CACGAGCCAC      900
    ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
    CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA     1000
    TCGTGAAGAT GGTGCCGCGA AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
30  TACGCGCCCG TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTG     1099
  
```

2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

```

50  TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
    GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA      100
    TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
    ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
    CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
55  TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
    GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
    GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
    GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC      450
    GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
60  GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC      550
  
```

```

AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCCGT GGGCCGCGTG      600
GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA      650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG      750
5  AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA     1000
10 TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTT      1098

```

15 2) INFORMATION FOR SEQ ID NO: 519

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*
 (B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

```

30 CTCGACAAGC-TGAAGGCGGA GCGCGAGCGC GGCATCACGA TCGACATTGC      50
GCTGTGGAAG TTCGAGTCGC CCAAGTCTGT GTTCACGATC ATCGATGCGC      100
CCGGCCACCG CGACTTCATC AAGAACATGA TCACCGGCAC GTCGCAGGCC      150
GACGCCGCCA TCCTGATGAT CGACTCGACC CAGGGCGGCT TCGAGGCTGG      200
35 CATCTCGAAG GACGGCCAGA CCCGCGAGCA CGCGCTGCTC GCCTTCACGC      250
TTGGTGTGAA GCAGATGGTG GTGTGCTGCA ACAAGATGGA CGACAAGACG      300
GTGCAGTACT CGCAGGCGCG CTACGAGGAG ATCAGCAAGG AGGTGGGCGC      350
GTACCTGAAG CGCGTCGGCT ACAACCCGGA GAAGGTGCGC TTCATCCCGA      400
TCTCGGGCTG GCAGGGCGAC AACATGATCG ACAAGTCGGA CAGCATGCCG      450
40 TGGTACAAGG GGCCACGCT GCTGGACGCG CTCGACATGC TGGAGGCGCC      500
GGTGGCGCCG GTGGACAAGC CGTGCCGCTT GCCCCTGCAG GACGTGTACA      550
AGATCGGCGG TATCGGGACG GTGCCCCTGG GCCGCGTGGA GACCGGCATC      600
ATGAAGCCTG GCGACGTGGT GACGTTTGCG CCCGCCAACG TGACGACGGA      650
GGTGAAGTCG ATCGAGATGC ACCACGAGCA GCTGGCGGAG GCGGTGCCCG      700
45 GCGACAACGT CGGCTTCAAC GTGAAGAACG TGTCGGTGAA GGACATCCGC      750
CGTGGTAAAC TGTGCGGCAA CTCGAAGAAC GACCCGCCGA AGGAGGCGGC      800
CGACTTCACG GCGCAGGTGA TCGTGCTGAA CCACCCTGGC CAGATCAGCA      850
ACGGCTACGC GCCGGTGCTG GACTGCCACA CGAGCCACAT CGCGTGCCGC      900
TTCGCGGATA TCGAGTCCAA GATCGACCGC CGTCTGGCA AGGAGCTGGA      950
50 GAAGAACCCC AAGGCGATCA AGTCCGGCGA TGCGGCCATC GTGAAGATGG     1000
TGCCGCAGAA GCCGATGTGC GTGGAGGTGT TCAACGACTA CCCGCCGCTG     1050
GGGCGCTTCG CTGTGCGCGA C

```

55

2) INFORMATION FOR SEQ ID NO: 520

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
(B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

```

CTCGACAAGC TGAAGGCGGA GCGCGAGCGC GGCATCACGA TCGACATTGC      50
GCTGTGGAAG TTCGAGTCGC CCAAGTCCGT GTTCACGATC ATCGATGCGC      100
CCGGCCACCG CGACTTCATC AAGAACATGA TCACGGGCAC GTCGCAGGCG      150
15 GACGCCGCCA TCCTGATGAT CGACTCGACG CATGGTGGCT TCGAGGCTGG      200
CATCTCGAAG GACGGCCAGA CCCGCGAGCA CGCGCTGCTT GCCTTCACTC      250
TTGGCGTGAA GCAGATGGTG GTGTGCTGCA ACAAGATGGA CGACAAGACG      300
GTGACGTACG CGCAGTCGCG CTACGATGAG ATCAGCAAGG AGGTGGGCGC      350
GTACCTGAAG CGCGTGGGCT ACAACCCGGA GAAGGTGCGC TTCATCCCGA      400
20 TCTCGGGCTG GCAGGGCGAC AACATGATCG AGAAGTCGGA CAACATGCCG      450
TGGTACAAGG GTCCCACGCT GCTGGACGCG CTCGACATGC TGGAGCCGCC      500
GGTGCGCCCG GTGGACAAGC CGCTGCGCCT GCCCTGCGAG GACGTGTACA      550
AGATCGGCCG TATCGGGACG GTGCCCCGTG CCCGCGTGGG GACCGGCATC      600
ATGAAGCCGG GCGACGTGGT GACGTTCCGC CCCGCCAACG TGACGACTGA      650
25 GGTGAAGTCG ATCGAGATGC ACCACGAGCA GCTGGCGGAG GCGCAGCCCG      700
GCGACAACGT CGGCTTCAAC GTGAAGAAGC TGTCTGGTGA GGACATCCGC      750
CGTGGTAACG TGTGCGGCAA CTCGAAGAAC GACCCGCCGA AGGAGGCGGC      800
CGACTTCACG GCGCAGGTGA TCGTGCTGAA CCACCCCGGC CAGATCAGCA      850
ACGGCTATGC GCCGGTGCTG GACTGCCACA CGAGCCACAT TCGTGCCGC      900
30 TTCGCGGAAA TCGAGTCCAA GATCGACCGC CGCTCCGGCA AGGAGCTGGA      950
GAAGAACCCC AAGGCGATCA AGTCTGGCGA TGCCGCGATC GTGAAGATGG     1000
TGCCGCAGAA GCCGATGTGC GTGGAGGTGT TCAACGACTA CGCGCCGCTG     1050
GGCCGCTTTG CCGTGCGCGA C                                     1071

```

35

2) INFORMATION FOR SEQ ID NO: 521

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1114 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania hertigi*
(B) STRAIN: ATCC 50125

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

```

TCGTTCAAGT ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG      50
CGGTATCACG ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCGG      100
55 TGTTCACGAT CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG      150
ATCACCGGCA CGTCGCAGGC GGATGCTGCC ATTCTGATGA TCGATTTCGAC      200
GCAGGGTGGC TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACGCGCGAGC      250
ACGCGCTGCT GGCCTTCACG CTGGGCGTGA AGCAGATGGT TGTGTGCTGC      300
AACAAGATGG ACGACAAGAC GGTGCAGTAC GCGCAGGCGC GCTACGAGGA      350
60 GATCAGCAAG GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCGG      400

```

```

    AGAAGGTGCG CTTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC      450
    GAGAAGTCCG ACAACATGTC GTGGTACAAG GGTCCCACGC TGCTGGAGGC      500
    GCTGGACATG CTGGAGGCGC CCGTGCGCCC GGTGGACAAG CCGCTGCGCC      550
    TGCCCCTGCA GGACGTGTAC AAGATCGGCG GCATTGGCAC GGTGCCGGTG      600
5   GGCCGTGTGG AGACCGGCAT CATGAAGCCC GGCACGTGG TGACGTTCGC      650
    GCCCGCCAAC GTGACGACGG AGGTGAAGTC GATCGAGATG CACCACGAGC      700
    AGCTGCAGGA GGCTGTGCCC GGCACAAACG TCGGCTTCAA CGTGAAGAAC      750
    GTGTGCGGTGA AGGACATCCG CCGTGGTAAC GTGTGTGGCA ACTCGAAGAA      800
    CGACCCGCCG AAGGAGGCGG CTGACTTCAC GGCACAGGTG ATCGTGCTGA      850
10  ACCACCCCGG CCAGATCAGC AACGGCTACG CGCCGGTGCT GGACTGCCAC      900
    ACCAGCCACA TCGCGTGCCG CTTGCGGAGC ATCGAGTCGA AGATCGACCG      950
    CCGCTCCGGC AAGGAGCTGG AGAAGAACCC CAAGTCCATC AAGTCCGGCG     1000
    ACGCCGCCAT CGTGAAGATG GTGCCGCAGA AGCCGATGTG CGTGGAGGTG     1050
    TTCAACGACT ACCCGCCGCT GGGCCGCTTT GCGGTGCGCG ACATGCGCCA     1100
15  AACCCTTGCC GTCG                                     1114

```

2) INFORMATION FOR SEQ ID NO: 522

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC-50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

```

35  TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
    GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA      100
    TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
    ACGTCGAGG CCGACGCCGC CATCTGTATG ATCGACTCGA CGCATGGCGG      200
    CTTGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
40  TTGCCTTCAC TCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
    GACGACAAGA CCGTGACGTA CGCGCAGTCT CGTACGATG AGATCAGCAA      350
    GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
    GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG      450
    GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
45  GCTGGAGCCG CCGGTGCGCC CCGTGGACAA GCGCTGCGC CTGCCCCCTGC      550
    AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGTGCCCGT GGGCCGCGTG      600
    GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCT CGCCCGCCAA      650
    CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
    AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTGCGTG      750
50  AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
    GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
    GCCAGATCAG CAACGGCTAT GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
    ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCGCTCCGG      950
    CAAGGAGCTG GAGAAGAACC CCAAGCGCAT CAAGTCTGGC GATGCCGCGA     1000
55  TCGTGAAGAT GGTGCCGCAG AAGCCGATGT CCGTGGAGGT GTTCAACGAC     1050
    TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC     1100
    CGTCCG                                     1106

```


2) INFORMATION FOR SEQ ID NO: 523

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

```

TACGCGTG GGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCGAAGTCC GTGTTTCACGA      100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
ACGTCGCAGG CGGACGCGGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
GACGACAAGA CGGTGATGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
GGAGGTGAGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
GCTTCATCCC GATCTCGGGG TGGCAGGGCG ACAACATGAT CGACAAGTCG      450
GACAACATGC CGTGGTACAA GGGTCCACG CTGCTGGACG CGCTCGACAT      500
GCTGGAGCCG CCGGTGCGCC CCGTGGACAA GCCGCTGCGC CTGCCCCCTGC      550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCCG GGGCCGCGTG      600
GAGACCGGGA TCATGAAGCC GGGCGACGTG GTGACGTTTC CGCCCGCCAA      650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
AGGCGCAGCC CGGCGACAAC GTGCGCTTCA ACGTGAAGAA CGTGTGCGTG      750
AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
GCCAGATCAG CAACGGCTAC GCGCCGCTGC TGGACTGCCA CACGAGCCAC      900
ATCGCGTGCC GCTTCGCGGA GATCGAGTCC AAGATCGACC GCCGCTCCCG      950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GACGCCGCGA     1000
TCGTGAAGAT GGTGCCGCGA AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC     1100
CGTCG                                         1105

```

2) INFORMATION FOR SEQ ID NO: 524

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

```

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCGAAGTCC GTGTTTCACGA      100

```

	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
5	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
10	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCCGGT	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
15	GAAGGAGGCG	CGCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
20	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

2) INFORMATION FOR SEQ ID NO: 525

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: II WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

40	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	GATCGACATT	GCGCTGTGGA	50
	AGTTCGAGTC	GCCCAAGTCG	GTGTTACACG	TCATCGATGC	GCCCGGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCGCAGG	CGGACGCGGC	150
	CATCCTGATG	ATCGACTCGA	CGCACGGTGG	GTTTCGAGGCT	GGCATCTCGA	200
	AGGACGGGCA	GACGCGCGAG	CACGCGCTGC	TTGCCTTCAC	TCTTGCGCTG	250
45	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGA	CGGTGATGTA	300
	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	GGAGGTGGGC	GCGTACCTGA	350
	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	GCTTCATCCC	GATCTCGGGC	400
	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	GACAACATGC	CGTGGTACAA	450
	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	GCTGGAGGCG	CCGGTGCGCC	500
50	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGCATCGGCA	CGGTGCCCCG	GGGCCGCGTG	GAGACCGGCA	TCATGAAGCC	600
	GGGCGACGTG	GTGACGTTTCG	CGCCCGCGAA	CGTGACGACG	GAGGTGAAGT	650
	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	AGGCGCAGCC	CGGCGACAAC	700
	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	AAGGACATCC	GCCGTGGGAA	750
55	CGTGTGCGGT	AACTCGAAGA	ACGACCCGCC	GAAGGAGGCC	GCCGACTTCA	800
	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	GCCAGATCAG	CAACGGCTAC	850
	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	ATCGCGTGCC	GGTTCGCGGA	900
	CATCGAGTCC	AAGATTGACC	GCCGCTCCGG	CAAGGAGCTG	GAGAAGAACC	950
	CCAAGGCGAT	CAAGTCCGGC	GATGCCGCGA	TCGTGAAGAT	GGTGCCGCAG	1000
60	AAGCCGATGT	GCGTGGAGAT	GTTCAACGAC	TACGCGCCGC	TTGGCCGCTT	1050

TGCTGTGCGC GACATGCGCC AAACCGTTGC C

1081

5 2) INFORMATION FOR SEQ ID NO: 526

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

20 AAATACGCGT GGGTGCTCGA CAAGCTGAAG GCGGAGCGCG AGCGCGGCAT 50
 CACGATCGAC ATTGCGCTGT GGAAGTTCTGA GTCGCCCCAAG TCCGTGTTCA 100
 CGATCATCGA TGCGCCCGGC CACCGCGACT TCATCAAGAA CATGATCACG 150
 GGCACGTGCG AGGCCGACGC CGCCATCCTG ATGATCGACT CGACGCATGG 200
 25 TGGCTTCGAG GCTGGCATCT CGAAGGACGG CCAGACCCGC GAGCACGCGC 250
 TGCTTGCTT CACKCTTGGC GTGAAGCAGA TGGTGGTGTG CTGCAACAAG 300
 ATGGACGACA AGACGGTGAC GTACGCGCAG TCGCGCTACG ATGAGATCAG 350
 CAAGGAGGTG GGC GCGTACC TGAAGCGCGT GGGCTACAAC CCGGAGAAGG 400
 TGCGCTTCAT CCCGATCTCG GGCTGGCAGG GCGACAACAT GATCGAGAAG 450
 30 TCGGACAACA TGCCGTGGTA CAAGGGTCCC ACGCTGCTGG ACGCGCTCGA 500
 CATGCTGAG CCGCCGCTGC GCGCCGTTGA CAAGCCGCTG CGECTGCCCC 550
 TGCAGGACGT GTACAAGATC GCGCGGTATCG GGACGGTGCC CGTGGGGCGC 600
 GTGGAGACCG GCATCATGAA GCCGGGCGAC GTGGTGACGT TCGCGCCCGC 650
 CAACGTGACG ACTGAGGTGA AGTCGATCGA GATGCACCAC GAGCAGCTGG 700
 35 CGGAGGCGCA GCCCGGCGAC AACGTCGGCT TCAACGTGAA GAACGTGTCTG 750
 GTGAAGGACA TCCGCCGTGG TAACGTGTGC GGCAACTCGA AGAACGACCC 800
 GCCGAAGGAG GCGGCCGACT TCACGGCGCA GGTGATCGTG CTGAACCACC 850
 CCGGCCAGAT CAGCAACGGC TACGCGCCGG TGCTGGACTG CCACACGAGC 900
 CACATTGCGT GCCGCTTCGC GGAAATCGAG TCCAAGATCG ACCGCCGCTC 950
 40 CGGCAAGGAG CTGGAGAAGA ACCCAAGGC GATCAAGTCT GGCGATGCCG 1000
 CGATCGTGAA GATGGTGCCG CAGAAGCCGA TGTGCGTGGA GGTGTTCAAC 1050
 GACTACGCGC CGCTGGGCCG CTTTGCCGTG CGCGACATGC GCCAAACCGT 1100
 TG 1102

45

2) INFORMATION FOR SEQ ID NO: 527

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neospora caninum*
 (B) STRAIN: Suarez-4

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

	GGACRAACTT	AAAGCTGAAC	GTGAGCGTGG	TATCACCATT	GATATCTCCC	50
	TGTGGAAATT	TGAGACCAGC	AAGTACTATG	TTACCATCAT	TGATGCCCCA	100
5	GGACACAGAG	ACTTCATCAA	AAACATGATT	ACAGGCACAT	CCCAGGCTGA	150
	CTGTGCTGTG	CTGATTGTTG	CTGCTGGTGT	TGGTGAATTT	GAAGCCGGTA	200
	TCTCCAAGAA	CGGGCAGACC	CGTGAGCATG	CCCTTNTGGC	TTACACCCTG	250
	GGTGTGAAAC	AACTAATTGT	TGGCGTTAAC	AAAAGKGATT	CCACTGAGCC	300
	ACCCTATAGC	CARAAGAGAT	ACGARGAAAT	TGTTAAGGAA	GTCAGCMCCT	350
10	AYNTTAAAAA	AATTGGYTAC	AACCCCGACA	CAGTANCATT	TGKGCCAATT	400
	TNTGGCTGGA	ATGGTGACAA	CATGCTGGAN	CCAAGTGCTA	ATATGCCATG	450
	GTTCAAGGGA	TGGAAGTCM	CCCGTAAGGA	CGGCAATGCC	AGKGAACCM	500
	CCCTGCTTGA	AGCTYTGGAT	TGCATTYTGC	CACCAAYTTG	CCCAACTGAC	550
	AAACCCCTTG	GTTTGCCTYT	CCAGGATGTC	TATAAAATTG	GKGGTATTGG	600
15	TACTGTCCCT	GTGGGTCGTG	TGGAGACTGG	TGTTCTCAAA	CCTGGCATGG	650
	TGGTCACCTT	TGCTCCAGTC	AATGTAACAA	CTGAAGTGAA	GTCTGTAGAA	700
	ATGCACCATG	AAGCATTGAG	TGAAGCCCTT	CCTGGGGACA	ATGTGGGCTT	750
	CAATGTCAAG	AACGTGTCTG	TCAAAGATGT	CCGTCGTGGC	AATGTGGCTG	800
	GTGACAGCAA	AAATGATCCA	CCCATGGAAG	CTGCTGGCTT	CACAGCTCAG	850
20	GTGATTATTT	TGAACCATCC	AGGCCAAATC	AGTGCTGGAT	ATGCACCTGT	900
	GCTGGATTGT	CACACAGCTC	ACATTGCTTG	CAAGTTTGCT	GAGCTGAAGG	950
	AGAAGATTGA	TCGTGCTTCT	GGGAAAAGC	TGGAAGATGG	CCCTAAATTC	1000
	TTGAAATCTG	GTGACGCTGC	CATCGTTGAT	ATGGTTCTTG	GCAAGCCCAT	1050
	GTGTGTCGAG	AGCTTCTCTG	ATTATCCTCC	CCTGGGCCGT	TTTGCTGTGC	1100
25	GTGAC					1105

2) INFORMATION FOR SEQ ID NO: 528

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 935 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Trichomonas vaginalis*
- (B) STRAIN: ATCC 30001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

45	GCACATCCCA	GGCTGATGCT	GCTATCCTTG	TCATCGACTC	CACACTCGGT	50
	GGYTTCTGAAG	CCGGTATCGC	TGAACAAGGC	CAGACACGTG	AACACGCTCT	100
	TCTTGCCCTTC	ACACTCGGCA	TCAAGCAGGT	CATTGTGCGC	GTCAACAAGA	150
	TGGATGACAA	GACAGTCAAC	TACAACAAGG	CYCGTTTCGA	CGAAATCACA	200
	GCCGAAATGA	CACGCATCCT	TACAGGCATC	GGCTACAAGC	CAGAAATGTT	250
50	CCGCTTCGTC	CCAATCTCCG	GCTGGGCTGG	CGACAACATG	ACAGAGAAGT	300
	CTCCAAACAT	GCCATGGTAC	AATGGCCCAT	ACCTTCTTGA	AGCCCTCGAT	350
	TCCCTTCAGC	CACCAAAGCG	CCCATTGAC	AAGCCACTCC	GTCTTCCACT	400
	CCAGGATGTC	TACAAGATCA	ACGGTATCGG	TACAGTTCCA	GTCGGCCGTG	450
	TCGAATCCGG	CACAATGAAG	CCAGGCATGA	TCGTTAACCT	CGCCCCATCC	500
55	ACAGTTACAG	CTGAAGTTAA	GTCCATCGAA	ATGCACCACG	AATCCCTTCC	550
	AGAGGCTCTT	CCAGGTGACA	ACATCGGCTT	CAACGTCAAG	AACGTTTCCA	600
	CAGCTGATGT	CAAGCGTGGC	TACGTGCTTG	GTGATACAAA	GCGTGACCCA	650
	CCAGTCGAAT	GCGCTTCTCT	CACAGCTCAR	ATGATCATCT	CCAACCACCC	700
	AGGCAAGATC	CACGCCGGCT	ACCAGCCAGT	TTTCGACTGC	CACACAGCTC	750
60	ACATCGCCTG	CAAGTTCGAC	AAGCTCATCC	AGCGTATCGA	TCGTGCGCCAC	800

GGCAAGAAGG	CTACAGAGAA	CCCAGAATAC	ATTCAGAAGG	ATGATGCCGC	850
TATCGTCGAG	GTTGTCCCAT	CCAAGCCACT	CGTCGTCGAG	TCCTTCCAGG	900
AGTACCCACC	ACTCGGCCGT	TTGCCCATCC	GTGAT		935

5

2) INFORMATION FOR SEQ ID NO: 529

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1065 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO795

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

AAGCTGAAGG	CTGAGCGCGA	ACGTGGTATC	ACGATCGACA	TTGCACTGTG	50
GAAATTTCGAG	TCACCCAAGT	CTGTCTTCAC	TATTATTGAT	GCTCCTGGGC	100
25 ACCGTGACTT	CATCAAGAAC	ATGATCACC	GCACATCGCA	AGCCGACGCA	150
GCCATCCTCA	TCATTGCCCTC	TGCGCAGGGT	GAGTTCGAGG	CTGGTATCTC	200
CAAGGATGGA	CAGACCCGCG	AGCACGCGTT	GCTGGCCTTC	ACTTTGGGTG	250
TGAAGCAGAT	GGTTGTGTGC	TGCAACAAGA	TGGACGACAA	GACTIONTGAAC	300
TACGGACAGG	AGCGGTATGA	CGAGATTGTG	AAGGAGGTGT	CTGCTTACAT	350
30 CAAGAAGGTT	GGGTACAACG	TGGAGAAGGT	GCGCTTCGTC	CCCATCTCCG	400
GATGGCAGGG	CGACAACATG	ATTGAGAAAT	CCGAGAAGAT	GCCATGGTAC	450
AAGGGTCCAA	CGCTCCTGGA	GGCACTAGAC	ATGCTGGAGC	CACCACTGCG	500
TCCGAGCGAG	AAGCCCCGTC	GTCTGCCACT	GCAGGACGTG	TACAAGATCG	550
GTGGTATTGG	CACCGTGCCC	GTTGGTCGTG	TGGAGACCGG	CGTGATGAAG	600
35 CCTGGTGATG	TGGTGACGTT	TGCCCCCGCC	AACGTGACGA	CCGAGGTGAA	650
ATCGATCGAG	ATGCACCACG	AGCAGCTCGC	TGAGGCGACC	CCCGGTGACA	700
ACGTGCGGCTT	TAACGTGAAG	AACGTTTCTG	TAAAGGACAT	CCGCCGTGGC	750
AACGTCTGCG	GTAACACCAA	GAACGACCCC	CCAAAGGAGG	CCGCCGACTT	800
CACGGCACAG	GTGATCATCC	TGAACCACCC	CGGACAGATT	GGAAACGGTT	850
40 ATGCGCCCCG	GCTGGACTGC	CACACATCGC	ACATTGCCTG	CAAGTTCGCG	900
GAGATCGAGT	CGAAGATCGA	CCGTCGCTCT	GGCAAGGAGC	TGGAGAAGGC	950
TCCCAAGTCG	ATCAAGTCTG	GCGACGCCGC	GATCGTGCGC	ATGGTGCCGC	1000
AGAAGCCTAT	GTGCGTGGAG	GTCTTCAACG	ACTACGCGCC	ACTCGGCCGC	1050
TTTGCCGTGC	GTGAC				1065

45

2) INFORMATION FOR SEQ ID NO: 530

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*
 (B) STRAIN: ATCC 11745

60

530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

	TTCGCGGAGG	GCGTGCCGCC	GGTGCTGACG	GCGCTGGACG	TGACGGAGGA	50
5	CCTCGGCCGC	GACGAGCCGC	TGACGCTGGA	GATTGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCCATGCAGA	CGACGGATCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTCGAC	GGGCGGCAAC	ATCTCCGTGC	CGGTTGGCCG	200
	CGAGACGCTG	GGCCGCATCT	TCAACGTGCT	CGGCGACGCG	ATCGACCAGC	250
	GCGGTGTGGT	GGGCGAGAAG	ATGCGCATGC	CGATCCACGC	CGAGGCGCCG	300
10	AAGCTGGCGG	ACCAGGCCGC	GGAGGACGCG	ATTCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CGTACTGCAA	GGGTGGCAAG	ATCGGGCTGT	400
	TCGGCGGTGC	TGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
	AACGTGGCCA	AGGGCCACGG	TGGTTTCTCC	GTGTTGCGCC	GCGTTGGCGA	500
	GCGCACCCGC	GAGGGCACGG	ATCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
15	TCATTGACCT	GAAGGCGAG	TCGAAGTGCG	TGCTGGTGTA	CGGCCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	TGCGCGTGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGTGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTTCATCG	700
	ACAACATCTT	CCGCTTCACC	CAGGCCAACT	CCGAGGTGTC	CGCCCTGCTG	750
	GGCCGCATTC	CCGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CCGAGGATCT	800
20	TGGTATGCTG	CAGGAGCGCA	TTACGTGCGAC	GACGAAGGGC	TCGATTACGT	850
	CTGTGCAGGC	CGTGTACGTG	CCGGCCGATG	ATATCACGGA	TCCGGCGCCG	900
	GCGACGACCT	TCTCGCACCT	GGATGCGACG	ACGGTGCTGG	ACCGCGCGGT	950
	TGCCGAGTCT	GGCATCTACC	CCGCCGTGAA	CCCGCTGGAG	TGCGCGTCGC	1000
	GTATCATGGA	CCCCGATGTG	ATCGACGTGG	ACCACTACAA	CGTTGCGCAG	1050
25	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTCG	1100
	CGTGCTGGGT	ATCGACGAGC	TGAGCGAGGA	GGACAAGCTT	GTGGTGGACC	1150
	GCGCTCGCAA	GGTGACGCGC	TTCTGTTCGC	AGCCGTTCCA	GGTGGCCGAG	1200
	GTGTTACCCG	GCATGACGGG	CCACTACGTG	CAGCTGGAGG	ACACAGTGGA	1250
30	GTCGTTCTCT	GGCCTGCTGA	TGGGCTCGTA	CGACCAGATC	CCGGAGA	1297

2) INFORMATION FOR SEQ ID NO: 531

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30816

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

	CTTCTCGGAG	GGCGTGCCGC	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	50
50	ACCTTGGCCG	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	100
	GCGAACACGG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
	GAAGTCGAAG	GTCGTGTGCA	CCGGCGGCAA	CATCTCTGTG	CCGCTGGGCC	200
	GTGAGACGCT	GGGCCGCATC	TTCAAYGTTT	TGGGCGACGC	GATCGACCAG	250
	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	300
55	GAAGCTGGCG	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	400
	TTCCGGCGGTG	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	500
	AGCGCACGCG	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550
60	GTGATTGACC	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	600

	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGCCGCATT	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
5	TTGGTATGCT	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTGC	1000
	CGTATCATGG	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
10	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTCACG	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	1250
	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTTCG	ACGACCAGAT	CCCGGAGA	1298

15

2) INFORMATION FOR SEQ ID NO: 532

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
35	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTCGAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
	TGAGACGCTG	GGCCGCATCT	TCAACGTTCT	GGGCGACGCG	ATCGACCAGC	250
	GCGGCCCCGT	GGGCGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCA	300
40	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
	TCGGCGGTGC	CGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCC	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
45	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	CGCGCGCGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGCGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTCATCG	700
	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CAGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
50	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	AACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGATACGT	CCAGCGGATG	ATATCACGGA	TCCCGCGCCC	900
	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
	GGCGGAGTCG	GGCATCTACC	CTGCCGTGAA	CCCGCTGGAG	TGCGCGTTCG	1000
	GTATCATGGA	CCCCGACGTG	ATCGATGTGG	ACCACTACAA	CGTTGCGCAG	1050
55	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGC	ATCGACGAGC	TGAGCGAGGA	AGACAAGGTT	GTTGTGGACC	1150
	GCGCGCGCAA	GGTGACCCGG	TTCCTGTGCG	AGCCGTTCCA	GGTTGCGGAG	1200
	GTGTTACCGG	GCATGACGGG	CCACTACGTG	CAGCTGGTCG	ACACGGTGGA	1250
	GTCGTTCTCT	GGCCTGCTGA	TGGGGTTCGTA	CGACCAGATC	CCGGAGA	1297

60

2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

5	CTTCTCGGAG	GGCGTGCCGC	CCGTACTGAC	GGCGCTGGAT	GTGACGGAGG	50
20	ACCTTGGCCG	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAT	100
	GCGAACACCG	GCCGCTGCAT	TCCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
	GAAGTCGAAG	GTTGTGTCTGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	200
	GTGAGACGCT	GGGCCGCATC	TTCAACGTTT	TGGGCGACGC	GATCGACCAG	250
	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	300
25	GAAGCTGGCG	GACCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	CCTCATTCTG	CCCTACTGCA	AGGGCGGCAA	GATCGGCCCTG	400
	TTCGGCGGTG	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GTGGCTTCTC	CGTGTTTGCC	GGCGTTGGCG	500
	AGCGCACGCG	CGAGGGCACG	GACCTATACC	TGGAGATGAT	GCAGTCGAAG	550
30	GTGATTGACC	TGAAGGGCGA	GTGGAAGTGC	GTGCTTGTGT	ACGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGCCGCATT	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCCGAGGATC	800
35	TTGGTATGCT	GCAGGAGCGC	ATCACATCGA	CGACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCGGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCCGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
40	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTTCG	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTTACG	GGCATGACGG	GCCACTACGT	GCAGCTGGCC	GACACGGTGG	1250
45	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTCGT	ACGACCAGAT	CCCGGAGA	1298

2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

```

5  CTTCTCGGAG GGCCTGCCGC CCGTACTGAC GCGCTGGAT GTGACGGAGG 50
   ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT 100
   GCGAACACCG GCCGCTGCAT TGCATGACAG ACGACGGACC TGCTGAAGCT 150
   GAAGTCGAAG GTTGTGTCTGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
   GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG 250
   CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
10  AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
   AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG 400
   TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
   CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTGTTGCC GCGCTTGGCG 500
   AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG 550
15  GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
   GAACGAGCCC CCGGTGTGCG GCGCGCGCGT TGCAGAGTCT GCGCTGACGA 650
   TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
   GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
   GGGCCGCATT CCGGCCGCCG TGGGCTACCA CCGGACGCTT GCCGAGGATC 800
20  TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG 850
   TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACTG ATCCCGCGCC 900
   CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950
   TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCTG 1000
   CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
25  GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100
   CCGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC 1150
   CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA 1200
   GGTGTTACAG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG 1250
   AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA 1298
30

```

2) INFORMATION FOR SEQ ID NO: 535

```

35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1301 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
40
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Leishmania gerbilli
          (B) STRAIN: ATCC 50121
45

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

```

50  GCACTTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG 50
   AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG 100
   GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA 150
   GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG 200
   GCCGTGAGAC GCTGGGCCGC ATCTTCAACG TTCTGGGCGA TGCGATCGAC 250
   CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC 300
55  CCCGAAGCTG CCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA 350
   TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY 400
   CTGTTCCGCG GTGCCGGTGT GGGCAAGACT GTGATCATCA TGGAGCTGAT 450
   CAACAACGTC GCGAAGGGCC ACGGTGGTTT CTCCGTGTTT GCCGGCGTTG 500
   GCGAGCGCAC GCGCGAGGGC ACGGACCTGT ACCTGGAGAT GATGCAGTCG 550
60  AAGGTGATTG ACCTGAAGGG CGAGTCGAAG TGCCTGCTTG TGTACGGGCA 600

```

```

GATGAACGAG CCCCCGGGTG CGCGCGCGCG CGTTGCGCAG TCTGCGCTGA 650
CGATGGCGGA GTACTTCCGC GACGTGGAGG GCCAGAACGT GCTGCTGTTC 700
ATCGACAACA TCTTCCGCTT CACGCAGGCG AACTCCGAGG TGTCCGCGCT 750
GCTGGGCCGC ATTCGGGCCG CCGTGGGCTA CCAGCCGACG CTTGCGGAGG 800
5 ATCTTGGTAT GCTGCAGGAG CGCATCACGT CGACAACGAA GGGGTTCGATC 850
ACGTCCGTGC AGGCCGTGTA CGTGCCAGCG GATGATATCA CGGATCCCGC 900
GCCCCGACG ACGTTCTCGC ACCTTGACGC GACGACTGTG CTGGACCGCG 950
CGGTGGCGGA GTCGGGCATC TACCCTGCCG TGAACCCGCT GGAGTGC GCG 1000
TCGCGTATCA TGGACCCCGA TGTGATCGAT GTGGACCACT ACAACGTTGC 1050
10 GCAGGATATC GTGCAGATGC TGACCAAGTA CAAGGAGCTG CAGGACATCA 1100
TTGCGGTGCT TGGCATCGAC GAGCTGAGCG AGGAAGACAA GGTGTGTTG 1150
GACCGCGCGC GCAAGGTGAC CCGGTTCTCTG TCGCAGCCGT TCCAGGTTGC 1200
GGAGGTGTTT ACGGGCATGA CGGGCCACTA CGTGCAGCTG GTCGACACGG 1250
TGGAGTCGTT CTCTGGCTTG CTGATGGGGT CGTACGACCA GATCCCGGAG 1300
15 A 1301

```

2) INFORMATION FOR SEQ ID NO: 536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

```

35 CTTCGCGGAG GGCCTGCCGC CCGTGCTGAC GTCGCTGGAT GTGACGGAGA 50
ACCTCGGCCG CGATGAGCCG CTGACGCTGG AGATTGTGCA GCACTTGGAC 100
GCGAACACCG GTCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
GAAGTCGAAG GTCGTGTCGA CCGGTGGCAA CATCTCTGTG CCTGTTGGCC 200
GCGAGACGCT GGGTTCGCAT TTCAACGTGC TTGGCGATGC GATTGACCAG 250
40 CGCGGCCCTG TGGGTGAGAA GATGCGCATG GCGATCCACG CCGAGGCGCC 300
GAAGCTGGCG GATCAGGCGG CAGAGGACAC GATCCTGACG ACCGGCATCA 350
AGGTGATCGA TCTTATTCTG CCGTACTGCA AGGGTGGTAA GATCGGTCTG 400
TTCGGTGGTG CCGGTGTAGG CAAGACTGTG ATTATTATGG AGCTGATCAA 450
TAACGTGGCG AAGGGCCACG GTGGGTTTTT CGTGTTTGCT GGCCTGGGCG 500
45 AGCGCACGCG CGAGGGCACT GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
GTGATTGACC TGAAGGGCGA ATCAAAGTGC GTGCTTGTGT ACGGACAGAT 600
GAACGAGCCC CCGGTGCGC GTGCGCGCGT TGCGCAGTCT GCGCTGACGA 650
TGGCCGAGTA CTTCGCGCAT GTGGAGGGCC AGAACGTGCT GCTGTTCATT 700
GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
50 GGGTCGCATT CCTGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800
TGGGCATGCT GCAGGAGCGC ATTACGTCGA CGACGAAGGG CTCGATTACG 850
TCTGTGCAGG CCGTGTACGT GCCTGCGGAT GATATCACGG ACCCGGCGCC 900
CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGTGC GG 950
TGGCAGAGTC GGGCATTTAC CCTGCGGTGA ACCCGCTGGA GTGCGCGT CG 1000
55 CGTATCATGG ACCCGGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCAT TG 1100
CCGTGCTTGG TATCGACGAG CTGACGAGG AGGACAAGGT TGTGGTGGAC 1150
CGCGCGCGCA AGTGACCCG GTTCCTGTCG CAGCCGTTCC AGGTTGCGGA 1200
GGTGTTCACT GGCATGACGG GTCACTACGT TCAGCTGGAG GACACGGTGG 1250
60 AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACGACCAGAT CCCGGAGA 1298

```

2) INFORMATION FOR SEQ ID NO: 537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

```

20  CTTCTCGGAG GCGGTGCCGC CCGTGCTGAC GCGCTGGAT GTGACGGAGG      50
    ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC      100
    GCGAACACCG GCCGCTGCAT TCGATGCAG ACGACGGACC TGCTGAAGCT      150
    GAAGTCGAAG GTTGTGTCTGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
    GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGATGC GATCGACCAG      250
25  CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
    GAAGCTGGCG GATCAGGCCG CAGAGGACAC GATCCTGACG ACCGGCATCA      350
    AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG      400
    TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
    CAATGTGCGG AAGGGCCACG GTGGTTTCTC CGTGTGTTGCC GGCGTTGGCG      500
30  AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG      550
    GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT      600
    GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCAGTCT GCGCTGACGA      650
    TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC      700
    GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CCGCGCTGCT      750
35  GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC      800
    TTGGTATGCT GCAGGAGCGC ATCACGTCGA CAACGAAGGG GTCGATCACG      850
    TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC      900
    CGCGACGACG TTCTCGCACC TGGATGCGAC GACTGTGCTG GACCGCGCGG      950
    TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG     1000
40  CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA     1050
    GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTG     1100
    CCGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC     1150
    CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA     1200
    GGTGTTACAG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG     1250
45  AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAG      1297

```

2) INFORMATION FOR SEQ ID NO: 538

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*

(B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

```

5  TTCTCGGAGG GCGTGCCGCC CGTGCTGACG GCGCTGGATG TGACGGAGGA      50
   CCTTGGCCGC GATGAGCCGC TGACGCTGGA GATCGTGCAG CACCTGGACG      100
   CGAACACCGG CCGCTGCATT GCGATGCAGA CGACGGACCT GTTGAAGCTG      150
   AAGTCGAAGG TTGTGTCGAC CGGCGGCAAC ATCTCTGTGC CGGTGGGCCG      200
   TGAGACGCTG GGCCGCATCT TCAACGTGCT GGGCGACGCG ATCGACCAGC      250
10  GCGGCCCCGT GGGTGAGAAG ATGCGCATGG CGATCCACGC CGAGGCCCCG      300
   AAGCTGGCGG ATCAGGCCGC GGAGGACACG ATCCTGACGA CCGGCATCAA      350
   GGTGATCGAC CTGATTCTGC CCTACTGCAA GGGTGGCAAG ATCGGCCTGT      400
   TTGGTGGCGC CGGTGTGGGC AAGACCGTGA TCATCATGGA GTTGATTAAC      450
   AACGTCGCGA AGGGCCACGG TGGTTTCTCG GTGTTTGCCG GCGTTGGCGA      500
15  GCGCACGCGC GAGGGCACGG ACCTGTACCT GGAGATGATG CAGTCGAAGG      550
   TGATTGACCT GAAGGCGAG TCGAAGTGCG TGCTTGTTGTA CGGGCAGATG      600
   AACGAGCCCC CGGGTGCGCG CGCGCGCGTT GCGCAGTCTG CGCTGACGAT      650
   GCGGGAGTAC TTCCGAGACG TGGAGGGCCA GAATGTGCTG CTGTTTCATCG      700
   ACAACATCTT CCGCTTCACG CAGGCGAACT CCGAGGTGTC TGCCTGCTG      750
20  GGCCGCATTC CGGCCGCCGT GGGCTACCAG CCGACGCTTG CGGAGGATCT      800
   TGGTATGCTG CAGGAGCGCA TCACGTCGAC GACGAAGGGG TCGATCACGT      850
   CCGTGCAGGC CGTGTACGTG CCTGCGGATG ATATCACGGA TCCGGCGCCC      900
   GCGACGACGT TCTCGCACCT GGACGCGACG ACTGTGCTGG ACCGCGCGGT      950
   GCGCGAGTCG GGGATCTACC CTGCCGTGAA CCCGCTGGAG TGCCTGCTGC      1000
25  GTATCATGGA CCCCAGTGTG ATCGACGTGG ACCACTACAA CGTTGCGCAG      1050
   GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC      1100
   GGTGCTTGGT ATCGACGAGC TGAGCGAGGA GGACAAGGTC GTGGTGGACC      1150
   GCGCGCGCAA GGTGACCCGG TTCTGTGTCG AGCCGTTCCA GGTTGCGGAG      1200
   GTGTTACGGG GCATGACGGG CCACTACGTG CAGCTGGCCG ACACGGTGGA      1250
30  GTCGTTCTCT GGGCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA      1297

```

2) INFORMATION FOR SEQ ID NO: 539

```

35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
40  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

```

45  CCITACATCC TBGTYGCICT IAACAAG

```

27

50 2) INFORMATION FOR SEQ ID NO: 540

```

      (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 23 bases
      (B) TYPE: Nucleic acid
55  (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG

23

5

2) INFORMATION FOR SEQ ID NO: 541

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

GTKGAAATGT TCCGCAAGCT GCT

23

20

2) INFORMATION FOR SEQ ID NO: 542

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

CGGAARTAGA ACTGSGGACG GTAG

24

35

2) INFORMATION FOR SEQ ID NO: 543

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

50 ATCTTAGTAG TTTCTGCTGC TGA

23

55

2) INFORMATION FOR SEQ ID NO: 544

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

5

AYGTTGTCGC CMGGCATTMC CAT

23

10 2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

15

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG

26

25

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

CCRCGICCGG TRATGGTGAA GAT

23

40

2) INFORMATION FOR SEQ ID NO: 547

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

GTACAGTTGC TTCAGGACGT ATC

23

55

2) INFORMATION FOR SEQ ID NO: 548

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548

10 ACGTTCGATT TCATCACGTT G

21

2) INFORMATION FOR SEQ ID NO: 549

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549

25

GAACGTGATA CTGACAAACC TTTA

24

30 2) INFORMATION FOR SEQ ID NO: 550

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550

GAAGAAGAAC ACCAACGTTG

20

45

2) INFORMATION FOR SEQ ID NO: 551

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551

GAAGAAAAA TCTTCGAAC TGGCTA

25

60

2) INFORMATION FOR SEQ ID NO: 552

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

TACACGGCCG GTGACTACG

19

2) INFORMATION FOR SEQ ID NO: 553

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

GGCCGTGTTG AACGTGGTCA AATCA

25

2) INFORMATION FOR SEQ ID NO: 554

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

G TTCCTTACA TCGTTGTTTT TCTC

24

2) INFORMATION FOR SEQ ID NO: 555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

TCTCGAACTT TCTCTATGTA TGCA

24

5

2) INFORMATION FOR SEQ ID NO: 556

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

CGGCGCNATC YTS GTTGTTG C

21

20

2) INFORMATION FOR SEQ ID NO: 557

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

35 CCMAGGCATR ACCATCTCGG TG

22

2) INFORMATION FOR SEQ ID NO: 558

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

50

TCITTYAART AYG CITGGGT

20

55 2) INFORMATION FOR SEQ ID NO: 559

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

542

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

CCGACRGCRA YIGTYTGICK CAT

23

10

2) INFORMATION FOR SEQ ID NO: 560

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

15 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

GAYTTCATYA ARAAYATGAT YAC

23

25

2) INFORMATION FOR SEQ ID NO: 561

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

ACIGTICGGC CRCCCTCACG GAT

23

40

2) INFORMATION FOR SEQ ID NO: 562

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

55 CARATGRAYG ARCCICCIGG IGYIMGIATG

30

60

2) INFORMATION FOR SEQ ID NO: 563

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563
10 GGYTGRTAIC CIACIGCIGA IGGCAT 26

15 2) INFORMATION FOR SEQ ID NO: 564

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564
TAYGGICARA TGAAYGARCC ICCIGGIAA 29

30 2) INFORMATION FOR SEQ ID NO: 565

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565
GGYTGRTAIC CIACIGCIGA IGGDAT 26

45 2) INFORMATION FOR SEQ ID NO: 566

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566
60 TTYGGIGGIG CIGGIGTIGG IAARAC 26

2) INFORMATION FOR SEQ ID NO: 567

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567
15 TCRTCIGCIG GIACRTAIAY IGCYTG 26

2) INFORMATION FOR SEQ ID NO: 568

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568
30 RTIATIGGIG CIGTIRTIGA YGT 23

2) INFORMATION FOR SEQ ID NO: 569

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569
RTIRTIGGIS CIGTIRTIGA TAT 23

2) INFORMATION FOR SEQ ID NO: 570

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

RTIRYIGGIC CIGTIRTIGA YGT

23

5

2) INFORMATION FOR SEQ ID NO: 571

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

RTIRTIGGIC CIGTIRTIGA TGT

23

20

2) INFORMATION FOR SEQ ID NO: 572

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

35 RTIRTIGGIS CIGTIRTIGA

20

2) INFORMATION FOR SEQ ID NO: 573

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

50

CCICCIACCA TRTARAAIGC

20

55 2) INFORMATION FOR SEQ ID NO: 574

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

60

546

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

ATIGCIATGG AYGGIACIGA RGG

23

10

2) INFORMATION FOR SEQ ID NO: 575

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

15

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

TIACCATTTC AGTACCTTCT GGTA

25

25

2) INFORMATION FOR SEQ ID NO: 576

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

AACTTCRTCA AGAAGGTYGG TTACAA

26

40

2) INFORMATION FOR SEQ ID NO: 577

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

CATGATTGAA CCATCCACCA

20

55

2) INFORMATION FOR SEQ ID NO: 578

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578
10 CATGATTGAA GCTTCCACCA 20

15 2) INFORMATION FOR SEQ ID NO: 579

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579
GAAGGCCGTG CTGGTGAGAA 20

30 2) INFORMATION FOR SEQ ID NO: 580

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580
GCTAAACCAG CTACAATCAC TCCAC 25

45 2) INFORMATION FOR SEQ ID NO: 581

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581
ACATCGGTGC ATTATTACGT GG 22

60

2) INFORMATION FOR SEQ ID NO: 582

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582
15 TTTCAACTTC GTCGTTGACA CGAACAGT 28

2) INFORMATION FOR SEQ ID NO: 583

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583
30 CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG 35

2) INFORMATION FOR SEQ ID NO: 584

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584
ACATGACACA TCTAAAACAA 20

2) INFORMATION FOR SEQ ID NO: 585

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

ACCACATACT GAATTCAAAG

20

5

2) INFORMATION FOR SEQ ID NO: 586

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

CAGAAGTATA CGTATTATCA

20

20

2) INFORMATION FOR SEQ ID NO: 587

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

35 CGTATTATCA AAAGACGAAG

20

2) INFORMATION FOR SEQ ID NO: 588

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

50

TCTTCTCAAA CTATCGTCCA

20

2) INFORMATION FOR SEQ ID NO: 589

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

550

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

GCACGAAACT TCTAAAACAA

20

10

2) INFORMATION FOR SEQ ID NO: 590

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

15

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

TATACGTATT ATCTAAAGAT

20

25

2) INFORMATION FOR SEQ ID NO: 591

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

TCCTGGTTCT ATTACACCAC

20

40

2) INFORMATION FOR SEQ ID NO: 592

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

55 CAAAGCTGAA GTATACGTAT

20

60

2) INFORMATION FOR SEQ ID NO: 593

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

20

TTCACCTAACT ATCGCCCACA

2) INFORMATION FOR SEQ ID NO: 594

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

20

ATTGGTATCC ATGACACTTC

2) INFORMATION FOR SEQ ID NO: 595

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

20

TTAAAGCAGA CGTATACGTT

2) INFORMATION FOR SEQ ID NO: 596

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

20

GAAATTATTG GTATCAAAGA

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME 2 DE 4

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME

THIS IS VOLUME 2 OF 4

NOTE: For additional volumes please contact the Canadian Patent Office

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME 3 DE 4

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME

THIS IS VOLUME 3 OF 4

NOTE: For additional volumes please contact the Canadian Patent Office

2) INFORMATION FOR SEQ ID NO: 597

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597
15 ATTGGTATCA AAGAAACTTC 20

2) INFORMATION FOR SEQ ID NO: 598

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598
30 AATTACACCT CACACAAAAT 20

2) INFORMATION FOR SEQ ID NO: 599

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599
CGGTGAAGAA ATCGAAATCA 20

2) INFORMATION FOR SEQ ID NO: 600

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

ATGCAAGAAG AATCAAGCAA

20

5

2) INFORMATION FOR SEQ ID NO: 601

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

GTTTCACGTG ATGATGTACA

20

20

2) INFORMATION FOR SEQ ID NO: 602

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

35 AAGTTGAAGT TGTTGGTATT

20

2) INFORMATION FOR SEQ ID NO: 603

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

50

GGTATTAAAG ACGAAACATC

20

2) INFORMATION FOR SEQ ID NO: 604

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

GGTGATGAAG TAGAAATCGT

20

10

2) INFORMATION FOR SEQ ID NO: 605

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

GAAATGTTCC GTAAATTATT

20

25

2) INFORMATION FOR SEQ ID NO: 606

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

ATTAGACTAC GCTGAAGCTG

20

40

2) INFORMATION FOR SEQ ID NO: 607

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACAC
60 GTGAACATAT CTTATTATCA CGTAACGTTG GTGTACCATA CATCGTTGTA

50
100

	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
	ATGTTCCAGT	TATCGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGACGAG	250
	TCTTATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
5	CCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGTGAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
	CGAAACATCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GACAACTTCG	GTGCTTTATT	ACGTGGTGTA	550
10	GCACGTGAAG	ATATCGAACG	TGGACAAGTA	TTAGCTAAAC	CAGCTACAAT	600
	CACCTCCACAC	ACAAAATTCA	AAGCTGAAGT	ATACGTATTA	TCAAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CAGACGTTAC	TGGTGTTGTA	GAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTTGCTAT	GGACGTTGAA	TTAATTCACC	800
15	CAATCGCTAT	CGAAGACGGA	A			821

2) INFORMATION FOR SEQ ID NO: 608

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

35	CGGAGCTATC	TTGGTAGTTT	CTGCTGCTGA	CGGCCCAATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	GTGTTTCCTTA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACRAATTC	CCTGGTGRCG	200
	ATGTTCTCTG	AGTTGCTGGA	TCAGCTTTGA	AAGCTCTAGA	AGGCGACGCT	250
40	TCATACGAAG	AAAAAATTCT	TGAATTAATG	GCTGCAGTTG	ACGAATACAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAGTTGTTG	GTATTGCTGA	450
	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
45	TAGACYACGC	TGAAGCTGGA	GACRACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCRT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
50	A					751

2) INFORMATION FOR SEQ ID NO: 609

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

10	CGGTGCGATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GCGWACCATA	CATCGTTGTT	100
	TTCTTGAACA	AAATGGATAT	GGTTGAYGAC	GAAGAATTGC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACC	TATTGTCTGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCCCTGT	AATCGCCGGT	TCTGCTTTGA	AAGCTCTTGA	AGGAGATCCT	250
15	TCATACGAAG	AAAAAATCAT	GGAATTGATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	ATTTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	GAAATCGTTG	GTATTGCTGA	450
	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
20	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACRAT	600
	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	TTATGTTTTG	ACAAAAGAAG	650
	AAGGTGGRCG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTTT	GAATTACCAG	AAGGAACTGA	750
25	A					751

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 891 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Haemophilus influenzae* Rd
(B) STRAIN: KW20
(C) ACCESSION NUMBER: extracted from U32739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

45	AATATGATTA	CTGGTGCGGC	ACAAATGGAT	GGTGCTATTT	TAGTAGTAGC	50
	AGCAACAGAT	GGTCCTATGC	CACAAACTCG	TGAACACATC	TTATTAGGTC	100
	GCCAAGTAGG	TGTTCCATAC	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	150
	GTAGATGACG	AAGAGTTATT	AGAATTAGTC	GAAATGGAAG	TTCGTGAACT	200
50	TCTATCTCAA	TATGACTTCC	CAGGTGACGA	TACACCAATC	GTACGTGGTT	250
	CAGCATTACA	AGCGTTAAAC	GGCGTAGCAG	AATGGGAAGA	AAAAATCCTT	300
	GAGTTAGCAA	ACCACTTAGA	TACTTACATC	CCAGAACCAG	AACGTGCGAT	350
	TGACCAACCG	TTCTTCTTTC	CAATCGAAGA	TGTGTTCTCA	ATCTCAGGTC	400
	GTGGTACTGT	AGTAACAGGT	CGTGTAAGAC	GAGGTATTAT	CCGTACAGGT	450
55	GATGAAGTAG	AAATCGTCGG	TATCAAAGAT	ACAGCGAAAA	CTACTGTAAC	500
	GGGTGTTGAA	ATGTTCCGTA	AATTACTTGA	CGAAGGTCGT	GCAGGTGAAA	550
	ACATCGGTGC	ATTATTACGT	GGTACCAAAC	GTGAAGAAAT	CGAACGTGGT	600
	CAAGTATTAG	CGAAACCAGG	TTCAATCACA	CCACACACTG	ACTTCGAATC	650
	AGAAGTGTAC	GTATTATCAA	AAGATGAAGG	TGGTCGTCAT	ACTCCATTCT	700
60	TCAAAGGTTA	CCGTCCACAA	TTCTATTTCC	TACAACAGA	CGTGACTGGT	750

ACAATCGAAT	TACCAGAAGG	CGTGGAATG	GTAATGCCAG	GCGATAACAT	800
CAAGATGACA	GTAAGCTTAA	TCCACCCAAT	TGCGATGGAT	CAAGGTTTAC	850
GTTCGCAAT	CCGTGAAGGT	GGCCGTACAG	TAGGTGCAGG	C	891

5

2) INFORMATION FOR SEQ ID NO: 611

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

CGGCGGTATC	TTAGTTGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
TTCTTAAACA	AAGTTGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
TGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
ATGTACCTGT	AATCGCTGGT	TCTGCATTAA	AAGCATTAGA	AGGCGATGCT	250
GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCAGTTG	ATGATTACAT	300
TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTATGCACGA	450
AACTTCTAAA	ACAAGTGTTA	CTGGTGTAGA	AATGTCCGT	AAATTATTAG	500
ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCA	550
CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCTATTAC	600
ACCACACACA	AAATTCAAAG	CTGAAGTATA	CGTATTATCT	AAAGATGAAG	650
GTGGACGTCA	CACTCCATTTC	TTCACATACT	ATCGCCCCACA	ATTCTATTTC	700
CGTACTACTG	ACGTAACCTG	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
TCGCTATCGA	AGACGGAA				818

40

2) INFORMATION FOR SEQ ID NO: 612

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

60	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
----	------------	------------	------------	------------	------------	----

	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
5	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCTTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGAGAAC	400
	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
10	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
15	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTC			825

20 2) INFORMATION FOR SEQ ID NO: 613

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 778 bases
	(B) TYPE: Nucleic acid
25	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Serratia ficaria</i>
	(B) STRAIN: ATCC 33105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

35	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCTTTC	ATCATCGTRT	100
	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	GCTGTCCGCT	TACGACTTCC	CTGGCGATGA	200
40	CCTGCCGGTG	ATTGCGGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	TAAAATCATC	GAGCTGGCTG	AMCMSCTGGA	TACTTACATC	300
	CCAGAACCAG	AGCGCGCTAT	CGACAAGCCG	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	GTTTACCGGT	CGTGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
45	ACCGTCAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCCATCAAG	600
	CCGCACACCC	AGTTCGATTC	AGAAGTGATC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACKCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
50	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCTG	GCGACAACGT	GAACATGA			778

55 2) INFORMATION FOR SEQ ID NO: 614

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 653 bases
	(B) TYPE: Nucleic acid
60	(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus malodoratus*

(B) STRAIN: ATCC 43197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

```

10 GTGCGATCTT AGTAGTATCA GCTACTGATG GTCCAATGCC TCAAACCTCGT      50
   GAACACATTT TGTTATCACG TCAAGTTGGT GTTAAGCACT TGATCGTTTT      100
   CTTGAACAAA GTAGATTTAG TTGATGACGA AGAATTGATC GACTTAGTTG      150
   AAATGGAAGT ACGTGAATTA CTTTCTGAAT ATGGTTTCCC AGGTGATGAT      200
15 ATTCCAGTGC TTAAAGGTTT TGCTTTGAAA GCATTAGAAG GCGATCCAGA      250
   ACAAGAACAA GTTATTCTTG ATTTGATGGA TACCGTTGAT GAATATATCC      300
   CAACACCTGA ACGTGACAAT GACAAACCGT TCTTGTTACC AGTTGAGGAT      350
   GTTTTCTCGA TCACAGGACG TGGTACTGTA GCTTCTGGTC GTATCGACCG      400
   TGGCGAAGTT AAAGTCGGCG ATGAAATTGA AATCATCGGG ATCAAACCTG      450
20 AAGTTCAAAA AGCAATCGTT ACTGGACTTG AAATGTTCCG TAAACATTG      500
   GATTATGGTG AAGCTGGCGA TAACGTTGGG GTTCTATTAC GTGGGATTAC      550
   ACGTGATGAA ATCGAACGTG GCCAAGTATT AGCTAAACCA GGTTCAATCA      600
   CACCACATAC TAAGTTCAAA GCCGAAGTAT ATGTGTTGAC GAAAGAAGAA      650
   GGT
25

```

2) INFORMATION FOR SEQ ID NO: 615

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus durans*

40 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

```

45 CCATTCTAGT TGTATCTGCA ACAGATGGAC CAATGCCACA AACACGTGAA      50
   CATATTTTAT TGTCACGTCA AGTAGGTGTT AAATATTTGA TCGTCTTCTT      100
   GAACAAAATC GACTTAGTAG ATGATGAAGA ATTGATTGAT CTTGTGCGAA      150
   TGGAAAGTTCG TGAATTATTA AGCGAATATG GTTCCCAGG TGACGATACA      200
   CCAGTCATCA AAGGTTTCAGC ATTAAGAGCT TTACAAGGAG ATCCTGATGC      250
   AGAAGCAGCT ATCATGGAAT TGATGGATAC TGTTGATGAA TATATCCCAA      300
50 CACCAGAACG TGATACAGAC AAACCATTAT TGTTACCAGT GGAAGATGTC      350
   TTCTCAATCA CAGGTCGTGG GACTGTTGCT TCAGGTCGTA TCGATCGTGG      400
   TGCAGTTCGT GTAGGTGATG AAATCGAAAT CGTCGGTATC AAACCTGAAA      450
   CACAAAAGC TGTGTAACT GGGGTCGAAA TGTTCCGCAA GACATTAGAC      500
   TATGGTGAAG CAGGAGATAA CGTTGGGGTA TTGTTACGTG GTATCCAACG      550
55 TGAAGATATC GAACGTGGAC AAGTAATCGC AAAACCAGGT TCAATCACAC      600
   CACATACAAA ATTCAAAGCA GAAGTGACG TATTGACAAA AGAAGAAGGT      650
   GGACGTCATA CACCATTCTT CAATAACTAT CGTCCACAAT TCTACTCCG      700
   TACAACCTGAC GTAACCTGAA CAATCGTTTT ACCTGGAGGC ACTGAAATGG      750
   TTATGCCTGG AGATAACGTA ACGATCGACG TTGAATTGAT CCATCCAGTT      800
60 GCCATCGAAA ACGGAACAAC TTTCTCTAT      829

```

2) INFORMATION FOR SEQ ID NO: 616

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
 (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

20	GGTGCAATTT TAGTAGTATC TGCTACTGAT GGCCCAATGC CACAAACACG	50
	TGAACATATC TTGTTATCAC GTCAAGTAGG GGTTAAACAC TTAATCGTCT	100
	TCTTGAACAA AGTTGATTTA GTTGATGATG AAGAATTGAT CGATTTAGTT	150
	GAAATGGAAG TTCGGGAATT GCTTCTGAA TATGGTTTCC CAGGCGATGA	200
	TATTCCAGTA CTTAAAGGTT CTGCTTTGAA AGCTTTAGAA GGCGATCCTG	250
25	AACAAGAACA AGTAATCCTT GACTTGATGG ATACGGTTGA TGAATACATC	300
	CCAACGCCTG AACGTGATAC TGACAAACCA TTCTTGTTAC CAGTCGAAGA	350
	TGTCTTCTCA ATCACAGGAC GTGGTACGGT TGCATCTGGT CGTATCGATC	400
	GTGGGGAAGT TAAAGTCGGT GATGAAGTTG AAATCATCGG GATCAAACCT	450
	GAAGTGCAAA AAGCTGTCGT AACTGGACTA GAAATGTTCC GTAAGACATT	500
30	GGATTACGGT GAAGCTGGCG ATAACGTTGG GGTTCATTA CGTGGGATTA	550
	CTCGTGATGA AATCGAACGT GGACAAGTAT TAGCTAAACC AGGTTCAATC	600
	ACTCCACATA CGAAATTCAG TGCAGAAGTT TATGTATTGA CGAAAGAAGA	650
	AGGTGGCCGT CATACGCCA	669

35

2) INFORMATION FOR SEQ ID NO: 617

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

	CGGGGCAATT TTAGTTGTAT CTGCAACTGA TGGCCCAATG CCACAAACAC	50
	GTGAACACAT TTTGTTAGCT CGTCAAGTAG GGGTTAAATA TTAAATCGTC	100
55	TTCTTGAACA AAACAGATTT AGTTGATGAT GAAGAATTAT TGGAAGTAGT	150
	TGAAATGGAA GTTCGTGAAT TATTAAATGA ATACAATTTC CCTGGCGATG	200
	ATATTCCTGT TATTCGCGGA TCTGCTTTAA AAGCATTAGA AGGCGATCCA	250
	GAACAAGAAG AAGTAATTAT GAACTTGATG GATACTGTGG ATGAATATAT	300
	CCCAACTCCA GAACGTGACA ATGATAAACC ATTCTTGTTA CCAGTGGAAG	350
60	ATGTCTTCAC AATTACTGGT CGTGGTACTG TTGCTTCAGG TCGTATCGAC	400

	CGTGGTAAAG	TCAACGTTGG	TGATGAAATT	GAAATTATCG	GAATTAAACC	450
	AGAAACACAA	AAAGCTGTTG	TAACCGGTTT	GGAAATGTTT	CGTAAAACTT	500
	TGGATTATGG	TGAAGCTGGT	GATAACGTTG	GGGTCTTATT	ACGTGGGATT	550
	ACTCGTGATG	AAGTAGAACG	TGGTCAAGTA	TTAGCAAAAC	CAGGTTCCAT	600
5	TACACCGCAT	ACCAAATTTA	AAGGTGAAGT	TTATATCTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCT	TTCTTTAATA	ACTATCGTCC	TCAATTTTAT	700
	TTCCGTACAA	CTGATGTGAC	TGGTAACATC	GCATTACCTG	AAGGAACTGA	750
	AATGGTAATG	CCTGGTGATA	ATGTAACAAT	TGAAGTTGAA	TTGATTCATC	800
	CAATCGCCGT	TGAAAAAGGG	ACTACTTTCT	CAATT		835

10

2) INFORMATION FOR SEQ ID NO: 618

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 673 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus avium*
 - (B) STRAIN: ATCC 14025
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

	GGTGCAATCC	TAGTAGTATC	AGCTACTGAT	GGTCCAATGC	CGCAAACACG	50
30	TGAACATATT	TTGCTATCAC	GGCAAGTGGG	TGTTAAACAC	TTAATCGTAT	100
	TTTTAAACAA	AGTTGATTTA	GTCGATGATG	AAGAAATGAT	CGATCTAGTT	150
	GAAATGGAAG	TCCGTGAATT	ACTTTCTGAA	TATGGTTTCC	CAGGTGACGA	200
	TATTCCAGTT	CTCAAAGGTT	CAGCTTTGAA	AGCATTAGAA	GGCGATCCTG	250
	AACAAGAACA	AGTAATCCTT	GATTTAATGG	ATACAGTTGA	CGAATATATC	300
35	CCAACTCCAG	AACGTGACAC	TGACAAGCCA	TTCTTGTTAC	CAGTCGAAGA	350
	TGTATTTTCT	ATCACTGGTC	GTGGGACTGT	AGCGTCTGGA	CGGATTGATC	400
	GTGGTGAAAGT	TAAAGTCGGC	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
	GAAATTCAAA	AAGCAGTCGT	AACTGGACTT	GAAATGTTCC	GTAAAACCTT	500
	AGATTATGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCATTAT	CGTGGGATTA	550
40	CACGTGATGA	AATCGAACGT	GGTCAAGTCT	TAGCTAAACC	AGGTTCAATC	600
	ACACCACATA	CAAAATTCAG	TGCAGAAGTT	TACGTATTGA	CGAAAGAAGA	650
	AGGTGGACGT	CATACACCAT	CTT			673

45

2) INFORMATION FOR SEQ ID NO: 619

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1713 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 55 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Saccharomyces cerevisiae*
 - (C) ACCESSION NUMBER: K00428
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

```

TTTCATATTT TTAAGGATTT TGTTTTAGCA CCCATCCGAC CTCAGTCAAT 50
ATATCCTTTT GCGACCAGGC TTTCTCCCT TTTGCTGCTA ACTGGTTACA 100
GATTTTCCCTA TTTTGGTCA TTTTATCTT TGAACTGAT TAAGCTGAAA 150
5 AAATTTGAGC TTCTTTGTTG TAAACTATTT TGTGCTTTCA GTTTTATTCT 200
AGCTCGACAA AGGTAACAGA CAAAATGTC AGCTTTATTA CCAAGATTAC 250
TCACAAGAAC AGCTTTTAAA GCTTCTGGGA AACTTCTGAG GCTCTCTTCA 300
GTAATTTCTA GGACCTTTTC TCAAACACT ACTTCCTATG CAGCTGCTTT 350
TGATCGTTCC AAACCGCATG TAAATATAGG TACGATCGGC CATGTTGATC 400
10 ATGGGAAGAC AACTTTAACC GCAGCCATTA CGAAAACGTT AGCCGCAAAA 450
GGTGGTGCCA ACTTCTTGGA CTATGCTGCC ATCGATAAGG CTCCGGAAGA 500
AAGAGCTCGT GGTATTACAA TTTCTACTGC ACACGTGGAA TACGAAACGG 550
CCAAGAGACA TTATTCTCAC GTCGACTGTC CAGGCCACGC TGATTACATC 600
AAGAATATGA TTACCGGTGC TGCTCAAATG GATGGTGCTA TCATTGTTGT 650
15 AGCTGCTACC GATGGACAAA TGCCCCAAC TAGAGAACAT TTTCTTTGG 700
CCAGACAAGT TGGTGTCCAA CATATTGTCG TTTTGTGTTA CAAGGTTGAT 750
ACCATTGATG ATCCAGAAAT GTTAGAGTTA GTCGAAATGG AAATGAGAGA 800
ACTTTTAAAC GAATATGGGT TTGACGGTGA TAATGCTCCA ATTATCATGG 850
GTTCTGCCCT TTGCGCTTTG GAAGGTCGCC AACCTGAAAT TGGGGAGCAG 900
20 GCCATCATGA AACTTTTGA TGCAGTGGAT GAGTATATTC CTACACCTGA 950
AAGAGATTTG AACAAGCCTT TCTTGATGCC CGTTGAAGAT ATCTTCTCTA 1000
TCTCCGGTAG AGGTACTGTG GTCACTGGTC GTGTGGAAAG GGGTAATTTA 1050
AAGAAAGGTG AGGAATTGGA AATTGTTGGT CACAACCTCA CCCCATTGAA 1100
AACACAGTT ACTGGTATTG AAATGTTTAG AAAGGAATTG GACTCTGCTA 1150
25 TGGCAGGTGA CAATGCCGGT GTTTTACTTA GAGGTATCAG GAGAGATCAA 1200
TTGAAGAGAG GTATGGTCTT AGCTAAGCCA GGTACCGTTA AAGCCCATAC 1250
AAAGATTCTA GCCTCTTTGT ACATTTTATC CAAAGAGGAA GGTGGTAGAC 1300
ATTCTGGGTT TGGTGAAAAC TACAGACCAC AAATGTTTAT AAGAACAGCT 1350
GATGTTACAG TTGTGATGAG ATTTCCCTAAG GAGGTTGAAG ATCATTCTAT 1400
30 GCAAGTTATG CCAGGTGACA ATGTTGAAAT GGAATGTGAT TTGATCCATC 1450
CTACCCCATT AGAAGTTGGT CAACGTTTCA ATATCAGAGA GGGTGGAAGA 1500
ACTGTTGGTA CCGGTCTAAT CACACGTATT ATTGAATAGA CTTATTGATG 1550
CAACTGGAGT ATATTTCTAT ATATTCTGTT CATTTCCCCT CTCATAATAT 1600
ATACTTGTTT CGTTAAAATT TTATACGTGT AAATAAAGTG CCATAAATTT 1650
35 TTCAGCTTTA CTTTTGGTAG AGTCCTGCTA GCACTAGATT TTACAATTTT 1700
ATGTGCACAC ACC 1713

```

40 2) INFORMATION FOR SEQ ID NO: 620

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

ATTGGTGCAT TGCTACGT

18

55 2) INFORMATION FOR SEQ ID NO: 621

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 751 bases
(B) TYPE: Nucleic acid

563

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: ATCC 19434

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

	TGGTGCATC	TTAGTTGTTT	CTGCAACTGA	CGGTCCGATG	CCTCAAACAC	50
	GTGAACACAT	TTTATTGTCA	CGCCAAGTTG	GTGTAAAATA	CCTGATTGTT	100
	TTCTTGAACA	AAGTTGATTT	AGTCGATGAT	GAAGAATTGA	TCGATTGTTG	150
15	AGAAATGGAA	GTTCGCGAGT	TATTGAGCGA	ATATGGTTTC	CCAGGCGATG	200
	ACACTCCTGT	GATCAAAGGT	TCCGCATTAA	AAGCATTGCA	AGGCGATCCA	250
	GATGCTGAAG	CTGCTATTAT	GGAATTGATG	GATACAGTAG	ATGAATATAT	300
	CCCAACACCA	GAACGTGATA	CAGATAAACC	ATTACTATTG	CCAGTGGAAG	350
	ACGTCTTCTC	AATTACAGGT	CGAGGAACTG	TTGCCTCAGG	TCGTATTGAT	400
20	CGTGGTGCTG	TTCGTGTCGG	TGATGAGGTA	GAGATCGTAG	GGATCAAACC	450
	TGAAACACAA	AAAGCAGTTG	TAACAGGTGT	AGAAATGTTC	CGTAAAACGT	500
	TAGATTACGG	GGAAGCTGGG	GATAACGTAG	GCGTGTGTTT	ACGGGGGATC	550
	CAACGTGACG	ATATCGAACG	TGGACAAGTA	CTTGCTAAAC	CAGGTTCCAT	600
	TACTCCACAT	ACAAAATTCA	AAGCAGAAGT	GTACGTGTTG	ACAAAAGAAG	650
25	AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTATCGTCC	ACAGTTCTAC	700
	TTCCGCACAA	CTGATGTTAC	AGGAACAATC	ACATTGCCAG	AAGATACAGA	750
	A					751

30

-2) INFORMATION FOR SEQ ID NO: 622

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 750 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*
(B) STRAIN: ATCC 13264

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

	GTCAAATGGG	ACGAATCCAG	ATTCCAAGAA	ATTGTCAAGG	AAACCTCCAA	50
	CTTTATCAAG	AAGGTTGGTT	ACAACCCAAA	GACTGTTCCA	TTCGTCCCAA	100
	TCTCTGGTTG	GAACGGTGAC	AACATGATTG	AAGCTACCAC	CAACGCTCCA	150
50	TGGTACAAGG	GTTGGGAAAA	GGAAACCAAG	GCCGGTGTCT	TCAAGGGTAA	200
	GACTTTGTTG	GAAGCCATTG	ACGCCATTGA	ACAACCATCT	AGACCAACTG	250
	ACAAGCCATT	GAGATTGCCA	TTGCAAGATG	TTTACAAGAT	TGGTGGTATT	300
	GGTACTGTGC	CAGTCGGTAG	AGTTGAAACC	GGTGTTCATC	AGCCAGGTAT	350
	GGTTGTTACT	TTCGCCCCAG	CTGGTGTTAC	CACTGAAGTC	AAGTCCGTTG	400
55	AAATGCATCA	CGAACAATTG	GAACAAGGTG	TTCCAGGTGA	CAACGTTGGT	450
	TTCAACGTCA	AGAACGTTTC	CGTTAAGGAA	ATCAGAAGAG	GTAACGTCTG	500
	TGGTGACGCT	AAGAACGATC	CACCAAAGGG	TTGCGCTTCT	TTCAACGCTA	550
	CCGTCATTGT	TTTGAACCAT	CCAGGTCAAA	TCTCTGCTGG	TTACTCTCCA	600
	GTTTTGGATT	GTCACACTGC	TCACATTGCT	TGTAGATTCT	ACGAATTGTT	650
60	GGAAAAGAAC	GACAGAAGAT	CTGGTAAGAA	GTTGGAAGAC	CATCCAAAGT	700

TCTTGAAGTC CGGTGACGCT GCTTTGGTCA AGTTCGTTCC ATCTAAGCCA

750

5 2) INFORMATION FOR SEQ ID NO:623

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

20 TCTTGAAAGC TTAAGGCCGA GCGAGAGCGA GGTATCACCA TCGACATTGC 50
 TCTTTGGAAG TTCGAGACCC CCAGGTACCA GGTACCGTC ATTGACGCCC 100
 CCGGTCACCG AGACTTCATC AAGAACATGA TCACCGGTAC CTCCAGGCT 150
 GACTGTGCCA TCCTCATCAT TGCCACCGGT ATCGGTGAGT TCGAGGCCGG 200
 25 TATCTCCAAG GACGGTCAGA CCCGAGAGCA CGCCTCCTC GCCTTCACCC 250
 TCGGTGTCAG GCAGCTCATT GTTGCTTGCA ACAAGATGGA CACCTGCAAG 300
 TGGTCCGAGG ACCGATTCAA CGAAATCGTC AAGGAGACCA ACGGTTTCAT 350
 CAAGAAGGTT GGTTACAACC CCAAGGCTGT CCCCTTCGTC CCCATCTCTG 400
 GTTGGCACGG TGACAACATG TTGGAGGAGA CCACCAAGTC AGTGAATCCG 450
 30 CTTCTACGTG ATGAGATGTT TTTCTGACTT TCCGTGCAGC ATGCCCTGGT 500
 ACAAGGGATG GACCAAGGAG ACCAAGTCTG GTGTTTCCAA GGGTAAGACC 550
 CTCCTCGAGG CCATCGACGC CATCGAGCCC CCTACCCGAC CCACCGACAA 600
 GCCCCTCCGT CTCCCTCTCC AGGACGTCTA CAAGATCGGT GGTATCGGCA 650
 CAGTCCCTGT CGGCCGAGTC GAGACCGGTG TCATCAAGGC CGGTATGTTG 700
 35 TCTCATCTCT CTGTCTCTGT AACATGCGTC TCGTAACATG CGCTTACTTC 750
 ATTTTCAGGT ATGGTCGTCA AGTTCGCCCC CACCAACGTC ACCACTGAAG 800
 TCAAGTCCGT TGAGATGCAC CACGAGCAGA TCCCGAGGG TCTTCCCGGA 850
 GACAACGTTG GTTTCAACGT CAAGAACGTT TCCATCAAGG ACATCCGACG 900
 AGGTAACGTC TGTGGTGACT CCAAGAACGA CCCCCTATG GAGGCTGCTT 950
 40 CTTTCAACGC CCAGGTTATC GTCCTTAACC ACCCTGGTCA GATCGGTGCC 1000
 GGTTACACCC CCGTTCTCGA CTGTCACTACT GCCCGTAAGC CTGACCCAAT 1050
 ACCTCCAACA TACCTTTGAA GCTGACCCTT TCTAGACATT GCCTGCAAGT 1100
 TTGCTGAGTT GATCGAGAAG ATTGACCGAC GAACCGGTAA GGTGATGGAG 1150
 GCCGCCCCCA AGTTCGTCAA GTCTGGTGAC GCCGCCATTG TCAAGCTTGT 1200
 45 TGCCCAAGAG CCCCTCTGTG TTGAGACCTA CGCCGACTAC CCCCCTCTTG 1250
 GTCGATTTCGC CGTCCGAGA 1269

50 2) INFORMATION FOR SEQ ID NO: 624

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

565

(A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 36801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

```

5      TCTGTCAAAT GGGACAAAAA CAGATTTGAA GAAATCATCA AGGAAACCTC      50
      CAACTTCGTC AAGAAGGTTG GTTACAACCC AAAGACTGTT CCATTCGTTC      100
      CAATCTCTGG TTGGAATGGT GACAACATGA TTGAACCATC CACCAACTGT      150
      CCATGGTACA AGGGTTGGGA AAAGGAAACC AAATCCGGTA AAGTTACTGG      200
10     TAAGACCTTG TTAGAAGCTA TTGACGCTAT TGAACCACCA ACCAGACCAA      250
      ATTGACAAACC ATTGAGATTG CCATTGCAAG ATGTTTACAA GATCGGTGGT      300
      ATTGGTACTG TGCCAGTCGG TAGAGTTGAA ACTGGTATCA TCAAAGCCGG      350
      TATGGTTGTT ACTTTCGCCC CAGCTGGTGT TACCACTGAA GTCAAATCCG      400
      TTGAAATGCA TCACGAACAA TTGGCTGAAG GTGTTCCAGG TGACAATGTT      450
15     GGTTCACACG TTAAGAACGT TTCCGTTAAA GAAATTAGAA GAGGTAACGT      500
      TTGTGGTGAC TCCAAGAACG ATCCACCAAA GGGTTGTGAC TCTTTCAATG      550
      CCCAAGTCAT TGTTTTGAAC CATCCAGGTC AAATCTCTGC TGGTTACTCT      600
      CCAGTCTTGG ATTGTCACCC TGCCCACATT GCTTGTAAT TCGACACTTT      650
      GGTTGAAAAG ATTGACAGAA GAACTGGTAA GAAATTGGAA GAAAATCCAA      700
20     AATTCGTCAA ATCCGGTGAT GCTGCTATCG TCAAGATGGT CCCAACCAAA      750
      CCA
  
```

25 2) INFORMATION FOR SEQ ID NO: 625

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

```

40     CGTTGAAGAC ACGACCCAAA GTATCC      26
  
```

2) INFORMATION FOR SEQ ID NO: 626

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

```

60     TACCACCTTT TAAGTAAGGT GCTAAT      26
  
```

2) INFORMATION FOR SEQ ID NO: 627

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627
ATTGTCTATA AAAATGGCGA TAAGTC 26

2) INFORMATION FOR SEQ ID NO: 628

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
30 (ii) MOLECULE TYPE: DNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628
AAAATGGCGA TAAGTCACAA AAAGTA 26

2) INFORMATION FOR SEQ ID NO: 629

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydia pneumoniae*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629
55 AAGTTCCATC TCAACAAGGT CAATA 25

2) INFORMATION FOR SEQ ID NO: 630

567

10

15

22

20

25

30

26

35

40

41

23

5

5

6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633

CAGACCAACY GAIAARCCIT TRAGAT

26

5

2) INFORMATION FOR SEQ ID NO: 634

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRRCIATTGC YATGGA

26

20

2) INFORMATION FOR SEQ ID NO: 635

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635

AAACCRGTIA RRGCRCTCT IGCTCT

26

35

2) INFORMATION FOR SEQ ID NO: 636

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636

ACTGGYGTTG AIATGTTCCG YAA

23

50

2) INFORMATION FOR SEQ ID NO: 637

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637

ACGTCAGTIG TACGGAARTA GAA 23

10

2) INFORMATION FOR SEQ ID NO: 638

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638

CCAATGCCAC AAACICGTGA RCACAT 26

25

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTCWACAC CWGTIACA 28

40

2) INFORMATION FOR SEQ ID NO: 640

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

55 TCCATGGTIT WYGGICARAT GAA 23

60 2) INFORMATION FOR SEQ ID NO: 641

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

TGATAACCWA CIGCIGAIGG CATACG

26

2) INFORMATION FOR SEQ ID NO: 642

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642

GGCGTIGGIG ARCGIACICG TGA

23

2) INFORMATION FOR SEQ ID NO: 643

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643

ACTGGIGTIG ARATGTTCCG YAA

23

2) INFORMATION FOR SEQ ID NO: 644

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644

ACGTCIGTIG TICKGAARTA GAA

23

2) INFORMATION FOR SEQ ID NO: 645

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645
15 ACGTCIGTIG TICKGAARTA RAA 23

2) INFORMATION FOR SEQ ID NO: 646

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646
30 ATCGACAAGC CITTCYTIAT GSC 23

2) INFORMATION FOR SEQ ID NO: 647

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647
ACGTCCGTSG TRCGGAAGTA GAACTG 26

2) INFORMATION FOR SEQ ID NO: 648

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648

ACGTCSGTSG TRCGGAAGTA GAACTG

26

5

2) INFORMATION FOR SEQ ID NO: 649

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

20 GTCCTATGCC TCARACWCGI GAGCAC

26

20

2) INFORMATION FOR SEQ ID NO: 650

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650

35 TTACGGAACA TYTCAACACC IGT

23

35

2) INFORMATION FOR SEQ ID NO: 651

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651

50

TGACGACCAC CITCYTCYTT YTTCA

25

55 2) INFORMATION FOR SEQ ID NO: 652

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Single

573

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652

CCWAYAGTIY KICCCICCYTC YCTIATA

27

10

2) INFORMATION FOR SEQ ID NO: 653

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

15

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

GAYTTCATIA ARAAYATGAT

20

25

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG

20

40

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA

20

55

2) INFORMATION FOR SEQ ID NO: 656

60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

AATTAATGGC TGCAGTTGAY GA

22

2) INFORMATION FOR SEQ ID NO: 657

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657

TTGTCCACGT TCGATRTCTT CA

22

2) INFORMATION FOR SEQ ID NO: 658

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658

GATYTAGTCG ATGATGAAGA ATT

23

2) INFORMATION FOR SEQ ID NO: 659

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659

GCTTTTTGIG TTTCWGGTTT RAT

23

2) INFORMATION FOR SEQ ID NO: 660

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660

15 GTAGAATTGA GGACGGTAGT TAG 23

2) INFORMATION FOR SEQ ID NO: 661

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661

30 GTAGAAATGT GGWCGATART TRT 23

2) INFORMATION FOR SEQ ID NO: 662

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

50 CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC 50
 GTGAGCACGT TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT 100
 GCTCTGAACA AGTGCGACAT GGTTGATGAT GAGGAAATCA TCGAGCTCGT 150
 CGAGATGGAG ATCCRTGAGC TGCTCGCTGA GCAGGATTAC GACGAAGAGG 200
 55 CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG CGACGAGAAG 250
 TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC 300
 AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA 350
 TCTTCACCAT CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT 400
 GGCTCCCTGA AGGTCAACGA GGACGTCGAG ATCATCGGTA TCCGCGAGAA 450
 60 KGCTACCACC ACCACCGTTA CCGGTATCGA GATGTTCCGT AAGCTTCTCG 500

```

ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG TGGCGTTAAG 550
CGCGAAGACG TTGAGCGTGG CCAGGTGTGT GTTAAGCCAG GCGCTTACAC 600
CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCGTGTCC AAGGACGAGG 650
GTGGCCGCCA CACCCCATTC TTCGACAACT ACCGCCCACA GTTCTACTTC 700
5 CGCACCACCG ACGTTACCGG TGTTGTGAAG CTTCTGAGG GCACCGAGAT 750
GGTCATGCCT GCGGACAACG TCGACATGTC CGTCACCCTG ATCCAGCCTG 800
TCGCTATGGA TGAGGGCCTG CGCTTCGCTA TC 832

```

10

2) INFORMATION FOR SEQ ID NO: 663

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1192 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
- (B) STRAIN: ATCC 10565

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

```

AACGGCGAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA 50
CACCGTGCGT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA 100
CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT 150
30 ACCTTGGGCC GGATCATCAA CGTTGTCCGT GAGCCCATCG ACGAGCGTGG 200
TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT 250
TCACCGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT 300
GTCGACTTGT TGGCTCCCTA CGCCCGTGGT GGTAAGATTG GTCTTTTCGG 350
TGGTGCCGGT GTCGGTAAGA CCGTGTTTAT CCAGGAGTTG ATTAACAACA 400
35 TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CCGTGAGCGT 450
ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT 500
CAACTTGAGG GGCAGACTCA AGGTGGCCTT GGTGTTCCGT CAGATGAACG 550
AGCCCCCGGG GGCTCGTGCC CGTGTCGCCT TGACCGGTTT GACCATTGCC 600
GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA 650
40 CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC 700
GTATCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT 750
TTGTTGCAGG AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT 800
GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCGCCA 850
CCACTTTCGC TCACTTGGAC GCCACCACCG TGTTGTCGCG TGGTATCTCC 900
45 GAGTTGGGTA TCTACCCCGC CGTCGACCCC TTGGACTCCA AGTCGAGATT 950
GTTGGACGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG 1000
TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT 1050
TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC 1100
CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTGCTGTC GCCGAGGTTT 1150
50 TCACTGGTAT CCCCGGTAGA TTGGTGAGAT TGCAGGACAC CG 1192

```

55

2) INFORMATION FOR SEQ ID NO: 664

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

5

AAYATGATIA CIGGIGCIGC ICARATGGA

29

10 2) INFORMATION FOR SEQ ID NO: 665

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(C) ACCESSION NUMBER: extracted from X00779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

25 ATGGGTAAAG AGAAGTCTCA CATTAAACGTT GTCGTTATCG GTCATGTCTGA 50
 TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA 100
 TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT 150
 AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG 200
 30 AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA 250
 AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG 300
 AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC 350
 TGGTGGTGTG GGTGAATTCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA 400
 GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT 450
 35 GCTGTCAACA AGATGGACTC CGTCAAAATGG GACGAATCCA GATTCCAAGA 500
 AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA 550
 AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT 600
 GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGGGAAA AGGAAACCAA 650
 GGCCGGTGTG GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG 700
 40 AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT 750
 GTTTACAAGA TTGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC 800
 CCGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTTGCCCCA GCTGGTGTGA 850
 CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT 900
 GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA 950
 45 AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG 1000
 GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA 1050
 ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC 1100
 TTGTAGATTG GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA 1150
 AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC 1200
 50 AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC 1250
 ACCATTAGGT AGATTCGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCTG 1300
 GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG 1350
 GCTGCTCAAA AGGCTGCTAA GAAATAA 1377

55

2) INFORMATION FOR SEQ ID NO: 666

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 1536 bases

578

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: extracted from M12082

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

	ATGGTTTTGC	CAAGACTATA	TACTGCTACA	TCCCGTGCTG	CTTTTAAAGC	50
	AGCCAAACAA	TCCGCTCCGC	TTCTATCCAC	TTCGTGGA	AGATGTATGG	100
15	CCTCAGCTGC	TCAATCTACT	CCAATCACCG	GTAAAGTTAC	CGCTGTCATT	150
	GGTGCCATTG	TTGACGTTCA	TTTTGAACAA	TCAGAGTTGC	CCGCTATTTT	200
	GAACGCTTTA	GAAATTAAAA	CACCTCAAGG	TAAGTTGGTT	TTGGAAGTTG	250
	CTCAACATTT	GGGTGAAAAC	ACTGTCAGAA	CCATTGCTAT	GGATGGTACC	300
	GAAGGTTTGG	TCCGTGGTGA	AAAGGTTCTT	GACACTGGTG	GCCCTATCTC	350
20	CGTCCCAGTT	GGGAGAGAAA	CTTTAGGGAG	AATCATCAAC	GTTATCGGTG	400
	AACCTATTGA	TGAAAGAGGT	CCAATTAAGT	CCAAACTAAG	AAAGCCAATT	450
	CACGCAGACC	CTCCTAGTTT	TGCAGAACAA	TCTACTTCGG	CTGAAATTTT	500
	GGAACAGGT	ATCAAAGTCG	TCGATCTATT	AGCTCCTTAT	GCCAGAGGTG	550
	GTAAGATTGG	TCTTTTCGGT	GGTGCAGGTG	TCGGTAAGAC	TGTGTTTCATT	600
25	CAAGAATTGA	TTAACAATAT	CGCCAAGGCC	CATGGTGGTT	TTTCCGTTTT	650
	CGCCGGTGT	GGTGAAAGGA	CCAGAGAGGG	TAATGACTTG	TACCGTGAAA	700
	TGAAGGAAAC	TGGAGTCATT	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	750
	GTTTTTCGGTC	AAATGAACGA	ACCTCCAGGA	GCCAGAGCCA	GAGTCGCTTT	800
	AACTGGTTTG	ACGATCGCTG	AATATTTTCTAG	AGATGAAGAA	GGTCAAGACG	850
30	TCTTGTGTGTT	TATCGACAAT	ATCTTTTAGAT	TTACTCAAGC	TGGTTCAGAA	900
	GTCTGTGCCC	TTTTTGGGTCG	TATTCATCT	GCCGTCGGTT	ATCAACCAAC	950
	TTTGGCCACT	GATATGGGTC	TCTTACAAGA	AAGAATTACC	ACCACAAAGA	1000
	AGGGTTCTGT	CACTTCTGTG	CAAGCCGTTT	ATGTTCCAGC	CGATGATTTA	1050
	ACAGATCCGT	TCCCGTCCAC	ATCTTTTGCC	CATTTGGACG	CATCATCCGT	1100
35	CTTGTCAGAA	GGTATTTTCAG	AATTAGGTAT	TTACCCTGCA	GTGGATCCAT	1150
	TGGATTCTAA	ATCAAGGTTA	TTGGATGCCG	CCGTTGTCGG	TCAAGAACAT	1200
	TATGACGTCG	CCTCCAAGGT	TCAAGAACT	TTACAGACCT	ATAAATCTTT	1250
	ACAAGATATC	ATTGCTATTT	TGGGTATGGA	TGAATTGTCC	GAACAAGATA	1300
	AACTAACTGT	CGAAAGGGCA	AGAAAGATTC	AAAGATTCTT	ATCTCAACCA	1350
40	TTTGCTGTGCG	CCGAAGTCTT	TACTGGTATC	CCAGGTAAAT	TAGTGAGATT	1400
	AAAGGACACC	GTTGCCTCGT	TCAAAGCCGT	TTTGGAAGGT	AAATACGATA	1450
	ATATACCAGA	ACATGCTTTC	TATATGGTTG	GTGGTATTGA	AGATGTTGTT	1500
	CGTAAAGCTG	AAAAGTTAGC	CCGTGAAGCC	AACTAG		1536

45

2) INFORMATION FOR SEQ ID NO: 667

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: Y

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

	CGGAAGGCGT	GCCGCCGGTG	TTAACTGCTT	TGGATGTGGT	GGAAAACTT	50
	GGCCGTGACG	AGCCCTTGAC	ACTTGAAATT	GTACAGCACT	TGGACGCCCCA	100
5	CACCGGCCGT	TGCATTGCCA	TGCAGACGAC	AGATCTGCTT	AAGCTGAAAT	150
	CGAAGGTAAGT	CTCGAGTGGC	GGGAACATTT	CTGTGCCTGT	GGGTCTGGGAG	200
	ACACTTGGCA	GAATCTTCAA	TGTGCTGGGC	GATGCCATTG	ACCAGCGCGG	250
	CCATGTTGGA	GAGAAGCAAC	GCATGCCTAT	TCACGCTGTG	GCACCAAAGT	300
	TGGCGGATCA	GGCGGCAGAG	GACACCATTG	TCACAACGGG	TATCAAGGTG	350
10	ATTGATCTGA	TTTTGCCCTA	CTGCAAGGGT	GGGAAGATTG	GTCTTTTGG	400
	TGGTGTGGC	GTGGGCAAGA	CGGTTATTAT	CATGGAACTT	ATTAACAACG	450
	TTGCCAAGGG	CCATGGTGGG	TTCTCCGTCT	TTGCGGGTGT	TGGTGAACGC	500
	ACGCGTGAGG	GGACGGATCT	TTACCTGGAG	ATGATGCAAT	CCAAAGTTAT	550
	TGACCTGAAG	GGTGACTCGA	AGTGTGTGTT	GGTGTATGGT	CAGATGAACG	600
15	AGCCTCCGGG	TGCCCGTGCT	CGTGTGGCGC	AGTCTGCCTT	GACAATGGCC	650
	GAGTACTTCC	GTGATGTGGA	AGGGCAAGAC	TGTGTGCTTT	TTATCGACAA	700
	CATTTTCCGC	TTTACGCAGG	CAAACTCTGA	GGTGTGAGCG	CTGTTGGGTC	750
	GTATTCCCGC	TGCCGTGCGC	TACCAGCCTA	CCCTTGCTGA	GGATCTTGGG	800
	CAGTTGCAGG	AGCGCATTAC	GTCCACGACA	AAAGGTTCCA	TTACCTCTGT	850
20	GCAGGCTGTG	TACGTGCCAG	CCGATGATAT	TACCGACCCT	GCGCCAGCAA	900
	CGACCTTTTC	CCACCTCGAT	GCCACGACGG	TGCTGGACCG	TGCCGTTGCC	950
	GAATCCGGCA	TTTACCCCGC	TGTCAACCCA	CTGGAGTGTG	CCTCGCGTAT	1000
	CATGGACCCG	GATGTAATCA	GCGTTGACCA	CTACAACGTG	GCGCAGGATG	1050
	TGGTGCAGAT	GCTTACCAAG	TACAAGGAGC	TGCAGGATAT	CATTGCGGTG	1100
25	CTTGGCATTG	ATGAGCTCAG	TGAGGAGGAT	AAACTTATCG	TGGACCGTGC	1150
	GCGTAAGGTG	ACAAAGTTTC	TCTCCCAGCC	TTTCCAGGTG	GCGGAGGTGT	1200
	TTACTGGCAT	GACAGGCCAC	TACGTGCAGC	TGGAGGAGAC	CATTGAGTCT	1250
	TTTTCCGGCC	TGTTGATGGG	CACATATGAT	CAGGTGCCCG	AGA	1293

30

2) INFORMATION FOR SEQ ID NO: 668

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1191 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium glutamicum*
 (C) ACCESSION NUMBER: X77034

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

	GTGGCAAAGG	CGAAGTTCGA	GCGTACCAAG	CCCCACGTAA	ACATCGGCAC	50
	CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCG	GCTATCACCA	100
50	AGGTTCTGGC	TGACACTTAC	CCTGAGCTCA	ACGAGGCTTT	CGCCTTCGAC	150
	TCCATCGATA	AGGCTCCTGA	GGAGAAGGAG	CGTGGCATCA	CGATCAACAT	200
	CTCCACCGTT	GAGTACCAGA	CTGAAAAGCG	CCACTACGCA	CACGTTGACG	250
	CTCCAGGCCA	CGCCGACTAC	ATCAAGAACA	TGATTACCGG	CGCTGCTCAG	300
	ATGGACGGCG	CAATCCTCGT	TGTTGCTGCT	ACCGACGGCC	CAATGCCTCA	350
55	GACCCGTGAG	CACGTTCTTC	TTGCTCGCCA	GGTTGGCGTT	CCTTACATCC	400
	TCGTTGCTCT	TAACAAGTGC	GACATGGTTG	AGGATGAGGA	AATCATCGAG	450
	CTCGTCGAGA	TGGAAGTTTC	TGAACTTCTT	GCTGAGCAGG	ACTACGACGA	500
	AGAGGCTCCA	ATTGTTTACA	TCTCCGCTCT	GAAGGCTCTT	GAGGGCGACG	550
	AGAAGTGGGG	CAAGCAGATC	CTTGAGCTCA	TGCAGGCTTG	CGATGACAAC	600
60	ATCCCTGACC	CAGTTCGTGA	GACCGACAAG	CCATTCCTCA	TGCCTATCGA	650

```

GGACATCTTC ACCATCACCG GTCGTGGCAC CGTTGTTACC GGTCGTGTTG 700
AGCGCGGTAC CCTGAACGTG AACGATGATG TTGACATCAT CGGCATCAAG 750
GAGAAGTCCA CCTCCACCAC CGTTACCGGT ATCGAGATGT TCCGTAAGCT 800
TCTTGACTCC GCTGAGGCTG GCGACAACCTG TGGTCTGCTT CTCCGTGGTA 850
5 TCAAGCGCGA AGATGTTGAG CGTGGCCAGG TTATCGTTAA GCCAGGCGCT 900
TACACCCCTC ACACCGAGTT CGAGGGCTCT GTCTACGTTT TGTCCAAGGA 950
TGAAGGTGGC CGCCACACCC CATTCCTCGA CAACTACCGT CCTCAGTTCT 1000
ACTTCCGCAC CACCGACGTT ACCGGTGTG TGAAGCTTCC AGAGGGCACC 1050
GAGATGGTCA TGCCTGGCGA CAACGTCGAC ATGTCCGTCA CCCTGATCCA 1100
10 GCCTGTCGCT ATGGACGAGG GCCTGCGTTT CGCTATCCGC GAAGGCTCCC 1150
GCACCGTTGG CGCTGGTCGT GTCACCAAGA TCATCAAGTA A 1191

```

15 2) INFORMATION FOR SEQ ID NO: 669

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 1383 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Escherichia coli
    (C) ACCESSION NUMBER: extracted from V00267

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

```

30 ATGGCTACTG GAAAGATTGT CCAGGTAATC GCGCCCGTAG TTGACGTCTGA 50
ATTCCCTCAG GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA 100
ATGGTAATGA GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT 150
ATCGTACGTA CCATCGCAAT GGGTTCCTCC GACGGTCTGC GTCGCGGTCT 200
35 GGATGTAAAA GACCTCGAAC ACCCGATTGA AGTCCCGGTA GGTAAGCGA 250
CTCTGGGCCG TATCATGAAC GTACTGGGTG AACCGGTCGA CATGAAAGGC 300
GAGATCGGTG AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA 350
CGAAGAGCTG TCAAACCTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA 400
TCGACCTGAT GTGTCCGTTT GCTAAGGGCG GTAAAGTTGG TCTGTTCGGT 450
40 GGTGCGGGTG TAGGTAAAAAC CGTAAACATG ATGGAGCTCA TTCGTAACAT 500
CGCGATCGAG CACTCCGGTT ACTCTGTGTT TGCGGGCGTA GGTGAACGTA 550
CTCGTGAGGG TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC 600
GACAAAGTAT CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAAACCG 650
TCTGCGCGTT GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG 700
45 AAGGTCGTGA CGTTCTGCTG TTCGTTGACA ACATCTATCG TTACACCCTG 750
GCCGGTACGG AAGTATCCGC ACTGCTGGGC CGTATGCCTT CAGCGGTAGG 800
TTATCAGCCG ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAACGTATCA 850
CCTCCACCAA AACTGGTTCT ATCACCTCCG TACAGGCAGT ATACGTACCT 900
CGGGATGACT TGA CTGACCC GTCTCCGGCA ACCACCTTTG CGCACCTTGA 950
50 CGCAACCGTG GTACTGAGCC GTCAGATCGC GTCTCTGGGT ATCTACCCGG 1000
CCGTTGACCC GCTGGACTCC ACCAGCCGTC AGCTGGACCC GCTGGTGGTT 1050
GGTCAGGAAC ACTACGACAC CGCGCGTGGC GTTCAGTCCA TCCTGCAACG 1100
TTATCAGGAA CTGAAAGACA TCATCGCCAT CCTGGGTATG GATGAACTGT 1150
CTGAAGAAGA CAAACTGGTG GTAGCGCGTG CTCGTAAGAT CCAGCGCTTC 1200
55 CTGTCCACAG CGTCTTCGT GGCAGAACTA TTCACCGGTT CTCCGGGTAA 1250
ATACGTCTCC CTGAAAGACA CCATCCGTGG CTTTAAAGGC ATCATGGAAG 1300
GCGAATACGA TCACCTGCCG GAGCAGGCGT TCTACATGGT CGGTTCCATC 1350
GAAGAAGCTG TGGAAAAAGC CAAAAAACTT TAA 1383

```

60

2) INFORMATION FOR SEQ ID NO: 670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*
 (B) STRAIN: NCTC 11638
 (C) ACCESSION NUMBER: extracted from AF004014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

20	ATGAAAGCGA	TGGAAGGTAA	AATCATTTCAG	GTTTTAGGCC	CGGTGGTAGA	50
	TGTGGAGTTT	GAATCCTATC	TGCCGGCGAT	TTTTGAAGCA	CTAGACATTA	100
	ATTTTGAAGT	TAATGGCGTT	CAAAAATCTT	TAGTTTTAGA	GGTGGCAGCC	150
	CATTTGGGTG	GTAATCGGGT	GCGAGCGATT	GCTATGGATA	TGACAGAAGG	200
	CTTAGTCCGT	AACCAAGCCG	TCAAAGCTCG	TGGCAAATG	ATTGAAGTGC	250
	CTGTGGGCGA	AGAAGTGTTA	GGGCGTATTT	TTAATGTTGT	GGGCGAGAGC	300
25	ATTGATAATT	TAGAGCCGCT	TAAGCCGTCC	TTAACTTGGC	CCATTTCACAG	350
	AAAAGCCCCCT	AGTTTTGAGC	AGCAAAGCAC	TAAAACAGAA	ATGTTTGAAA	400
	CCGGTATTAA	AGTCATTGAC	TTGCTCGCGC	CTTATTCTAA	GGGCGGTAAA	450
	GTAGGCTTGT	TTGGTGGGGC	TGGCGTAGGC	AAAACGGTGA	TCATTATGGA	500
	GCTTATCCAC	AATGTGGCTT	ATAAGCATAA	CGGGTATTCT	GTGTTTGCAG	550
30	GTGTGGGGGA	GCGCACCAGA	GAAGGGAACG	ATCTGTATTT	TGAGATGAAA	600
	GAAGGGGGCG	TTTTAGACAA	AGTTGCGTTG	TGCTATGGGC	AAATGAATGA	650
	GCCACCAGGT	GCAAGGAATC	GCATCGCATT	CACCGGCTTG	ACGATGGCGG	700
	AGTATTTCCG	TGATGAAAAG	GGCTTAGATG	TGTTGATGTT	TATTGATAAC	750
	ATCTTTAGAT	ACGCTCAAAG	CGGTGCGGAA	ATGAGCGCGC	TATTAGGCCG	800
35	TATCCCTTCA	GCGGTGGGGT	ATCAGCCCCA	GCTAGCCGGG	GAAATGGGGA	850
	AACTTCAAGA	CGGTATCGCT	TCCACTAAAA	ATGGCTCTAT	CACTTCGGTT	900
	CAAGCGGTGT	ATGTGCCAGC	AGACGACTTG	ACTGACCCAG	CCCCTGCTTC	950
	GGTGTTTGCG	CATTTAGATG	CGACTACGGT	GTTGAATAGA	AAGATCGCTG	1000
	AAAAAGGGAT	TTATCCGGCG	GTGGATCCTT	TGGATTCCAC	TTCAAGGATT	1050
40	TTAAGCCCTC	AAATGATTGG	CGAGAAGCAC	TATGAAATCG	CCACCGGTAT	1100
	CCAGCAAGTT	TTGCAAAAAT	ACAAGGATTT	GCAAGATATT	ATTGCGATTT	1150
	TGGGATTGGA	CGAATTGAGC	GAAGAGGATA	AAAAAACGGT	TGAAAGGGCC	1200
	AGAAAAATTG	AGAAGTTTTT	ATCCCAGCCG	TTTTTTGTGG	CTGAAGTGTT	1250
	TACAGGAAGT	CCCGGTAAGT	ATGTGACTCT	CCAAGAGACT	TTAGAGGGCT	1300
45	TTGGAGGGAT	TTTAGAGGGC	AAATACGATC	ACATTCCTGA	AAACGCGTTT	1350
	TACATGGTGG	GCAGCATTCA	AGAGGTTTTA	GAAAAAGCTA	AAAACATGAA	1400
	AAATTCCTAA					1410

2) INFORMATION FOR SEQ ID NO: 671

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium acetobutylicum*
 (B) STRAIN: DSM 792
 (C) ACCESSION NUMBER: extracted from AF101055

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

```

10  ATGCCAGAAC ATGTAGGTAA AATTGTTTCAG GTAATAGGAC CTGTTGTGGA      50
    TATTAAATTT GATGCAGAGA ACCTTCCTGA CATCTATAAT TCCATAGAAA      100
    TAGATATGGG AGATAATAAA AAACCTCATTG CTGAAGTTGA ACAACATGTA      150
    GGAGATGACA TAGTAAGAAC AATAGCAATG GAAGGTACTG ACGGATTAAA      200
    AAGAGGAATG GAAGCAGTTA ACACTGGTAA ACCAATATCT GTACCAGTTG      250
    GAGAAAATGT TTTAGGACGT CTTTTTAATG TTTTAGGTCA GACAATAGAT      300
    GAAGCAGGAG ACATGAATGC TGATAAGTAT TATCCAATTG ATAGACCAGC      350
15  TCCAACCTTT GAAGAACAAT CAGTTCAACC AGAAATGTTT GAAACAGGTA      400
    TTAAGGTTAT AGATTTACTT GCTCCATATC AAAAGGGTGG AAAAATCGGT      450
    TTGTTTCGGT GTGCCGGTGT TGGTAAAACA GTTCTTATTC AGGAACTTAT      500
    AAATAATATA GCAAAAGAAC ACGGTGGATT ATCAGTATTC ACAGGTGTTG      550
    GAGAAAGAAC AAGAGAAGGT AATGACCTTT ATTATGAAAT GAAAGATTCA      600
20  GGAGTTATAA ATAAACAGC TCTAGTATTT GGTCAGATGA ATGAACCACC      650
    TGGCGCTAGA ATGAGAGTTG CTTTAACAGG ACTTACAATG GCTGAATATT      700
    TTAGAGACAA AGGTCAAGAT GTGCTTCTAT TTATAGATAA TATATTCAGA      750
    TTTACACAAG CTGGTTCAGA GGTTTCAGCT TTAAGTGGTA GAATACCTAG      800
    TGCCGTTGGT TATCAGCCAA CACTTGCAAA TGAAATGGGT GCTCTTCAAG      850
25  AGAGAATAAC ATCAACAAAA CAGGGTTCAA TCACATCCGT TCAGGCTGTA      900
    TATGTTCCCT CTGATGACCT TACAGACCCA GCTCCAGCAA CAACATTTAC      950
    GCATCTTGAT GCAACAACAG TTCTTTCAAG AGAAATATCA AACTTAGGAA     1000
    TATATCCTGC AGTTAGTCCT CTTGAATCAA CTTCAAGAAT ACTTGATCCA     1050
    AGAATTGTTG GAGAAGAGCA TTATGAAAGT GCTAACAAGG TTAAACATAT     1100
30  ACTTGAAAGA TATCAAGAAC TTCAAGATAT CATAGCTATA CTTGGTGTTG     1150
    ATGAACTTTC AGATGAGGAT AGATTGTTAG TTGGAAGAGC AAGAAGAGTA     1200
    CAGAGATTCT TATCTCAAGC TTTTAGTGTT GCTGAACAAT TTACAGGAAT     1250
    GAAAGGTCAG TTTGTACCTG TAAAAGATAC TATAAGAAGT TTTAAAGAAA     1300
    TATTAGATGG TAAGTGTGAT GATCTTCCAG AAGCTGCATT TTTATTTGCA     1350
35  GGAACAATAG AAGATGTAA AGAAAAAGCT AAAAAAATGA TGGAAAGCTA     1400
    A
  
```

40 2) INFORMATION FOR SEQ ID NO: 672

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cytophaga lytica*
 (B) STRAIN: DSM 2039
 (C) ACCESSION NUMBER: M22535

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

```

60  ATGTCTAAAG TTACAGGTAA AGTTTCCCAA ATTATTGGCC CAGTTATAGA      50
    TGTGGAGTTC CAAGCAGGGG TAGATCTTCC AAAAAATTTAT GATTCATTAG      100
    AAATTAAGAA AGCAGATGGA TCAATTTTGG TTTTGGAAGT ACAATCACAC      150
    ATTGGTGAGA ACACAGTAAG AACTATATCT ATGGATTCTT CTGATGGTTT      200
  
```

	AAGTCGTGGA	GCAGAGGTTA	ATGCAACAGG	AAGCGCTATA	CAAATGCCAG	250
	TTGGAGATGA	CGTTTACGGA	CGTTTATTTA	ACGTAATTGG	AGACGCTATT	300
	GATGGTCTTG	GGAATTTACC	AAAATCTGGT	AAAGATGGTT	TGCCAATACA	350
	CAGAGAGGCA	CCAAAATTTG	AAGACTTATC	TACTTCTACA	GAAGTATTAT	400
5	TTACAGGTAT	TAAAGTAATT	GACCTTATTG	AGCCTTATGC	AAAAGGTGGT	450
	AAGATTGGTT	TATTTGGAGG	TGCCGGAGTA	GGTAAAACAG	TATTAATTCA	500
	GGAATTAATT	AACAACATTG	CAAAAGGTCA	CGGTGGACTT	TCTGTATTTG	550
	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ACGATTTACT	ACGTGAGATG	600
	TTAGAGTCTG	GTATTATTAA	ATACGGAGAT	GACTTTATGC	ACTCTATGGA	650
10	AGAAGGTGGT	TGGGATTTAT	CTAAAGTTGA	TAAATCTGTA	ATGAAAGATT	700
	CTAAAGCAAC	CTTTGTATTT	GGACAAATGA	ATGAGCCACC	AGGAGCACGT	750
	GCACGTGTTG	CATTATCTGG	TTTAACTATT	GCAGAATATT	TCCGTGATGG	800
	AGCAGGTGAA	GGTCAAGGTA	AAGATGTACT	TTTCTTTGTG	GATAACATTT	850
	TCCGTTTTAC	ACAAGCTGGT	TCTGAGGTAT	CTGCATTACT	TGGTCGTATG	900
15	CCATCTGCGG	TAGGTTACCA	ACCAACATTA	GCAACAGAAA	TGGGTGCTAT	950
	GCAAGAGCGT	ATTACATCAA	CAAAAAGAGG	TTCTATTACA	TCTGTACAGG	1000
	CGGTTTACGT	ACCTGCGGAT	GATTTAACGG	ATCCAGCACC	GGCAACTACC	1050
	TTTGCTCACT	TAGATGCAAC	AACGGTATTG	TCTCGTAAAA	TTGCAGAGTT	1100
	AGGTATTTAC	CCAGCGGTAG	ATCCATTAGA	TTCTACTTCT	AGAATCTTAG	1150
20	CTCCAGAAAT	TTTAGGAAAA	GATCACTACT	CTTGTGCACA	ACGTGTAAAA	1200
	GAGTTGTTAC	AACGTTATAA	AGAATTACAA	GATATTATTG	CTATCCTTGG	1250
	TATGGAAGAA	TTATCTGAGG	AAGATAAAAT	GGCAGTTGGT	AGAGCAAGAC	1300
	GTGTACAACG	TTTCTTATCT	CAGCCTTTCC	ACGTAGCAGA	GCAATTTACA	1350
	GGTCTTAAAG	GTGTTTTAGT	AGATATCAAG	GATACTATTA	AAGGATTTAA	1400
25	TATGATTATG	GATGGTGAAT	TAGATCACTT	ACCAGAATCT	GCATTTAACC	1450
	TTAAAGGTAC	TATTGAAGAA	GCTATAGAAG	CAGGAGAAAA	AATGCTTGCT	1500
	GAAGCATAA					1509

30

2) INFORMATION FOR SEQ ID NO: 673

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia risticii*
 (B) STRAIN: HRC-IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

	CCTAAAATAT	ATGATGCATT	ATATGTAAAA	CTAGATAATG	AAAATTTGTG	50
	TTTAGAAGTT	TCACAAATTA	TTGGAGATAA	TGTTGTTAGA	TGTATTGCAA	100
	TGGGAGCTAC	TTATGGATTA	AATCGTGGTT	TAGAAGTAGT	TTGTTTCAGGA	150
50	AATCCAATTC	AGGTTCCCTGT	AGGTGAACAA	GTTTTAGGTA	GAATGTTTAA	200
	TGTTGTTGGT	AAAACAATTG	ACAATCTTGA	ATCTTTAGAT	GATAAAAATA	250
	TAAAAATGAT	GCCAATTCAT	CGAAATCCAC	CATCATTTGA	AGAGCAATCC	300
	AATGAAATTG	AAATTTTTGA	AACAGGCATT	AAAGTTATTG	ATTTATTAAT	350
	TCCATATGCT	AAAGGTGGTA	AGATTGGATT	ATTTGGTGGA	GCAGGGGTTG	400
55	GGAAAACGGT	TCTTGTTCAA	GAATTAATTC	ACAATATCGC	AAAAGGTCAT	450
	GGTGGTCTAT	CTGTTTTTGC	TGGAGTTGGT	GAAAGAAGTC	GTGAAGGTAA	500
	TGACTTGTAT	TATGAAATGA	TTGAAGGTGG	AGTTATAGAT	AAAACAGCCT	550
	TAGTGTTTGG	GCAAATGAAT	GAACCTCCTG	GCGCAAGAAT	GCGCGTAGCA	600
	TTAACTGCTT	TAACAATGGC	TGAATATTTT	CGTGATGTTT	AAAACCAAGA	650
60	TGTTTTGTGA	TTTATTGATA	ATATCTTTAG	ATTTACACAA	GCTGGTAGTG	700

AAGTTTCAGC	ATTATTAGGA	AGAATGCCAT	CTGCTGTTGG	TTATCAACCA	750
ACTTTGGCAT	ATGAAATGGG	ATTGTTACAA	GAAAGAATCA	CTTCCACTAA	800
AAGTGGTTCT	ATAACATCT				819

5

2) INFORMATION FOR SEQ ID NO: 674

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

AGAGCGAAGT	ACCAAGTGTT	TACGATGCTC	TGAATGTTGT	GGATTCCAAA	50
GAACGTCTGG	TTCTGGAAGT	TCAACAGCAG	CTAGGCGGTG	GCGTGATTCTG	100
25 CGCTATCGTT	ATGGGTAGCT	CGGATGGTTT	ACGTCGTGGA	ATGACAGTAC	150
AAAACACTGG	CGCTCCAATT	TCAGTACCAG	TAGGTACTAA	AACCCTAGGT	200
CGTATCATGA	ACGTGCTTGG	TGATGCGATT	GACGAACGTG	GCGACATTGG	250
CGCAGAAGAG	GTGTACTCGA	TTCACCGTCC	TGCTCCAAGC	TACGAAGAAC	300
AGTCTAGTGC	AAC TGAAC TT	TTGGAAACGG	GTGTTAAGGT	TATCGACCTG	350
30 ATCTGTCCGT	TTGCGAAAGG	CGGTAAAATC	GGTCTGTTCTG	GTGGTGCGGG	400
TGTAGGTAAG	ACCGTTAACA	TGATGGAAC T	TATCAACAAC	ATCGCGCTAC	450
AGCACTCAGG	TTTGTCAGTA	TTTGCTGGGG	TAGGTGAGCG	TACTCGTGAG	500
GGTAACGACT	TCTACCACGA	AATGCAGGAA	GCGGGCGTTG	TAAACGTTGA	550
ACAACCAGAA	CTGTCGAAAG	TAGCGATGGT	TTACGGTCAG	ATGAACGAGC	600
35 CACCAGGCAA	CCGTCTGCGT	G TAGCACTGA	CTGGTCTGAC	TATGGCGGAA	650
AAGTTCCGTG	ATGAAGGCCG	TGACGTACTG	CTGTTTATCG	ACAACATCTA	700
CCGTTACACC	CTAGCGGGAA	CGGAAGTATC	TGCTCTGCTT	GGCCGTATGC	750
CTTCAGCGGT	AGGTTACCAA	CCAACACTGG	CTGAAGAGAT	GGGTGTTCTG	800
40 CAAGAACGTA	TCACGTCAAC	CAAAAAAGGT	TCTATCACCT		840

2) INFORMATION FOR SEQ ID NO: 675

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

CGGCGGTATC	CTAGTTGTAG	CGGCAACTGA	CGGTCCAATG	CCACAAACTC	50
60 GTGAGCACAT	CCTGCTGGGT	CGCCAAGTAG	GTATTCCTTA	CATCATCGTA	100

	TTCATGAACA	AGTGTGACAT	GGTTGACGAT	GAAGAGCTTC	TAGAGCTGGT	150
	AGAGATGGAA	GTTTCGTGAGC	TGCTGTCTGA	GTACGATTTT	CCAGGTGATG	200
	ACCTGCCAGT	AATCCAAGGT	TCAGCACTAG	GCGCGCTAAA	CGGCGAAGCA	250
	CAGTGGGAAG	CGAAGATTGT	TGAGCTAGCA	GAAGCACTGG	ATACTTAYAT	300
5	TCCAGAGCCA	GAGCGTGCAG	TAGACATGGC	ATTCTTGATG	CCAATCGAAG	350
	ACGTATTCTC	AATCCAAGGT	CGTGGTACAG	TAGTAACTGG	CCGTATCGAG	400
	CGCGGCATCC	TGAAAGTGGG	TGACGAAGTA	GCGATCGTTG	GTATCAAAGA	450
	GACAGTAAAA	ACGACCTGTA	CAGGTGTAGA	GATGTTCCGT	AAGCTGCTTG	500
	ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	CACTRCTACG	TGGTACTAAG	550
10	CGTGAAGAAG	TAGAGCGTGG	TCAAGTACTG	GCGAAGCCAG	GTTCAATCAC	600
	ACCACACACT	AAGTTCGAAT	CAGAAGTATA	CGTACTGTCA	AAAGATGAAG	650
	GTGGCCGTC	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC	ACGTAACAGG	CAGCATTGAG	CTACCAGARG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGACAACG	TGAAGATGGT	TGTAGACCTG	ATTGCACCAA	800
15	TCGCGATGGA	CGAAGGTCTA	CGCTTCGC			828

2) INFORMATION FOR SEQ ID NO: 676

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*
 (B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

35	CTTCTCGGAT	GGCGTGCCGC	CGGTGCTGAC	GGCGCTGGAC	GTGACGGAGG	50
	AACTCGGGCG	CGACGAGCCG	CTGACGCTAG	AGATCGTGCA	ACACTTGGAC	100
	GCGCACACCG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TACTGAAGCT	150
	GAAGTCGAAG	GTCGTGTCGA	CCGGCGGGAA	CATCTCTGTG	CCTGTGGGCC	200
	GCGAGACGCT	TGGCCGCATC	TTCAACGTAC	TGGGCGACGC	GATTGACCAG	250
40	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CGGAGGCGCC	300
	GAAGCTGGCG	GACCAGGCGG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AAGTGATCGA	TCTGATCCTG	CCGTACTGCA	AGGGCGGCAA	GATCGGTCTG	400
	TTCCGGCGGTG	CCGGTGTGGG	GAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GTGGCTTCTC	CGTGTTCCGC	GGCGTTGGGG	500
45	AGCGCACCCG	CGAGGGGACG	GATCTGTACC	TGGAGATGAT	GCAATCGAAG	550
	GTGATCGACC	TGAAAGGTGA	GTCGAAGTGT	GTGCTTGTGT	ACGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCCGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CAGCGCTGCT	750
50	GGGCCGCGATC	CCCGCCGCTG	TGGGCTACCA	ACCGACGCTT	GCGGAGGATC	800
	TCCGGCATGTT	GCAGGAGCGC	ATCACGTCGA	CGACGAAGGG	GTCGATCACG	850
	TCTGTGCAGG	CGGTGTACGT	GCCTGCGGAT	GATATCACGG	ATCCC GCGCC	900
	GGCGACGACA	TTCTCGCACC	TGGACGCGAC	GACGGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	TGGCATCTAC	CCCGCGGTCA	ACCCACTGGA	GTGCGCGTCG	1000
55	CGTATCATGG	ACCCTGATGT	GATCGACGTG	GATCACTACA	ACGTTGCGCA	1050
	GGACATTGTT	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	TATCGACGAG	CTGACCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGTGCGCGCA	AGGTGACCCG	GTTCTGTCA	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTTACT	GGCATGACAG	GCCATTACGT	ACAGCTGAGC	GACACGGTGG	1250
60	AGTCGTTTCTC	CGGTTTGCTG	ATGGGGTCGT	ACGACCAGAT	TCCGGAGA	1298

2) INFORMATION FOR SEQ ID NO: 677

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

20	CAAGCTCAAG TCTGAGCGTG AGAGAGGTAT TACTATTGAC ATTACTCTCT	50
	GGAAATTGA GACCCAGAAA TACGAGTACA CTGTCATAGA CGCACCTGGT	100
	CATCGTGACT TTATCAAAAA TATGATTACT GGGACTTCAC AAGCCGACGT	150
	TGCTATGCTT GTCGTTCTTG CTGAATCTGG CGGATTCGAG GCTGCTTTTT	200
	CCAAAGAAGG TCAGACCCGT GAACACGCCT TACTAGCCTT CACACTTGGC	250
25	GTCAAACAGA TGATTGTTGC TATTAACAAA ATGGATTCTT GTCAGTACAA	300
	GGAGGATCGT TATATGGAAA TTTTCAAGGA AGTACAGCAG TACTTGAAGA	350
	AGGTGGGTTA CAAAGTTGAA AGCGTGCCGT TTGTTGCTAT TTCAGGATTC	400
	CACGGTGACA ACATGGTTGA AAAATCTACT AACATGCCTT GGTATAAGGG	450
	TAAGACCCTC GTAGAGGCAC TTGATCAAAT GGAGCCTCCA AAACGTCCGG	500
30	TCGAAAAACC TCTTAGATTG CCCCTGCAGT CAGTCTATAA AATTGGAGGT	550
	ATTGGTACGG TACCAGTCGG AAGGGTCGAA ACAGGACAAC TGAAAGCAGG	600
	AATGATCATT ACTTTTGCCC CCACTGGTTT GACCACTGAA TGTAATCTG	650
	TTGAAATGCA TCACGAGGTT GTGGAAGTGG CTAGCCCCGG TGATAACGTT	700
	GGATTTAATG TCAAGAATGT GTCTGTAAAG GATATTAAGA GAGGAAATGT	750
35	GGCTTCGGAT TCGAAAAATG ACCCAGCCAA GGAAGCTACC TCTTTCTCTG	800
	CACAACCTCAT GTACTCAAT CACCCTGGTA CCATCAAGGC CGGTTACTCA	850
	CCTGTGGTTG ATTGCCATAC TGCCCACATT GCTTGCAAAT TCGAATCTCT	900
	AGACACTAGG ATTGACAAGC GTACTGGCAA GACTTTGGAA GAAAATCCTA	950
	AGACTATTAA GAATGGTGAC GCTGCCATGG TGACTATGAA ACCAAATAAA	1000
40	CCCATGGTTG TGGAAACTTT CACCGACTAC GCCCCGTTGG GCCGGTTCGC	1050
	CGTGCGTGAT ATGCGCCAAA CCGTTGCCGT CGG	1083

2) INFORMATION FOR SEQ ID NO: 678

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: Lev-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCT CACGGTGGTT 50
 ACTCTGTCTT CACTGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG 100
 TACCACGAAA TGAGGGAGAC TGGTGTATC AACCTTGAGG GTGACTCCAA 150
 GGTGCTCTT GGTGAGTTCT TTTTCTTCTT CAGGCTAATT AGTCGATGAC 200
 5 GTGGGCCCTG ACTAAAAGT TTTCTTCCAG TCTTCGGTCA GATGAACGAG 250
 CCCCCTGGAG CCCGTGCCCCG AGTTGCCCTT ACTGGTTTGA CCATTGCCGA 300
 GTAATTCCGT GACGAGGAAG GCCAGGATGT GTTGCTTTTC ATTGACAACA 350
 TTTTCCGATT CACCCAGGCC GGTTCGAGG TGTCTGCCTT GCTCGGTCGT 400
 ATCCCCCTCTG CCGTCGGTTA CCAGCCCACT CTTTCCACCG ACATGGGTGG 450
 10 TATGCAGGAG CGAATGTAGG TTGCATTCTC TGTGATTTTA CGGCAAGCCT 500
 TGACTTTTTT TTTCTAGTAC CACCACCAAG AAGGGTTCCA TTACCTCCGT 550
 C 551

15

2) INFORMATION FOR SEQ ID NO: 679

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA
 25
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT 50
 ACTCCGTCTT CACCGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG 100
 TACCACGAAA TGAGGGAGAC TGGTGTATC AACCTTGAGG GTGACTCCAA 150
 35 GGTGCTCTT GGTGAGTTCT TTTTCTTGGG AGCTAATTAG TCGATGACGT 200
 GGGCCCTGAC CAAAACCGTT TCTTTCAGTC TTCGGTCAGA TGAACGAGCC 250
 CCCTGGAGCC CGTGCCCGAG TTGCTCTTAC TGGTTTGACC ATTGCCGAGT 300
 ACTTCCGTGA CGAGGAAGGC CAGGATGTGT TGCTTTTCAT TGACAACATT 350
 TTCCGATTCA CCCAGGCCGG TTCCGAGGTG TCTGCCTTGC TCGGTTCGTAT 400
 40 CCCCTCTGCC GTCGGTTACC AGCCCACTCT TTCCACCGAT ATGGGTGGTA 450
 TGCAAGAGCG AATGTAAGTT GCATTTTTTG TGATTTTACG GCAAGTCTTG 500
 ACTTACATTT TTTTCTAGCA CCACCACCAA GAAGGGTTCC ATTACCTCCG 550
 TC 552

45

2) INFORMATION FOR SEQ ID NO: 680

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 1018 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 55 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cunninghamella bertholletiae*
 (B) STRAIN: ATCC 42115

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

```

5  TCTCCCTGCT ATTTTAAACG CTCTTGAAGT TAAGGATCAT GCTGGTGGTC 50
   GTCTTGTTCT TGAAGTTGCT CAACACTTGG GTGAAAACAC TGTACGTACT 100
   ATTGCTATGG ATGGTACTGA AGGTAAGTTT ATTTTtagAT GATCATAAAT 150
   AATTGATCAT AATGATAAAA AAAAAAGAAG AAGAAGAACA GGATGTATAT 200
   AATGGTTAAT AAATAATATT TTCATATTGK ATATAACTAT TTAATCTGTT 250
   TTTTTTCTT CATGATTATA TATATATATG TMCTAATATC TAATATGAAC 300
   CTTTTTTATA AAATTAATCA GGTCTTGTCC GTGGTCAAAA GGTGTTGAT 350
10  ACTGGTGCTC CTATTACCAT TCCTGTTGGT AAGGAAGTTC TTGGTCGTAT 400
   CATCAACGTT ATTGGTGAAC CCATTGATGA ACGTGGTCCT ATTAAGGCCA 450
   AGTCTCACCG TGCTATTCAC GCTGAAGCTC CAGAATTCGT TGATCAATCT 500
   CCTACTCCCG AAATTCCTGA AACTGGTATT AAGGTTGTCG ATTTATTAGC 550
   TCCTTATGTA CTGGGTGGTA AGATTGGTCT TTTCGGTGGT GCTGGTGTAG 600
15  GTAAAACTGT CTTGATTCAA GAACCTATTA ACAACATTGC TAAAGCCCAT 650
   GGTGGTTACT CTATTTTCTG TGGTGTGGT GAACGTACTC GTGAAGGTAA 700
   CGATTTATAC CACGAAATGA TGGAACTGG TGTCATTAAA CTTGAAGGTG 750
   ACTCCAAGTG TGCTCTTGTA TTCGGTCAAA TGAACGAACC TCCTGGTGCT 800
   CGTGCCCGTG TTGCTTTAAC TGGTTTAAAC ATTGCTGAAT ACTCCGTGA 850
20  TGAAGAAGGT CAAGATGTGT TACTTTTCAT TGATAACATT TTCCGTTTCA 900
   CTCAAGCTGG TTCTGAAGTA TCTGCCCTTT TAGGTCGTAT TCCATCTGCT 950
   GTAGGTTACC AACCCACTTT ATCTACTGAT ATGGGTGGTA TGCAAGAACG 1000
   TATTACTACT ACCAAGAA 1018

```

25

2) INFORMATION FOR SEQ ID NO: 681

```

30  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Single
     (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

```

40  GGISSITTYG GIISIGGIAA RAC 23

```

2) INFORMATION FOR SEQ ID NO: 682

```

45  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 26 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Single
     (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

```

55  GTIACIGGYT CYTCRAARTT ICCICC 26

```

2) INFORMATION FOR SEQ ID NO: 683

60

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

GTIACIGGIT CISWIAWRTC ICCICC

26

2) INFORMATION FOR SEQ ID NO: 684

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (C) ACCESSION NUMBER: M64984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

30	ATGGCTGGTG	CTTTAGAAAA	CGCAAGAAAA	GAAATTAAAC	GTCTTTCATT	50
	AGATGACACC	AATGAATCCC	AATATGGTCA	AATCTATTCT	GTTTCCGGTC	100
	CGGTTGTTAT	TGCCGAAAAC	ATGATGGGAT	GTGCCATGTA	CGAATTGGTT	150
	AAAGTTGGTC	ATGATAATTT	AGTTGGGGAA	GTTATTAGAA	TTAATGGTGA	200
	TAAAGCAACC	ATTCAAGTTT	ATGAAGAAAC	TGCAGGGGTC	ACTGTTGGTG	250
35	ATCCAGTTTT	AAGAACTGGT	AAACCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAATGGAAA	CTATTTATGA	TGGTATTCAA	AGACCTTTAA	AAGCCATTAA	350
	AGATGAATCC	CAATCTATTT	ATATCCCAAG	AGGTATTGAT	GTTCTGCTT	400
	TATCAAGAAC	TGTTCAATAT	GATTTCACTC	CAGGTCAATT	GAAAGTTGGT	450
40	GATCATATCA	CTGGTGGGGA	CATTTTTGGT	TCTATTTATG	AAAACCTCTT	500
	ATTGGATGAC	CATAAGATTT	TGTTACCTCC	AAGAGCAAGA	GGTACTATTA	550
	CTTCTATTCG	TGAAGCCGGT	TCTTATAATG	TTGAAGAACC	AGTTTTGGAA	600
	GTTGAATTTG	ATGGTAAGAA	ACATAAATAC	TCTATGATGC	ATACATGGCC	650
	AGTTAGAGTT	CCAAGACCAG	TTGCTGAAAA	ATTGACTGCT	GATCATCCAT	700
45	TGTTGACCGG	TCAAAGAGTC	TTGGATTCTT	TATTCCCATG	TGTTCAAGGT	750
	GGTACTACTT	GTATCCCAGG	GGCTTTTGGT	TGTGGTAAAA	CTGTTATTTT	800
	TCAATCTTTG	TCCAAATTCT	CCAACCTCTG	TGTTATTATC	TATGTTGGTT	850
	GTTCCTACTA	AGGTACTCAA	GTCATGATGG	CTGATGGTGC	CGACAAATCT	900
	ATTGAATCTA	TTGAAGTTGG	TGACAAAGTC	ATGGGTAAAG	ATGGTATGCC	950
50	AAGAGAAGTT	GTTGGCTTAC	CAAGAGGTTA	TGATGATATG	TACAAGGTTT	1000
	GTCAACTTTT	TAGTACTAGA	CGTAATGCTA	AATCCGAAGG	CTTGATGGAT	1050
	TTCACTGTTT	CTGCTGATCA	TAAACTTATC	TTGAAAACCT	AACAAGATGT	1100
	CAAGATTGCT	ACACGTAAAA	TTGGTGCCAA	CACCTATACT	GGTGTACTTT	1150
	TCTATGTTTT	GGAAAAGACT	AAGACTGGTA	TTGAATTAGT	TAAAGCCAAG	1200
55	ACTAAAGTTT	TCGGTCATCA	TATCCATGGT	CAAAATGGCG	CTGAAGAAAA	1250
	AGCTGCTACT	TTTGCTGCTG	GCATTGACTC	TAAAGAATAC	ATTGATTGGA	1300
	TCATTGAAGC	TAGAGATTAT	GTACAAGTTG	ATGAAATTGT	CAAGACCAGC	1350
	ACCACTCAAA	TGATCAACCC	AGTTCATTTT	GAATCTGGTA	AACCTCGGTAA	1400
	CTGGTTACAC	GAACACAAGC	AAAACAAATC	ACTTGCTCCA	CAATTGGGTT	1450
60	ACTTGTTGGG	TACTTGGGCT	GGTATTGGAA	ATGTTAAATC	TTCTGCTTTC	1500

```

ACCATGAACT CCAAAGATGA TGTAAATTA GCTACAAGAA TTATGAACTA 1550
CTCTTCAAAA TTGGGCATGA CTTGTTCTTC TACTGAATCC GGTGAACTCA 1600
ATGTCGCTGA AAACGAAGAA GAATTTTTCATAAACCTTGG TGCTGAAAAG 1650
GATGAAGCTG GTGATTTCAC TTTTGATGAA TTTACCGATG CTATGGATGA 1700
5 ATTGACTATC AATGTTTCATG GTGCAGCTGC AAGCAAGAAG AACAAATTTGT 1750
TGTGGAATGC TTTGAAATCT CTTGGTTTCA GAGCCAAGTC TACTGATATT 1800
GTCAAGAGTA TTCCTCAACA TATTGCTGTT GATGATATTG TTGTCAGAGA 1850
ATCTTTGATT GCCGGTTTAG TTGATGCTGC TGGTAATGTT GAAACCAAAT 1900
CCAATGGTTC TATTGAAGCT GTTGTAGAA CTTCTTTCAG ACATGTCGCT 1950
10 AGAGGTCTTG TCAAGATTGC TCATTCTTTG GGTATTGAAT CATCTATTAA 2000
TATTAAAGAT ACTCACATTG ATGCTGCTGG TGTAGACAA GAATTTGCTT 2050
GTATTGTCAA TTTGACTGGT GCTCCACTTG CTGGTGTCTT TTCTAAATGT 2100
GCACTTGCAA GAAACCAAAC TCCAGTTGTC AAATTTACCA GAGACCCAGT 2150
TTTGTTC AAC TTTGATTTGA TCAAATCTGC AAAAGAAAAC TATTATGGTA 2200
15 TTGTTTGGC TGAAGAACT GATCATCAAT TCCTTTTATC CAACATGGCC 2250
TTGGTGCACA ACTGTGGTGA ACGTGGTAAT GAGATGGCTG AAGTTTTGAT 2300
GGAATTCCCA GAATTGTTTA CTGAAATTTT TGGTAGAAAA GAACCAATTA 2350
TGAAACGTAC CACTTTGGTT GCCAATACTT CTAATATGCC AGTCGCTGCC 2400
AGAGAAGCTT CTATTTATAC TGGTATTACA TTGGCTGAAT ATTTTCAGAGA 2450
20 TCAAGGTAAG AATGTTTCTA TGATTGCTGA TTCTTCTTCA CGTTGGGCTG 2500
AAGCTTTGAG AGAAATTTCT GGTAGATTGG GTGAAATGCC TGCTGATCAA 2550
CGTTTCCCAG CTTATTTGGG TGCTAAATTG GCTTCTTTCT ATGAGCGTGC 2600
CGGTAAAGCC ACTGCTTTGG GTTCACCAGA TAGAGTTGGT TCAGTTTCTA 2650
TTGTTGCTGC TGTCTCTCCA GCTGGTGGTG ATTTCTCTGA TCCAGTTACT 2700
25 ACTTCTACTT TGGGTATTAC TCAAGTTTTC TGGGGGTTGG ATAAGAAATT 2750
GGCCCAAAGA AACATTTTCC CATCTATTAA CACCAGTGTT TCTTATTCTA 2800
AATACACCAA TGTTTTGAAC AAATACTATG ATTCCAATA TCCAGAATTC 2850
CCACAATTGA GAGACAAAAT TAGAGAAATT TTATCTAATG CTGAAGAATT 2900
GGAACAAGTT GTTCAATTAG TTGGTAAATC TGCATTGTCT GATTCTGATA 2950
30 AGATTACTTT AGATGTTGCT ACCTTGATTA AAGAAGATTT CTGCAACAA 3000
AATGGTTATT CTTCATATGA TGCATTCTGT CCAATTTGGA AGACTTTTGA 3050
TATGATGAGA GCATTTATTT CATATTATGA TGAAGCACAA AAAGCAATTG 3100
CCAATGGTGC TCAATGGTCT AAATTAGCTG AAAGTACTAG TGATGTTAAA 3150
CATGCTGTTT CTTCAGCTAA ATTCTTTGAA CCATCAAGAG GTCAAAAAGA 3200
35 AGGTGAAAAA GAATTTGGAG ATTTATTAAC CACTATCTCC GAAAGATTG 3250
CTGAAGCTTC AGAATAA 3267

```

40 2) INFORMATION FOR SEQ ID NO: 685

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1782 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
(B) STRAIN: ATCC 9790
(C) ACCESSION NUMBER: D17462

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

```

TTGCAAATTG GAAAAATCAT AAAAGTCTCC GGTCTCTCG TTATGGCAGA 50
AAATATGTCA GAAGCAAGTA TTCAAGACAT GTGTTTAGTG GGAGATTAG 100
GAGTCATCGG CGAAATCATT GAGATGCGTC AAGATGTGGC GTCTATTCAA 150
60 GTATATGAAG AAACCTCAGG AATTGGTCCC GGAGAACCTG TTCGTTCCAC 200

```

	TGGGGAAGCA	CTATCTGTTG	AGCTAGGACC	AGGAATCATT	TCACAAATGT	250
	TTGACGGGAT	TCAAAGACCA	CTGGATACAT	TTATGGAAGT	GACTCAAAGT	300
	AACTTCTTAG	GACGTGGGGT	CCAATTACCA	GCTTTAGATC	ATGAGAAACA	350
	ATGGTGGTTT	GAAGCGACAA	TCAAGAAGG	AACAGAAGTA	AGTGCTGGAG	400
5	ACATCATTTG	GTACGTGGAT	GAAACGAAGA	TCATTCAGCA	CAAAATCATG	450
	GTCCCTAATG	GTATCAAAGG	AACTGTACAA	AAAATTGAAT	CTGGATCATT	500
	TACGATCGAT	GATCCGATTT	GTGTGATCGA	AACGGAACAA	GGCTTAAAAG	550
	AGCTGACGAT	GATGCAAAAA	TGGCCAGTAC	GTCGTGGTCG	ACCAATCAAA	600
	CAAAAAATTAA	ATCCAGATGT	ACCGATGATC	ACCGGTCAAA	GGGTCATTGA	650
10	CACGTTTTTC	CCAGTAACTA	AAGGAGGAGC	GGCAGCCGTT	CCAGGTCCGT	700
	TTGGTGCAGG	GAAGACAGTT	GTGCAACACC	AGATTGCTAA	GTGGTCGGAC	750
	GTAGATCTAG	TGGTTTACGT	TGGTTGTGGG	GAACGAGGAA	ATGAAATGAC	800
	GGATGTCGTC	AATGAATTTT	CTGAACTGAT	CGATCCAAAT	ACAGGCGAGT	850
	CTTTGATGGA	ACGAACGTG	TTGATCGCTA	ATACATCGAA	CATGCCAGTA	900
15	GCTGCTCGAG	AAGCTTCTAT	TTATACGGGA	ATCACGATTG	CCGAGTACTT	950
	CCGTGACATG	GGGTATGATG	TAGCAATCAT	GGCAGATTCC	ACTTCTCGTT	1000
	GGGCAGAAGC	ACTGCGTGAA	ATGAGCGGAC	GTTTAGAAGA	AATGCCTGGT	1050
	GATGAAGGTT	ATCCCCTTA	TCTGGGCTCT	CGTCTAGCTG	AATACTATGA	1100
	ACGTTCAGGA	CGTGTCATTG	CTCTAGGCTC	TGACCAACGT	GAGGCGAGTA	1150
20	TCACTGCCAT	CAGTGCGGTT	TCTCCTTCTG	GTGGAGATAT	CTCTGAACCA	1200
	GTGACTCAA	ATACCTTACG	TGTGGTGAAG	GTTTTCTGGG	GATTAGATTC	1250
	TAGTCTTGCT	CAAAAAAGAC	ATTTTCCATC	GATTAAGTGG	ATCCAAAGTT	1300
	ACTCATTATA	TTCAACAGAA	GTTGGCAGAT	ATATGGATCA	AATCTTACAA	1350
	CAGGATTGGT	CTGATATGGT	AACTGAAGGC	ATGCGGATCT	TGCAAGAAGA	1400
25	AGAACAATTA	AATGAAAATCG	TGCGCTTGGT	AGGGATCGAT	TCGCTTTCTG	1450
	ATAACGATCG	CTTGACCCTT	GAAGTAGCAA	AATCGATTCTG	AGAAGACTAT	1500
	TTACAACAAA	ATGCTTTTGA	TGATGTAGAT	ACGTTTACTT	CAAGAGAAAA	1550
	ACAATTCAAC	ATGTTGAAAG	TTATTTTGAC	TTTGGGAAA	GAAGCTCGAA	1600
	AAGCCTTATC	GTTGGGAGCG	TACTTCAATG	AAATCATGGA	AGGTACAGTA	1650
30	GCGGTCAGAG	AACGCATTAG	TCGGAGCAAG	TATATTCCAG	AAGAAGAGTT	1700
	AGCCAAAATT	AGTAGTATAA	ATGAAGAAAT	CAAAGAAACG	ATCCAATTGA	1750
	TTGTTTCAGA	AGGAGGGATG	ACCGATGATT	AA		1782

35

2) INFORMATION FOR SEQ ID NO: 686

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1781 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

50	CAGGGACATG	TTATAGAAGC	TTATGGAAAC	TTGTTACGTG	TACGCTTTGA	50
	CGGATATGTT	AGACAAGGTG	AAGTTGCATA	TGTCAACGTA	GATAATACCT	100
	GGTTAAAAGC	AGAAGTGATT	GAAGTTGCTG	ATCAAGAAGT	CAAGGTTTCAG	150
	GTATTTGAAG	ATACACAAGG	CGCGTGTCTG	GGAGCTCTTG	TTACGTTTTTC	200
55	AGGACATCTT	TTAGAAGCCG	AGTTAGGGCC	TGGCTTGCTT	CAGGGCATTT	250
	TCGATGGACT	TCAAAATCGT	CTTGAGGTGC	TAGCTGAAGA	TAGTTCTTTC	300
	TTGCAGAGAG	GCAAGCATGT	TAATGCTATT	TCTGATCATA	ATTTATGGAA	350
	TTATACTCCC	GTAGCTTCTG	TTGGGGATAC	TTTAAGACGA	GGAGATCTTC	400
	TAGGAACAGT	ACCTGAAGGA	CGATTTACTC	ATAAGATTAT	GGTTCCTTTT	450
60	TCTTGCTTTC	AAGAGGTTAC	CCTGACTTGG	GTAATTTCTG	AAGGAACCTA	500

	TAATGCTCAT	ACTGTGGTCG	CAAAAGCTCG	AGATGCTCAG	GGTAAAGAAT	550
	GTGCC'TTTAC	TATGGTGCAA	AGATGGCCGA	TCAAACAAGC	TTTTATTGAA	600
	GGAGAGAAGA	TCCCTGCGCA	TAAGATTATG	GATGTGGGTT	TGCGAATCTT	650
	AGATACGCAA	ATTCCAGTAT	TGAAGGGGGG	AACTTTCTGT	ACCCCAGGAC	700
5	CTTTTGGTGC	AGGGAAAACA	GTCTTACAAC	ACCATCTTTC	TAAGTACGCT	750
	GCTGTAGATA	TTGTGATTTT	GTGTGCGTGC	GGAGAGCGTG	CTGGTGAAGT	800
	TGTTGAGGTA	TTACAAGAGT	TCCCTCATCT	TATCGACCCC	CATACCGGAA	850
	AGTCTTTAAT	GCACAGAACA	TGTATTATTT	GTAACACATC	ATCCATGCCT	900
	GTGGCTGCCC	GAGAGTCTTC	GATCTATTTA	GGAGTGACGA	TTGCAGAATA	950
10	CTATCGCCAG	ATGGGACTAG	ATATTCTGCT	TTTAGCTGAT	TCTACATCCC	1000
	GATGGGCACA	AGCCCTTAGA	GAGATTTCCG	GACGTCTTGA	AGAAATCCCT	1050
	GGAGAGGAAG	CATTTCCCTGC	ATACCTGTCT	TCTAGAATAG	CTGCTTTTTTA	1100
	TGAGCGAGGA	GGAGCTATCA	CCACGAAAGA	TGGTTCTGAA	GGATCTTTAA	1150
	CTATATGTGG	TGCGGTGTCT	CCTGCAGGAG	GAAACTTTGA	AGAACCAGTC	1200
15	ACTCAATCTA	CATTAGCTGT	ATCTCGAGCG	TTCTGTGGTC	TTTCAAAGC	1250
	ACGAGCTGAC	GCACGTAGGT	ATCCTTCAAT	AGACCCTTTG	ATTTCTTGGT	1300
	CAAAATATTT	GAACCAGGTA	GGACAAATTT	TAGAAGAGAA	GGTTTCAGGC	1350
	TGGGGTGGTG	CTGTGAAAAA	AGCAGCACAG	TTTCTAGAGA	AAGGTTTCAGA	1400
	AATCGGCAAG	CGTATGGAAG	TTGTCACTGA	AGAAGGGGTT	TCTATGGAAG	1450
20	ACATGGAAAT	CTACTTAAAG	GCAGAACTTT	ATGATTTTGT	TkATCTCCAG	1500
	CAGAACGCAT	TCGATCCTGT	GGACTGTTAT	TGTCCTTTTG	AGAGACAGAT	1550
	AGAGTTATTT	TCATTAATCA	GTCGTATTTT	TTGATGCTAAA	TTTGT'TTTTG	1600
	ATAGTCTCTGA	TGATGCAAGA	AGCTTTT'TCC	TTGAGCTGCA	GAGCAAGATT	1650
	AAGACATTAA	ATGGCCTGAA	ATTTCTTTCA	GAGGAATATC	ATGAGAGTAA	1700
25	AGAGGTCATA	GTTAGACTGT	TGGAAAAAAC	AATGGTACAA	ATGGCGTAAG	1750
	GATATGCAAA	CAATCTACAC	AAAATAACT	G		1781

30 2) INFORMATION FOR SEQ ID NO: 687

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Halobacterium salinarum*
 (C) ACCESSION NUMBER: S56356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

45	ATGAGTCAAG	CTGAAGCAAT	CACTGACACC	GGCGAAATCG	AGAGCGTGAG	50
	CGGTCCGGTC	GTGACCGCCA	CGGGCCTCGA	CGCGCAGATG	AACGACGTGC	100
	TCTACGTGGG	CGACGAGGGT	CTGATGGGCG	AGGTCATCGA	GATCGAAGGC	150
	GACGTAACCA	CCATCCAGGT	CTACGAGGAG	ACGTCCGGCA	TCGGGCCGGG	200
50	CCAGCCCGTC	GACAACACGG	GCGAACCCTG	CACCGTGGAC	CTGGGGCCCGG	250
	GGATGCTGGA	TTCCATCTAC	GATGGTGTGC	AGCGTCCACT	GGACGTCCCTC	300
	GAAGACGAGA	TGGGGGCGTT	CCTCGATCGC	GGTGT'TGACG	CACCCGGCAT	350
	CGACCTCGAC	ACCGACTGGG	AGTTCGAGCC	CACCGTCGAG	GCGGGCGACG	400
	AGGTCGCGGC	CGGCGATGTC	GTCGGCACC	TCGACGAAAC	GGTCAGCATC	450
55	GAACACAAGG	TTCTGGTGCC	CCCCCGCAGT	GACGGCGGCG	AAGTCGTCGC	500
	CGTCGAATCC	GGCACGTTCA	CCGTCGACGA	CACGGTCGTC	GAGTTGGACA	550
	CCGGCGAGGA	GATCCAGATG	CACCAAGAGT	GGCCGGTCCG	CCGCCAGCGC	600
	CCCACCTCG	ACAAGCAGAC	GCCGACGGAG	CCGCTGGTGT	CCGGCCAGCG	650
	CATCCTCGAC	GGCCTGTTCC	CGATCGCGAA	AGGCGGGACG	GCCGCGATCC	700
60	CGGGGCCGTT	CGGGTCCGGG	AAGACGGTCA	CCCAGCAGTC	CCTCGCGAAG	750

	TTCGCCGACG	CGGACATCGT	TGTCTACATC	GGCTGTGGTG	AGCGCGGCAA	800
	CGAGATGACG	GAAGTCATCG	AGGACTTCCC	GGAGCTGCCC	GACCCCCAGA	850
	CCGGGAACCC	GCTGATGGCC	CGCACCACGC	TCATCGCGAA	CACGTCTGAAC	900
	ATGCCGGTTG	CCGGGCGTGA	GTCTCTGCATT	TACACGGGAA	TCACCATCGC	950
5	GGAGTACTAC	CGCGACATGG	GCTACGACGT	GGCGCTGATG	GCCGACTCCA	1000
	CCTCGCGGTG	GGCGGAGGCC	ATGCGGGAGA	TCTCCTCGCG	ACTCGAGGAG	1050
	ATGCCCGGCG	AGGAGGGGTA	TCCCGCGTAC	CTGGCCGCCC	GCCTCTCGGA	1100
	GTTCTACGAG	CGCGCCGGCT	ACTTCGAGAA	CTTCAACGGG	ACCGAGGGCT	1150
	CCATCTCGGT	CATCGGTGCG	GTGTCGCCCG	CCGGCGGGGA	CTTCTCCGAG	1200
10	CCGGTCACCC	AGAACACGCT	GCGCATCGTG	AAGACGTTCT	GGGCGCTTGA	1250
	CTCGGACCTC	GCCGAGCGCC	GGCACTTCCC	GGCGATCAAC	TGGGACGAGT	1300
	CCTACAGCCT	CTACAAGGAC	CAACTCGACC	CGTGGTTCAC	GGACAACGTC	1350
	GTCGACGACT	GGGCCGAGCA	GCGCCAGTCG	GCGGTCGACA	TCCTCGACGA	1400
	GGAATCCGAA	CTCGAAGAGA	TCGTGCAGCT	CGTCGGGAAG	GACGCGCTGC	1450
15	CCGAGGACCA	GCAGCTCACG	CTGGAAGTCG	CGCGGTACAT	CCGCGAGGCG	1500
	TGGCTCCAGC	AGAACGCGCT	CCACGACGTG	GATCGCTACT	GCCCCCCCGA	1550
	GAAGACGTAC	GCCATCCTCT	CCGGCATCAA	GACGCTTCAC	GAGGAGTCCT	1600
	TTGAGGCGTT	GGACGCCGGT	GTGCCAGTCG	AGGAGATCAC	GTCGATCGAC	1650
	GCCGCGCCCG	GCCTGAATCG	TCTCGGCACG	ACGCCCACG	ACGAGCACGA	1700
20	GGCGGAGGTC	GCGGAGATCA	AACAGCAGAT	TACCGAGCAG	CTTCGGGAGC	1750
	TCTACTGA					1758

25 2) INFORMATION FOR SEQ ID NO: 688

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 3118 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: Human
 (C) ACCESSION NUMBER: L09234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

40	GAATTCGGGC	AGCTGACTAG	TCTTGTGATT	GGGGTCCTGG	GCTGATAAAA	50
	TCATTCCAAA	TGACGAGCAC	ATTGATAAAG	ACGTCCGATG	AGGACCGGGA	100
	GTCCAAATTC	GGCTTTGTTT	TTGCCGTATC	TGGACCTGTG	GTGACAGCTG	150
	AACGAATGGC	CGGTTCTGCT	ATGTACGAAC	TGGTGCGTGT	CGGTTATTAT	200
45	GAAGTGGTCG	GAGAGATCAT	CCGGTTGGAG	GGTGACATGG	CAACAATCCA	250
	AGTATACGAA	GACACCTCAG	GTGTGACAGT	AGGCGATCCC	GTGCTGCGCA	300
	CAGGCAAGCC	GCTGTCCGTG	GAAGTGGGAC	CCGGAATCAT	GGGCAGCATC	350
	TTCGACGGTA	TCCAGCGACC	GCTGAAGGAT	ATCAATGAAC	TGTCAAATAG	400
	TATCTACATC	CCGAAAGGTG	TCAATGTGCC	TGCCCTGAGT	CGCACTGCAC	450
50	AGTGGGACTT	CAGTCCCCTG	AGTGTCAAGG	TTGGAAGCCA	CATTACTGGT	500
	GGTGACCTGT	ACGGTTTGGT	CCACGAAAAT	ACTCTGGTGA	AACACAAGTT	550
	GCTGCTGCCG	CCCCGTGCCA	AGGGAAGTGT	CACGTACATT	GCAGAACCTG	600
	GAAACTACAC	AGTTGATGAT	GTTGTCCTGG	AGACAGAATT	TGACGGCGAG	650
	CGATCAAAGT	TCACCATGCT	GCAAGTGTGG	CCTGTACGTC	AGCCCAGGCC	700
55	TGTTACAGAA	AAGTTGCCAG	CTAACTACCC	CCTCCTTACT	GGCCAGCGTG	750
	TGCTCGACTC	CCTATTCCCG	TGTGTCCAGG	GTGGAACAAC	AGCTATTCTT	800
	GGGGCCTTCG	GATGTGGCAA	GACTGTAATA	TCACAGTCTT	TGTCAAATAA	850
	CTCAAATCC	GATGTAATTA	TCTATGTAGG	TTGTGGTGAG	CGAGGTAATG	900
	AAATGTCAGA	AGTACTCAGG	GATTTCCCGC	AGTTGTCGTT	GGAGATTGAT	950
60	GGTGTGACTG	AATCAATCAT	GAAGAGAACA	GCCCTGGTCG	CAAACACATC	1000

	AAACATGCCT	GTGGCTGCTC	GAGAAGCATC	TATCTACACA	GGTATTACAC	1050
	TGTCAGAAATA	CTTCAGGGAC	ATGGGTTACA	ATGTATCCAT	GATGGCTGAC	1100
	TCAACTTCAC	GATGGGCCGA	AGCTCTTCGA	GAAATCTCAG	GTCGATTGGC	1150
	TGAAATGCCT	GCCGACAGCG	GTTATCCCGC	CTACCTAGGT	GCACGACTTG	1200
5	CCAGTTTCTA	CGAGCGTGCC	GGCCGTGTGA	AGTGCTTGGG	TAACCCAGAC	1250
	AGGGAGGGCT	CCGTGAGTAT	AGTGGGCGCC	GTGTCGCCGC	CCGGTGGAGA	1300
	CTTCTCAGAT	CCCGTGACGA	CGGCCACACT	AGGTATCGTC	CAGGTGTTCT	1350
	GGGGTCTCGA	CAAGAACTT	GCCCAGCGAA	AGCACTTCCC	ATCCATCAAC	1400
	TGGCTCATCT	CGTAGAGTAA	ATACATGCGT	GCTCTGGATG	ACTTCTACGA	1450
10	CAAGAATTTT	CCAGAGTTTG	TCCCCTGCG	TACAAAGGTG	AAGGAGATTT	1500
	TGCAGGAGGA	AGAAGACCTG	TCTGAAATTG	TGCAGTTGGT	CGGTAAAGCT	1550
	TCATTGGCAG	AAACTGACAA	GATCACACTT	GAGGTTGCCA	AACTATTAAA	1600
	GGATGATTTT	CTGCAACAGA	ACAGCTATTC	ACCATATGAC	CGTTTCTGCC	1650
	CATTCTACAA	GACAGTAGGA	ATGCTGAAAA	ATATGATTGC	TTTCTACGAT	1700
15	ATGTCTCGGC	ATGCAGTTGA	ATCTACTGCT	CAGAGCGAGA	ACAAGATCAC	1750
	TTGGTAATCT	ATTAGAGATT	CTATGGGCAA	TATTCTGTAT	CAGCTTTCCT	1800
	CCATGAAATT	CAAGGATCCA	GTCAAGGATG	GAGAAGCGAA	GATCAAGGCA	1850
	GACTTTGAGC	AGCTTCATGA	AGACATTCAG	CAAGCCTTCA	GGAACCTGGA	1900
	GGATTAAAGT	GGTAGCTGCC	AGTGGTTCTC	TCGGTGCAGT	TGTCACATTT	1950
20	GGCAAGCTCT	GTAGGGTTGC	CGAGTGGCAT	CGGTGCTAGA	CACCTGAGCA	2000
	TTCCTTTGCC	ACATAAAGAC	TAAAGCAGGT	GGAATTTTCA	TTGTAAAAAG	2050
	CTGGTTCCAT	TGGTGCTAAG	ATTATGTTGT	GCCCTTTTCT	GCTTCTCACA	2100
	TTCCAACAGA	GGAAATTTACT	TCCAGTTTTC	TTCCATTTTC	CTCCTCATTT	2150
	TAAGTGTCTG	TACAGAGGCA	ATAATCTGAT	AACTCTGTAC	CGTCACTTAC	2200
25	AAGCAGGGAG	AATTTGTAAT	TATTACAAAT	CCCATTATCT	CTGTGCACCA	2250
	CAGCCTTGTA	AATTCATTTG	TCCCAGGACT	CCCTCTTGTC	TGTACGTGAG	2300
	ATTGCCGTCT	GTATGTATGT	ACACACCGTA	CTGCAGTATT	TGAAGTCAGT	2350
	CAGAAGGTGA	ATTACACCAC	TTACTCATTG	TGTCACGTAG	CAAGTGTGCA	2400
	AACTGCCATC	CATTGTCCTA	TTTATTCACA	TAAGTAGTTT	TCTTTGCATT	2450
30	TCCAGTGTTG	CAAATTGTGT	TTAGAAAATT	ATGCCATCGA	GACTGGTCTGA	2500
	ACCTCACATT	GTAATCTCAGT	ATTTACACAC	ACGTTTACTT	GCTACAGAAA	2550
	TGTAGAAAAA	ATAATTGTTG	TATATTGAAA	GTACAAGTGA	CAAAGTTGCA	2600
	TTTAAAATGG	TGAATGTATT	TTATATTTCT	TTTGTAGACA	CAAGAGTTAA	2650
	TGCATTTTGC	TTAATGGAGA	TGTATGTAAA	CCTAAAATAG	CAGTTTGTGC	2700
35	ACAAATTATG	TATATGTGAA	ATGGAGATGG	TTTCTAATTT	GCTGATTGAT	2750
	TGCCAGTATT	AATTTAAACA	ACTGTAGTTG	TGGGATGTAG	TGGGAAGATT	2800
	TTTTTTTTCC	TATAAAATG	GTGGATGTAT	GTGTCGGAGA	TTTTGATTGT	2850
	ATGTGTAAAA	TAGTGATCCC	AGTAACTGTA	AAGCTTTAGA	ATACAGTTAC	2900
	TGACTGTATA	GTTGTACAGG	TGTTGTTACT	TTTAAGAATT	TATTGACACA	2950
40	AAGGTGAAAG	TCTATTATTG	TATTGTAAAT	TTTAAAGCAT	TTAAGGTTTA	3000
	AAAATCCTAC	TTCTGTGTAT	AAATGTTACC	ATTCCTCATA	TAACATAACT	3050
	GTGTAGAAAT	ACAGTCAACT	TCATGTTTCA	TAGCATTTCA	CTGTTGTCAC	3100
	ATAAATTATG	CCCGGAAT				3118

45

2) INFORMATION FOR SEQ ID NO: 689

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Plasmodium falciparum*
 (B) STRAIN: 3D7
 (C) ACCESSION NUMBER: L08200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

	ATGACAAAAG	TTGCTGTTGA	AAAAGAGGAA	CCAGGAGTTG	TTTATAAGGT	50
5	GGCTGGTTCA	TTAGTTATTG	CTGAGAATAT	GAGTGGAAC	CGTATGTACG	100
	AGTTAGCTAA	AGTAGGATGG	AATAAATTGG	TTGGAGAAAT	TATTAGATTA	150
	GAAGGGAATT	ATGCATATAT	ACAAGTTTAT	GAAGATACTT	CAGGTTTATC	200
	TGTAGGAGAC	CCTGTTATAA	AAACAGGAAA	TGCTTTATCA	GTCGAATTGG	250
	GTCCTGGTAT	TTTAGATAAT	ATTTATGATG	GTATTCAAAG	ACCATTAGAA	300
10	AGAATAGCAA	ATGTGTGTGG	TGATGTATAT	ATATATAAAG	GTATTGATAT	350
	GACATCTTTA	GATCATGATA	AACAATGGCA	ATTTTATGCT	GATAAGAAAT	400
	TAAAATTAAA	TGATATTGTT	ACTGGTGGAG	ATATCTTTGG	ATTTGTTGAT	450
	GAAAATAAAT	TATTTAAAGA	ACACAAAATT	ATGGCTCCAC	CTAATGCTAA	500
	AGGGAGGCTT	ACATATATTG	CTCCAGATGG	ATCATATACT	TTAAAAGATA	550
15	AAATATTTGA	ATTAGAATAT	CAAGGAAAAA	AATATACATA	TGGTTTATCT	600
	CATTTATGGC	CTGTTCTGTA	TCCTAGACCT	GTTTTAGAAA	AGGTAACAGG	650
	GGATACTTTA	TTATTAACAG	GGCAAAGAGT	TTTAGATTCT	TTATTTCCAA	700
	CAGTTCAAGG	AGGTACTTGT	GCTATTCCCT	TGTCATTGGG	TTGTGGAAAA	750
	ACTTGTGTTT	CTCAGGCCTT	ATCAAAATAT	TCTAATAGTG	AAGTTATTAT	800
20	ATATGTAGGA	TGTGGTGAAA	GAGGTAATGA	AATGGCTGAA	ATTTTATCCG	850
	ACTTTCCTGA	ATTAACACT	AAAGTAGATA	ATGAAGATGT	AGGTATTATG	900
	CAAAGAACGT	GTTTAGTTGC	TAATACTTCT	AACATGCCTG	TCGCTGCAAG	950
	AGAAGCTAGT	ATTTATACAG	GTATTACTTT	ATGTGAATAT	TTCCGTGATA	1000
	TGGGTTATAA	TGCTACCATG	ATGGCTGATA	GTACAAGTAG	ATGGGCAGAA	1050
25	GCCTTAAGAG	AAATTTTCAGG	ACGTTTAGCT	GAAATGCCTG	CAGATAGTGG	1100
	TTATCCAGCT	TATTTAGGTG	CTAGATTAGC	TTCTTTTAT	GAACGTGCAG	1150
	GAAAAGTCAA	ATGTATTGGT	TCTCCATCTC	GTATAGGATC	CATTACAATT	1200
	GTGGGTGCTG	TGTCTCCACC	AGGTGGTGAT	TTCTCTGACC	CTGTAACTAC	1250
	AGCAACCATG	TCTATTGTTC	AAGCATTTTG	GGGTTAGAT	AAAAAACTAG	1300
30	CTCAAAGAAA	ACATTTCCCT	TCTGTTAATT	GGTCTACATC	CTTTTCAAAG	1350
	TATGTCAGAC	AATTAGAACA	ATACTTTGAT	AATTTTGATC	AAGATTTCTT	1400
	ATCTTTAAGA	CAAAAAATTA	GTGATATTTT	ACAACAAGAA	AGTGACTTGA	1450
	ATGATATTGT	TCAACTAGTA	GGAAAGGATT	CATTATCAGA	AGACCAAAAA	1500
	GTTGTTATAG	AAGTAGCCAA	AATTATTAGA	GAAGATTTTC	TTCAACAAAA	1550
35	TGCATTTAGC	GATTATGATT	ATATGTGCCC	ATTACAAAAA	ACAGTTGGTA	1600
	TGATGAGAAT	TATTTGCCAC	TTTTATGCTC	AATGCTTAAG	AACATTACAA	1650
	GAATATGACT	CAAGAGAAAG	AAAAATTGGT	TGGGGATCTA	TATATAATAC	1700
	ATTAAGACCA	ACTATAAATA	AAATTACACA	TATGAAATTT	GAAAACCCAA	1750
	AAAATTCAGA	TGAATATTTT	AAAAGTATT	TTAAGGCACT	TGAAGAAGAA	1800
40	ATAACAGTAG	GTTTAAGAAA	CTTGATGGAA	AAATGA		1836

2) INFORMATION FOR SEQ ID NO: 690

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3216 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55

- (A) ORGANISM: *Saccharomyces cerevisiae*
- (B) STRAIN: X2180-1A
- (C) ACCESSION NUMBER: J05409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

60

	ATGGCTGGTG	CAATTGAAAA	CGCTCGTAAG	GAAATAAAAA	GAATCTCATT	50
	AGAAGACCAT	GCTGAATCTG	AATATGGTGC	CATCTATTCT	GTCTCTGGTC	100
	CGGTCGTCAT	TGCTGAAAT	ATGATTGGTT	GTGCCATGTA	CGAATTGGTC	150
	AAGGTCGGTC	ACGATAACCT	GGTGGGTGAA	GTCATTAGAA	TTGACGGTGA	200
5	CAAGGCCACC	ATCCAAGTTT	ACGAAGAAAC	TGCAGGCCTT	ACGGTCGGTG	250
	ACCCTGTTTT	GAGAACAGGT	AAGCCTCTGT	CGGTAGAATT	GGGTCCTGGT	300
	CTGATGGAAA	CCATTTACGA	TGGTATTCAA	AGACCTTTGA	AAGCCATTAA	350
	GGAAGAATCG	CAATCGATTT	ATATCCCAAG	AGGTATTGAC	ACTCCAGCTT	400
	TGGATAGGAC	TATCAAGTGG	CAATTTACTC	CGGGAAAGTT	TCAAGTCGGC	450
10	GATCATATTT	CCGGTGGTGA	TATTTACGGT	TCCGTTTTTG	AGAATTCGCT	500
	AATTTCAAGC	CATAAGATTC	TTTTGCCACC	AAGATCAAGA	GGTACAATCA	550
	CTTGGAATTG	TCCAGCTGGT	GAGTACACTT	TGGATGAGAA	GATTTTGGAA	600
	GTTGAATTTG	ATGGCAAGAA	GTCTGATTTT	ACTCTTTACC	ATACTTGGCC	650
	TGTTCTGTGT	CCAAGACCAG	TTACTGAAAA	GTTATCTGCT	GACTATCCTT	700
15	TGTTAACAGG	TCAAAGAGTT	TTGGATGCTT	TGTTTCCTTG	TGTTCAAGGT	750
	GGTACGACAT	GTATTCCAGG	TGCTTTTGGT	TGTGGTAAGA	CCGTTATCTC	800
	TCAATCTTTG	TCCAAGTACT	CCAATTCTGA	CGCCATTATC	TATGTCGGGT	850
	GCTTTGCCAA	GGGTACCAAT	GTTTTAATGG	CGGATGGGTC	TATTGAATGT	900
	ATTGAAAACA	TTGAGGTTGG	TAATAAGGTC	ATGGGTAAAG	ATGGCAGACC	950
20	TCGTGAGGTA	ATTAATTTGC	CCAGAGGAAG	AGAACTATG	TACAGCGTCG	1000
	TGCAGAAAAG	TCAGCACAGA	CCCCACAAAA	GTGACTCAAG	TCGTGAAGTG	1050
	CCAGAATTAC	TCAAGTTTAC	GTGTAATGCG	ACCCATGAGT	TGGTTGTTAG	1100
	AACACCTCGT	AGTGTCCGCC	GTTTGTCTCG	TACCATTAAG	GGTGTGCAAT	1150
	ATTTTGAAGT	TATTACTTTT	GAGATGGGCC	AAAAGAAAGC	CCCCGACGGT	1200
25	AGAATTGTTG	AGCTTGTCAA	GGAAGTTTCA	AAGAGCTACC	CAATATCTGA	1250
	GGGGCCTGAG	AGAGCCAACG	AATTAGTAGA	ATCCTATAGA	AAGGCTTCAA	1300
	ATAAAGCTTA	TTTTGAGTGG	ACTATTGAGG	CCAGAGATCT	TTCTCTGTTG	1350
	GGTTCCCATG	TTCGTAAAGC	TACCTACCAG	ACTTACGCTC	CAATTCTTTA	1400
	TGAGAATGAC	CACTTTTTCG	ACTACATGCA	AAAAAGTAAG	TTTCATCTCA	1450
30	CCATTGAAGG	TCCAAAAGTA	CTTGCTTATT	TACTTGGTTT	ATGGATTGGT	1500
	GATGGATTGT	CTGACAGGGC	AACTTTTTTCG	GTTGATTCCA	GAGATACTTC	1550
	TTTGATGGAA	CGTGTTACTG	AATATGCTGA	AAAGTTGAAT	TTGTGCGCCG	1600
	AGTATAAGGA	CAGAAAAGAA	CCACAAGTTG	CCAAAACGTG	TAATTTGTAC	1650
	TCTAAAGTTG	TCAGAGGTAA	TGGTATTCGC	AATAATCTTA	ATACTGAGAA	1700
35	TCCATTATGG	GACGCTATTG	TTGGCTTAGG	ATTCTTGAAG	GACGGTGTCA	1750
	AAAATATTCC	TCTTTTCTTG	TCTACGGACA	ATATCGGTAC	TCGTGAAACA	1800
	TTTCTTGCTG	GTCTAATTGA	TTCTGATGGC	TATGTTACTG	ATGAGCATGG	1850
	TATTAAAGCA	ACAATAAAGA	CAATTCATAC	TTCTGTCAGA	GATGGTTTGG	1900
	TTTCCCTTGC	TCGTTCTTTA	GGCTTAGTAG	TCTCGGTTAA	CGCAGAACCT	1950
40	GCTAAGGTTG	ACATGAATGG	CACCAAACAT	AAAATTAGTT	ATGCTATTTA	2000
	TATGTCCTGGT	GGAGATGTTT	TGCTTAACGT	TCTTTCGAAG	TGTGCCGGCT	2050
	CTAAAAAATT	CAGGCCTGCT	CCCGCCGCTG	CTTTTGCACG	TGAGTGCCGC	2100
	GGATTTTATT	TCGAGTTACA	AGAATTGAAG	GAAGACGATT	ATTATGGGAT	2150
	TACTTTATCT	GATGATTCTG	ATCATCAGTT	TTTGCCTTGCC	AACCAGGTTG	2200
45	TCGTCCATAA	TTGCGGAGAA	AGAGGTAATG	AAATGGCAGA	AGTCTTGATG	2250
	GAATTCCCAG	AGTTATATAC	TGAAATGAGC	GGTACTAAAG	AACCAATTAT	2300
	GAAGCGTACT	ACTTTGGTCG	CTAATACATC	TAACATGCCG	GTTGCAGCCA	2350
	GAGAAGCTTC	TATTTACACT	GGTATCACTC	TTGCAGAATA	CTTCAGAGAT	2400
	CAAGGTAAAA	ATGTTTCTAT	GATTGCAGAC	TCTTCTTCAA	GATGGGCTGA	2450
50	AGCTTTGAGA	GAAATTTCTG	GTCGTTTGGG	TGAGATGCCT	GCTGATCAAG	2500
	GTTTCCCAGC	TTATTTGGGT	GCTAAGTTGG	CCTCCTTTTA	CGAAAGAGCC	2550
	GGTAAAGCTG	TTGCTTTAGG	TTCCCCAGAT	CGTACTGGTT	CCGTTTCCAT	2600
	CGTTGCTGCC	GTTTTCGCCAG	CCGGTGGTGA	TTTCTCAGAT	CCTGTTACTA	2650
	CTGCTACATT	GGGTATCACT	CAAGTCTTTT	GGGGTTTAGA	CAAGAAATTG	2700
55	GCTCAAAGAA	AGCATTTCCC	ATCTATCAAC	ACATCTGTTT	CTTACTCCAA	2750
	ATACACTAAT	GTCTTGAACA	AGTTTATATG	TTCCAATTAC	CCTGAATTTC	2800
	CTGTTTTAAG	AAGTCGTATG	AAGGAAATTC	TATCAAACGC	TGAAGAATTA	2850
	GAACAAGTTG	TTCAATTAGT	TGGTAAATCG	GCCTTGCTCTG	ATAGTGATAA	2900
	GATTACTTTG	GATGTTGCCA	CTTTAATCAA	GGAAGATTTT	TTGCAACAAA	2950
60	ATGGTTACTC	CACTTATGAT	GCTTCTGTGC	CAATTTGGAA	GACATTTGAT	3000

	ATGATGAGAG	CCTTCATCTC	GTATCATGAC	GAAGCTCAAA	AAGCTGTTGC	3050
	TAATGGTGCC	AACTGGTCAA	AACTAGCTGA	CTCTACTGGT	GACGTTAAGC	3100
	ATGCCGTTTC	TTCATCTAAA	TTTTTTGAAC	CAAGCAGGGG	TGAAAAGGAA	3150
	GTCCATGGCG	AATTCGAAAA	ATTGTTGAGC	ACTATGCAAG	AAAGATTTCG	3200
5	TGAATCTACC	GATTAA				3216

2) INFORMATION FOR SEQ ID NO: 691

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1860 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Schizosaccharomyces pombe*
 - (B) STRAIN: 972 h-
 - (C) ACCESSION NUMBER: S47814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

25	ATGGCGGGAG	GAATTGAACT	GGCCAAGAAG	GCTATCAGGA	GCCTCAAAAA	50
	TTACGACGAG	CATGAAAACC	GATATGGATC	TATTTTCAGC	GTTTCTGGTC	100
	CTGTCGTTGT	TGCAGCCAAT	ATGCTTGGAT	GTTTCGATGTA	CGAACTCGTT	150
	CGCGTTGGTC	ATGAAGAACT	AGTTGGTGAA	GTAATTCGTA	TCCATCAAGA	200
30	TAAATGTACT	ATTCAAGTAT	ACGAAGAGAC	GTCCGGTCTC	ACTGTTGGTG	250
	ATCCTGTCCA	ACGCACTGGA	AAGCCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAGCTGAGA	CTATTTATGA	TGGTATCCAA	CGTCCGTTAA	AGCAAATTTT	350
	CGACAAATCT	CAAAGTATTT	ATATTCCTAG	AGGTATTAAT	ACAGAATCAC	400
	TTAATCGTGA	GCATAAGTGG	GATTTACAC	CAAATAAGGA	TTTACGCATT	450
35	GGCGATCATG	TATCCGGTGG	TGATGTTTTC	GGTTCGTAT	TTGAAAACCTC	500
	TCTTTTCAAT	GATCATAAAA	TTATGTTACC	CCCTAGAGCC	CGTGGTACCG	550
	TCACATATAT	TGCTGAAGCT	GGATCATACC	ATGTTGATGA	AAAACCTTCTT	600
	GAAGTCGAGT	TTAATGGCAA	GAAACATTCT	TTTAGTATGT	TGCATACTTG	650
	GCCTGTCCGT	GCTGCTCGTC	CAGTTGCGGA	CAACTTAACT	GCTAATCAAC	700
40	CTTTATTGAC	TGGTCAACGT	GTTTTGGATG	CGTTATACCC	CTGTGTTCAA	750
	GGTGCGACTA	CTGCTATCCC	CGGTGCCTTT	GGTTGTGGTA	AAACAGTTAT	800
	TTCACAAATCT	CTTTCTAAGT	ACTCTAATTC	TGATTTGATT	GTTTACGTCG	850
	GTTGTGGTGA	ACGTGGAAC	GAAATGGCAG	AAGTGTTAAT	GGATTTCCCA	900
	GAACATAACAA	TTGATATTAA	TGGTAAACCA	GAGCCCATTA	TGAAGCGTAC	950
45	TACATTGGTA	GCCAACACTT	CTAACATGCC	TGTCGCTGCT	CGTGAAGCTT	1000
	CCATTTATAC	CGGTATTACA	CTTGCTGAAT	ATTATCGTGA	TCAAGGTAAG	1050
	AACGTTTCAA	TGATGGCTGA	TTCTACATCT	CGTTGGGCTG	AAGCTTTGCG	1100
	TGAAATTTCT	GGTCGTTTGG	CTGAGATGCC	TGCCGATTCT	GGTTATCCCG	1150
	CTTATTTGGG	TGCCAAATTG	GCTTCTTTTT	ACGAACGTGC	TGGTCGTGCT	1200
50	CGTTGCTTGG	GAAGTCCTGA	CCGTGAAGGA	ACAGTTTCAA	TTGTTGGAGC	1250
	TGTTTCTCCT	CCGGGTGGTG	ATTTTCTGA	TCCTGTTACT	AGTGCAACCT	1300
	TGGGAATTGT	TCAAGTCTTC	TGGGGTTTGG	ACAAGAAATT	GGCCCAACGT	1350
	AAACACTTTC	CCTCAATCAA	CACCTCTCTT	TCCTATTCTA	AATACATCAA	1400
	TGCTTTGCAA	CCTTGGTATG	AGGAAAGAGT	TCCAGGCTTT	AATACTCTTC	1450
55	GTGATCAAAT	CAAACAGATC	ATTCAACAAG	AAGATTCCAT	GTTGGAAATT	1500
	ATTCAAGTTGG	TTGGTAAGTC	GGCTCTTTCT	GAAACGGATA	AAGTTACTTT	1550
	GGACATAGCC	GGTATTATTA	AGAATGACTT	CTTACAACAA	AACGGTTATT	1600
	CTGATTACGA	TCGCTGTTGC	CCTCTTTACA	AGACTTATCA	TATGATGCGA	1650
	AACATGATTG	CTTACTACAC	AAAGGCTAAA	AGTGCCGTTG	AAACTGGTAG	1700
60	CGTTCCTTGG	TCAAAGATTA	AAGAAAGTAC	TTCAGATATC	TTTTATGAGT	1750

TAACCTCGAT	GAAATTCGAA	AACCCTAATG	AAGGCGAGAA	GGAAATAGTC	1800
GAACACTATG	AAACTCTGCA	CAAGAAGATT	GAGGACAAGT	TTCACACTCT	1850
GA CTGAGTAA					1860

5

2) INFORMATION FOR SEQ ID NO: 692

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma congolense*
 (B) STRAIN: IL3000
 20 (C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692

25	ATGACGAGCG	ATAAAAACCC	TTACAAAACA	GAGCAGCGCA	TGGGGGCCGT	50
	GAAGGCCGTC	TCCGGGCCAG	TTGTCAATTGC	TGAAAACATG	GGCGGTAGCG	100
	CTATGTATGA	GCTTGTGCAG	GTAGGTTCCCT	TCCGGTTAGT	GGGCGAGATC	150
	ATTCGTCTAG	AGGGCGATAC	CGCCACTATT	CAGGTCTATG	AGGAAACAGG	200
	TGGCCTCACT	GTCGGAGACC	CGGTGTACTG	TACGGGTAAG	CCTCTTTCGC	250
	TTGAGCTTGG	ACCTGGAATC	ATGCTGAAA	TATTTGACGG	TATCCAGCGG	300
30	CCTCTTGACA	CCATCTACCG	CATGGTGGAA	AACGTGTTTA	TCCCCAGGGG	350
	CGTTCAGGTG	AAGTCACTCA	ATGACCAGAA	ACAGTGGGAC	TTTAAGCCAT	400
	GCCTGAAGGT	TGGAGATCTT	GTGTCTGGTG	GTGATATCAT	TGGCTCAGTG	450
	GTGGAGAACT	CTCTCATGTA	CAATCACAGC	ATTATGATTC	CGCCCAATGT	500
	GCGGGGCCGT	GTTACTTCCA	TTGTTCCCTC	AGGAAATTAC	ACCCTCCAAG	550
35	ATGACATTAT	TGAATTGGAA	TATAATGGGA	CAGTGAAATC	ACTAAAACCT	600
	ATGCATCTGT	AGCCAGTACG	GACCCGCGCT	CCTGTGGCGT	CAAAAGAATC	650
	CGGCAATCAT	CCGCTTCTCA	CCGGACAGCG	TGTGCTCGAT	GCTCTCTTTC	700
	CATCCGTCCA	GGGTGGAACA	TGCGCCATCC	CTGGCGCGTT	TGGATGCGGA	750
	AAGACGGTTA	TCAGTCAGGC	TCTTTCGAAG	TTCTCCAACA	GCGACGCTGT	800
40	TATCTATGTC	GGCTGCGGCG	AGCGTGGGAA	TGAGATGGCA	GAGGTGCTCA	850
	TGGACTTCCC	CACACTCACC	ACCGTTATTG	ATGGTCGTGA	GGAGTCCATC	900
	ATGAAGCGTA	CCTGCCTGGT	GGCAAACACC	TCAAATATGC	CTGTCGCTGC	950
	TCGTGAGGCG	TCTATTTACA	CTGGCATCAC	TTTAGCTGAG	TATTATCGTG	1000
	ATATGGGCAA	GCACATTGCT	ATGATGGCCG	ACTCTACCTC	TCGATGGGCT	1050
45	GAGGCTCTCC	GTGAGATCTC	TGGGCGTCTC	GCTGAAATGC	CCGCTGATGG	1100
	TGGTTACCCT	GCGTACCTCA	GTGCGCGTCT	TGCTTCCTTC	TACGAGCGTG	1150
	CGGGGCGCGT	GACATGCATC	GGTGGGCCAA	AACGCGAGGG	CTCAGTAACC	1200
	ATCGTTGGTG	CCGTTTCTCC	TCCTGGAGGT	GACTTTTCTG	ACCCAGTGAC	1250
	GTCCGCTACG	CTTGGTATTG	TGCAAGTCTT	TTGGGGTCTT	GAGAAGCGTC	1300
50	TTGCGCAACG	TAAACACTTT	CCTTCTGTTA	ATTGGCTCAT	TTCTTATTCA	1350
	AAATACCTTA	ATGCTTTGGA	GCCCTTCTTC	AACACGCTTG	ACCCTGACTA	1400
	CATGCGCCTG	CGGTCAGTTG	CTGCGGAGAT	CCTTCAGCGT	GAGGAAGAGT	1450
	TGCAAGAAAT	TGTTCAACTT	GTGCGTAAGG	ACTCACTTTC	GGAGTCTGAC	1500
	AAAATTTATC	TAGAAACGGC	TAAGGTTATT	CGTGAAGAGT	TTCTCCAGCA	1550
55	GAATGCCTTT	ACGCCGTACG	ACAAGTATTG	CCCGCCGTAC	AAGACCTGCT	1600
	GGATGCTACG	TAACATTGTC	GCGTTCTACG	AGGAGAGCCA	GCGCGTTGTA	1650
	GCTGAGTCCG	CTGGGGAACCT	TAAGATTACG	TGGAACCTACA	TTCTGTGAAAT	1700
	GATTCCTCAT	ATTTACACGG	GTTTAACTGA	GATGAAGTTC	CGTGATCCTC	1750
	AGGAGGGTGA	GGAGGCCAAC	GTAGAATTCT	ACAGAAAACA	AAATGAGGAA	1800
60	ATTGTCAGCG	CATTGCGCTC	GCTGCTGCAA	TAA		1833

2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thermus thermophilus*
 (B) STRAIN: HB8
 (C) ACCESSION NUMBER: D63799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

20	ATGATCCAAG	GGGTGATCCA	GAAGATCGCG	GGCCCCGGCGG	TGATCGCCAA	50
	GGGCATGCTC	GGGGCCCCGCA	TGTACGACAT	CTGCAAGGTG	GGCGAAGAGG	100
	GCCTCGTG	CGAGATCATC	CGCCTGGACG	GGGACACGGC	CTTCGTCCAG	150
	GTCTACGAGG	ACACCTCGGG	CCTAAAGGTG	GGGGAGCCCG	TGGTCTCCAC	200
25	GGGCCTTCCC	TTGGCGGTGG	AGCTCGGCCC	CGGGATGCTG	AACGGCATCT	250
	ACGACGGCAT	CCAGCGCCCC	CTGGAGCGCA	TCCGGGAGAA	GACGGGGATC	300
	TACATCACCC	GGGGCGTGGT	GGTCCACGCC	CTGGACCGGG	AGAAGAAGTG	350
	GGCCTGGACG	CCCATGGTCA	AGCCCCGGGA	CGAGGTGCGG	GGGGGTATGG	400
	TCCTGGGCAC	GGTGCCCCGAG	TTCGGCTTCA	CCCACAAGAT	CCTGGTACCC	450
30	CCGGACGTGC	GGGGCCGGGT	CAAGGAGGTG	AAGCCCGCCG	GGGAGTACAC	500
	CGTGGAGGAG	CCGGTGGTGG	TCCTCGAGGA	CGGCACCGAG	CTCAAGATGT	550
	ACCACACCTG	GCCCGTTTCG	CGGGCGAGGC	CCGTGCAAAG	GAAGCTTGAC	600
	CCCAACACCC	CCTTCCTCAC	GGGGATGCGC	ATCCTGGACG	TCCTCTTCCC	650
	CGTGGCCATG	GGGGGCACCG	CCGCCATCCC	TGGGCCCTTC	GGCAGCGGCA	700
35	AGACCGTGAC	CCAGCAGTCC	CTGGCCAAGT	GGTCCAACGC	CGACGTGGTG	750
	GTCTACGTGG	GCTGCGGGGA	GCGGGGGAAC	GAGATGACCG	ACGTGCTCGT	800
	GGAGTTCCCC	GAGCTCACCG	ACCCCAAGAC	GGGTGGGCCC	TTGATGCACC	850
	GCACCGTCCT	CATCGCCAAC	ACCTCCAACA	TGCCCCGTGG	CGCCCCGCGAG	900
	GCCAGCATCT	ACGTGGGCGT	GACCATCGCC	GAGTACTTCC	GCGACCAGGG	950
40	CTTCTCCGTG	GCCCTCATGG	CCGACTCCAC	GAGCCGCTGG	GCCGAGGCTT	1000
	TGCGCGAGAT	CTCTAGCCGC	CTCGAGGAGA	TGCCCCGCCA	GGAGGGCTAC	1050
	CCGCCCTACC	TCGCCGCCAG	GCTCGCCGCC	TTCTACGAGC	GGGCGGGCAA	1100
	GGTCATCACC	CTGGGCGGCG	AGGAGGGGGC	GGTGACCATC	GTGGGGGCGG	1150
	TCTCCCCGCC	GGGCGGCGAC	ATGTCCGAGC	CCGTGACCCA	GTCCACCTTG	1200
45	AGGATCGTGG	GGGCCTTCTG	GCGGCTTGAC	GCCTCCCTGG	CCTTCCGCCG	1250
	CCACTTCCCC	GCCATCAACT	GGAACGGCTC	CTACAGCCTC	TTCACCTCCG	1300
	CCCTTGACCC	CTGGTACCGG	GAGAACGTGG	CCGAGGACTA	CCCCGAGCTC	1350
	CGCGACGCCA	TCTCCGAGCT	TTTGACGCGG	GAGGCGGGCC	TCCAGGAGAT	1400
	CGTCCAGCTC	GTGGGGCCGG	ACGCCCTCCA	GGACGCCGAG	CGCCTCGTCA	1450
50	TTGAGGTGGG	CCGGATCATC	CGCGAGGACT	TCCTGCAGCA	GAACGCCTAC	1500
	CACGAGGTGG	ACGCCTACTG	CTCCATGAAG	AAGGCCTACG	GGATCATGAA	1550
	GATGATCCTC	GCCTTCTACA	AGGAGGCGGA	GGCGGCCATC	AAGCGGGGGG	1600
	TTTCCATAGA	CGAGATCCTG	CAGCTCCCCG	TTCTGGAGCG	CATCGGCCGC	1650
	GCCCCGTACG	TGAGCGAGGA	GGAGTTCCCC	GCCTACTTTG	AGGAGGCCAT	1700
55	GAAGGAGATC	CAGGGGGCCT	TCAAGGCTGG	CCTAAAGGGG	GAGAGATGGA	1750
	CCTTCTGA					1758

2) INFORMATION FOR SEQ ID NO: 694

600

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

CGGCGCIATC YTS GTTGTTG C

21

2) INFORMATION FOR SEQ ID NO: 695

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

GTTTCACGTG ATGACGTACA

20

2) INFORMATION FOR SEQ ID NO: 696

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

ATIGGICAYR TIGAYCAYGG IAARAC

26

2) INFORMATION FOR SEQ ID NO: 697

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

CCIACIGTIC KICCRCCYTC RCG

23

2) INFORMATION FOR SEQ ID NO: 698

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: extracted from J01690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

```

20 GTGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTTA ACGTTGGTAC      50
   TATCGGCCAC GTTGACCACG GTAAACTAC TCTGACCGCT GCAATCACCA      100
   CCGTACTGGC TAAAACCTAC GGCGGTGCTG CTCGTGCATT CGACCAGATC      150
   GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCTTCTCA      200
   CGTTGAATAC GACACCCCGA CCGGTCAC TA CACACGTA GACTGCCCCG      250
25 GGCACGCCGA CTATGTTAAA AACATGATCA CCGGTGCTGC TCAGATGGAC      300
   GGCGCGATCC TGGTAGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG      350
   TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCGGTAC ATCATCGTGT      400
   TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGCTGGT      450
   GAAATGGAAG TTCGTGAAC TCTGTCTCAG TACGACTTCC CGGGCGACGA      500
30 CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCACGCAG      550
   AGTGGGAAGC GAAAATCCTG GAACTGGCTG GCTTCCTGGA TTCTTATATT      600
   CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA      650
   CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC      700
   GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      750
35 ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      800
   CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC      850
   GTGAAGAAAT CGAACGTGGT CAGGTAAGT CTAAGCCGGG CACCATCAAG      900
   CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG      950
   CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      1000
40 GTACTACTGA CGTGAAGTGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG      1050
   GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      1100
   CGCGATGGAC GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG      1150
   TTGGCGCGGG CGTTGTTGCT AAAGTTCTGG GCTAA      1185

```

2) INFORMATION FOR SEQ ID NO: 699

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

GTIACIGGYT CYTYRARRTT ICCICC

26

2) INFORMATION FOR SEQ ID NO: 700

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

15 TIRTIGAYGT CGARTTCCCT CARG

24

2) INFORMATION FOR SEQ ID NO: 701

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
25 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

30 GTGTTACGA TCATCGATGC G _____

21

35 2) INFORMATION FOR SEQ ID NO: 702

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG

20

50 2) INFORMATION FOR SEQ ID NO: 703

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

TATGGAAATT CGAAACATCT

20

5

2) INFORMATION FOR SEQ ID NO: 704

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

AGTGCTCCAA TTAATGTTGG

20

20

2) INFORMATION FOR SEQ ID NO: 705

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705

35 GTACAGTTCC AATACCTGAA

20

2) INFORMATION FOR SEQ ID NO: 706

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706

50 TGAAATCTTC ACATCCAACA

20

55 2) INFORMATION FOR SEQ ID NO: 707

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

604

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707

TWACCATTTC AGTACCTTCT GTAA

25

10

2) INFORMATION FOR SEQ ID NO: 708

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

15 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708

TCRTCCATIC CIARIATIGC IATAT

26

25

2) INFORMATION FOR SEQ ID NO: 709

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1656 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Borrelia burgdorferi*

(C) ACCESSION NUMBER: extracted from AE001122

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

	ATGAATGAAG	TTTTATTTGT	AAAGACTGCT	GGTAGGAATT	TAAAAGCAGA	50
	AGTAATTCGT	ATTAGGGGCA	ATGAAGTTGA	TGCACAGGTT	TTTGAATTGA	100
45	CAAAAGGGAT	ATCTGTTGGA	GACCTAGTTG	AATTTACAGA	CAAACCTTTTA	150
	ACAGTTGAAC	TCGGACCAGG	GCTTTTAACT	CAAGTATATG	ATGGGCTTCA	200
	AAATCCTTTG	CCTGAATTGG	CTATTCAATG	TGGATTTTTT	TTAGAAAGGG	250
	GAGTATATTT	AAGGCCCTTG	AATAAAGATA	AAAAGTGGAA	TTTTAAAAAA	300
	ACCTCCAAAG	TTGGAGATAT	CGTTATTGCA	GGAGATTTTT	TAGGTTTTGT	350
50	AATTGAGGGA	ACTGTTCAAC	ATCAAATAAT	GATTCCATTT	TATAAAAGGG	400
	ATTCTTATAA	AATTGTGGAG	ATTGTAAGTG	ATGGCGACTA	TTCGATTGAT	450
	GAGCAAATTG	CTGTAATTGA	AGATGATTCT	GGTATGAGGC	ATAATATTAC	500
	AATGTCTTTT	CATTGGCCTG	TTAAAGTTCC	TATTACTAAT	TATAAGGAAC	550
	GCCTTATTCC	TAGTGAACCT	ATGTTGACTC	AAACTAGAAAT	TATAGATACA	600
55	TTTTTCCCAG	TTGCCAAAGG	TGGAACTTTT	TGCATTCCGG	GTCCTTTTGG	650
	AGCAGGAAAA	ACGGTCTCTC	AGCAGGTTAC	AAGTCGAAAT	GCTGATGTTG	700
	ATGTAGTGAT	TATTGCAGCT	TGTGGTGAGC	GAGCAGGAGA	AGTGGTAGAA	750
	ACTCTTAAAG	AATTTCCCGA	ATTAATGGAT	CCAAAAACCG	GCAAATCTTT	800
	AATGGACAGG	ACTTGATATTA	TTTGTAATAC	ATCTTCAATG	CCAGTTGCAG	850
60	CTAGAGAAGC	TTCTGTTTAT	ACTGCTATTA	CTATTGGTGA	GTATTACAGG	900

```

CAAATGGGCC TTGATATTCT TCTTTTGGCA GATTCAACTT CAAGATGGGC      950
TCAAGCAATG AGAGAAATGT CTGGACGCCT TGAGGAAATT CCTGGCGAGG      1000
AGGCTTTTCC GGCATATCTT GAGTCTGTTA TTGCTTCCTT TTATGAAAGG      1050
GCAGGTATTG TAGTTCTTAA TAATGGGGAT ATTGGATCTG TAACAGTTGG      1100
5  TGGCTCTGTA AGTCCTGCTG GTGGTAATTT TGAAGAGCCA GTTACTCAAG      1150
CAACTTTAAA AGTTGTAGGA GCATTTACAG GGCTTACAAG AGAAAGGTCT      1200
GATGCTAGGA AATTTCCAGC TATTAGTCCCT CTTGAATCTT GGAGTAAATA      1250
TAAAGGCGTT ATTGATCAAA AAAAGACTGA ATATGCAAGA TCTTTTTTGG      1300
TGAAAGGTAA TGAAATTAAT CAAATGATGA AAGTTGTGG AGAAGAAGGC      1350
10 ATAAGTAACG ATGATTTTTT AATTTATTTA AAATCCGAGC TACTTGATTC      1400
GTGCTATTGG CAGCAAAATT CATTGATTC TATTGATGCT GCTGTTAGTT      1450
CAGAGCGTCA AAATTATATG TTTGATATAG TTTATAACAT TCTTAAACT      1500
AACTTTGAGT TTTCTGATAA ACTTCAAGCA AGAGATTTTA TAAATGAGTT      1550
AAGGCAAAAT CTTTTAGACA TGAATCTTTC TTCTTTTAAG GATCATAAGT      1600
15 TTAATAAATT GGAGCATGCT TTGGGTGAAT TGATAAATTT TAAAAAGGTA      1650
ATTTAG

```

20 2) INFORMATION FOR SEQ ID NO: 710

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: extracted from AE000520

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

```

GTGATCAAAG ACGATGTGGT TACAGGCCGT GTAGTGAGGG TGTCTGGTCC      50
CATTGTGTAT GCCGAGGGCC TCTCTGCGTG CAGCGTATAC GATGTTGTCTG      100
ACGTAGGGGA AGCATCGCTC ATCGGAGAAA TTATCCGGTT GGATGAGAGC      150
40 AAGGCGGTCTG TGCAAGTATA CGAGGATGAC ACAGGTATGC GAGTCGGGGA      200
GAAGGTGACA AGCTTGCGTC GACCACTCTC AGTCCGCTTA GGGCCTGGAT      250
TAATCGGCAC CATTATGAC GGTATTCAGC GCCCACTTGA GCGCCTCTTC      300
CAAGAAGACG GCGCCTTCTT GCGTCCTGGT GCGCGTTTAC AACCGCTTGA      350
TGGCTCCGTA CGCTGGGATT TTCGTCCTCA TTGTAACGAG CGCGGTGAGG      400
45 CCCTGTGCGC GGGGATTCCG ATTGCACCTG GGTCACTGTT AGGGACCGTG      450
CAGGAGACTC CTTCTGTTGT GCACACTATC ATGGTTCCTC CTGACATCCG      500
GGGGAGCGTG CTATCTTCGT TCAAGGGCGC AGGTGCTTAC ACAATAGATG      550
AAGAAATTGG ACGCACTGAT CTTGGTGAGC CGCTTTTTCT ATCCCACTAC      600
TGGCCAGTGC GTCGTGCGCG TCCTTTTCAGC AAAAAACTTG CAGTGTGTGA      650
50 GCCACTAGTT ACTGGACAGC GGGCGATTGA TGTTTTCTTC CCCCTATCAA      700
AGGGAGGAAC GCGGGCTATT CCAGGGGGAT TTGGAAGTGG GAAGACAATG      750
ACGCAGCATG CCGTTGCCAA GTGGTGTGAT GCAGATATTA TCGTGACAT      800
CGGCTGCGGA GAGCGGGGCA ACGAGATGAC AGACGTGCTC TCTGAATTTT      850
CCAAACTCAT CGATCCGCGC ACAGGACGCT CTCTTATGGA GCGGACGATT      900
55 TTGATCGCAA ATACGTCCAA TATGCCTGTG TCCGCACGCG AGGTGTCGCT      950
GTATTCAGGG ATTACCCTTG CGGAATACTA CCGTGATATG GGTATGCATG      1000
TGGCCATCAT GGCTGATTCT ACCAGCCGCT GGGCGGAGGC GCTGCGTGAA      1050
TTGTCTGGGC GCATGGAAGA AATGCCTGCG GAGGAGGGAT TCCCTGCGTA      1100
CCTTCCGACG CGTCTTGACG AATTTTATGA GCGCGCAGGA CGCGTGAAA      1150
60 CCTGTGTGGC GCGCGAGGGC TCTGTGAGCA TCATTGGTGC TGTTTCTCCC      1200

```

	CTGGGTGGAG	ATTTCTCTGA	GCCGGTGACG	CAGCACACAA	AGCGCTTCAT	1250
	CCGTTGCTTT	TGGGCCTTGG	ATCGTGAAC	TGCACACGCG	CGTCATTACC	1300
	CTGCCATTGG	GTGGATAGAT	TCATACTCTG	AATATGCGCA	GGAAGTAAGT	1350
	GCATGGTGGA	GTAAGTATGA	CCC GCGCGCA	GGCGCGTTGC	GCGCCGCAGC	1400
5	CTTGGAATTTG	CTGAGAAAGG	AACAGCGGTT	ACAGCAAATT	GTCAGGCTTG	1450
	TCGGTCCTGA	TGCGCTGCCT	GGAGAAGATC	GTCTGGTGCT	AATGGTGTGT	1500
	GAAATGATCA	AAGGTGGCTT	TCTGCAGCAG	AACGCTTTTG	ATCCGACGGA	1550
	TGTGTTCTCC	TGTCCCGAAA	AGCAGGTGCA	GATCTTGCGT	ACCATAGTGG	1600
	ATTTTACGA	ACGTGCCGTG	GTGCTGCTGC	GTGCAGGTAT	TTCGCTTTCT	1650
10	GCGCTGTCCC	AGCTTTCGTG	CCGGGAGCTC	ATCGTACGTA	TGAAAACACTAC	1700
	GTACGGGAAT	GAGGATGTAC	ACAAGATGCA	GAAAGTGTAC	GACACGATGT	1750
	GCACTGAGTT	TGACCAACTG	AGTGTGTGTG	CTGCCGCGCG	CACACAAGGG	1800
	GGGGAGAAAG	TCGAATGA				1818

15

2) INFORMATION FOR SEQ ID NO: 711

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1779 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Chlamydia trachomatis*
- (B) STRAIN: MoPn
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

	CAGGGCTATG	TCGTAGAAGC	TTACGGAAAT	TTATTGCGGG	TGCATTTTGA	50
	TGGGCATGTG	CGTCAAGGAG	AAGTGGCCTA	TGTCAGCGTG	GATGATACTT	100
35	GGTTGAAAGC	GGAAATTATA	GAAGTTGTGG	GAGATGAGGT	TAAAGTCCAA	150
	GTTTTTGAGG	AAACTCAAGG	AATTTCTCGA	GGCGCTTTGG	TAACCTTTTC	200
	CGGGCATTTA	TTAGAAGCGG	AACTTGGGCC	CGGTCTATTG	CAAGGTATTT	250
	TTGACGGACT	TCAGAATCGC	TTAGAGGTAT	TGGCAGATAC	AAGCTTGTTT	300
	TTGAAAAGAG	GGGAGTATGT	TAATGCCATT	TGTCGGGAAA	CTGTATGGGC	350
40	TTATACGCAA	AAGGCTTCTG	TCGGGGATGT	TCTATCTCGG	GGAGATGTGC	400
	TTGGTACAGT	AAAGGAAGGG	CGGTTTGATC	ATAAAATCAT	GGTTCCTTTC	450
	TCTTGTTTTG	AGGAAGTGAC	TATCACTTGG	GTCATTTCTT	CAGGAGATTA	500
	CACTGTTGAT	ACCGTTATTG	CTAAAGGACG	TACTGCTTCA	GGAGCCGAGC	550
	TTGAATTTAC	AATGGTTCAG	AAATGGCCCA	TTAAACAGGC	TTTTTTTAGAA	600
45	GGGGAAAAGG	TACCGTCTCA	TGAAATTATG	GATGTTGGGT	TACGAGTATT	650
	AGATACTCAG	ATCCCCGTCT	TAAAGGGAGG	AACTTTTTGT	ACTCCAGGGC	700
	CTTTTGGTGC	AGGAAAGACC	GTTTTACAGC	ACCATTTATC	TAAGTATGCA	750
	GCTGTAGATA	TCGTAGTTTT	GTGTGCTTGT	GGAGAGCGAG	CTGGAGAGGT	800
	TGTAGAAATT	CTTCAGGAGT	TCCCGCATTT	GACAGATCCT	CATACGGGGC	850
50	AGTCTTTGAT	GCATAGGACC	TGTATTATTT	GTAATACATC	TTCCATGCCT	900
	GTAGCAGCTA	GAGAGTCCTC	CATTTATTTG	GGTATTACTA	TAGCAGAATA	950
	TTACCGTCAA	ATGGGGTTGC	ATGTTTTGTT	ATTGGCTGAC	TCGACATCTA	1000
	GATGGGCTCA	AGCTTTAAGG	GAAATTTTCA	GGCGATTAGA	AGAAATCCCT	1050
	GGAGAAGAAG	CTTTCCCAGC	CTATTTGGCG	TCTCGAATAG	CAGCTTTTTA	1100
55	TGAGCGAGGC	GGGGCTGTGA	AAATGAAAGA	TGGATCGGAA	GGCTCCTTGA	1150
	CTATCTGTGG	AGCGGTTTCT	CCCGCAGGAG	GAAATTTTGA	AGAGCCTGTT	1200
	ACACAAGCAA	CTTTATCTGT	TGTTGGGGCT	TTCTGTGGGC	TTTCTAAGGC	1250
	TAGAGCAGAT	GCTAGACGGT	ATCCTTCTAT	TGATCCGATG	ATTTTCATGGT	1300
	CTAAGTACTT	GGATTCTGTG	CGCGAGATTT	TAGAGAAAAA	AGTTCCAGGA	1350
60	TGGGGAGATT	CCGTTAAAAA	AGCTTCTCGT	TTCTTAGAAG	AAGGAGCAGA	1400

```

AATTGGTAAG CGAATAGAAG TTGTTGGGGA AGAAGGGATT TCTATGGAAG 1450
ATATAGAAAT CTTTTTGAAG TCAGAGTTGT ATGATTCTCTG TTACTTACAG 1500
CAAAACGCTT TCGATGCAGA GGAAGTGTAT TGTCCCTTTG ATCGTCAAAT 1550
AGAGCTTTTT TCTTTAATGA GTCATATTTT TAGCTCTAGA TTCTGTTTTG 1600
5 ATTGTCCAGA TAATGCTCGG AGTTTCTTTT TAGAGCTTCA AAGTAAATTT 1650
AAAACGCTGA ATGGTCAAAA ATTCCTTTCT GAAGACTATC AGAAGGGGCT 1700
AGAAGTGATC TATAAACTAT TAGAAAGCAA AATGGTGCAG ACGGCGTAGG 1750
TATGCAAACA ATATATACAA GAATTACGG 1779

```

10

2) INFORMATION FOR SEQ ID NO: 712

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 965 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Enterococcus faecalis
    (B) STRAIN: V583

```

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712

```

GTGCAAATTG GAAAAATTGT CAAAGTTTCA GGTCCCTTGA TTTTAGCTGA 50
AAACATGTCA GATGCTAGTA TCCAAGACAT TTGTCATGTA GGAGATTTAG 100
30 GCGTTATCGG AGAGATTATT GAAATGCGAG GCGACGTCGC TTCGATTCAA 150
GTATATGAAG AAACAACAGG CATTGGACCA GGAGAACCAG TTATTTCAAC 200
AGGAGAACCA TTATCTGTTG AATTAGCCCC AGGTTTAATT GCCGAAATGT 250
TTGATGGTAT TCAACGACCA TTGGATACAT TTCAAGAAGT AACCCACAGT 300
AACTTTTTAG GCCGTGGCGT TAAAATTGAT GCGTTAGATC GTGAGAAAAA 350
35 ATGGACGTTT GAACCAACTG TGGCAGTTGG TGAAGAAGTG TCGGCAGGTG 400
ACATCGTCGG TGTGTTTCAA GAAACACCGA TTATTCAACA TAAAATTATG 450
GTGCCTTTCG GCGTTTCAGG AACGATTGCC GAAATTAAAG CAGGTGACTT 500
TGCCATTGAT GAAACAGTTT ACTCAGTGGA AACGGCTAAA GGAACGGAAA 550
GTTTTAGCAT GATGCAAAAA TGGCCCGTTC GGCGGGGACG TCCCATTTTA 600
40 GAAAAACTAA GTCCCAAAGT ACCGATGGTG ACCGGACAAC GCGTAATTGA 650
TACCTTTTTT CCAATTACGA AAGGCGGAGC GGCAGCAGTT CCAGGACCAT 700
TTGGCGCTGG AAAAACAGTC GTTCAGCACC AAATTGCTAA GTGGGCCGAT 750
GTCGACTTAG TCGTTTACGT TGGTTGTGGG GAACGCGGGA ATGAAATGAC 800
AGATGTTTTA AATGAATTTT CAGAATTAAT TGACCCAACA ACTGGTGAGT 850
45 CTTTGATGAA TCGGACGATT TTAATTGCGA ATACGTCAA TATGCCGGTA 900
GCGGCACGGG AAGCCTCGAT TTATACAGGG ATTACCATTG CAGAATATTT 950
CCGTGATATG GGTTA 965

```

50

2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 1737 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Methanosarcina barkeri*

(C) ACCESSION NUMBER: extracted from J04836

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

	GTGGAAGTAA	AAGGTGAAAT	TTATCGTGTG	TCTGGGCCTG	TCGTCACCGC	50
	CATCGGCTTG	CAGGCAAAAA	TGTATGACCT	GGTCAAAGTC	GGTAATGAAG	100
	GTTTAATGGG	TGAAGTCATT	CAGATATTAG	GGCCCAAGAC	CATCATCCAG	150
10	GTATATGAAG	AGACCGCAGG	TATCAAGCCA	GGGGAACCCT	GTGTATCTAC	200
	AGGGTCGTCT	CTGTCCGTAG	AACTTGGTCC	GGGTCTTCTT	TCCAGTATTT	250
	ATGACGGGGT	TCAAAGGCCCT	CTGCACGTCC	TGCTTGAAAA	AATGGGTTAGC	300
	TTCATCCAGA	GAGGTGTCAG	CGCAGATGGG	CTTGATCATA	AGAAACTCTG	350
	GGATTTCAAA	CCCATTGTCA	AGAAGGGCGA	TTCCGTAAAA	GGTGGAGACG	400
15	TAATTGGTGT	TGTACAGGAA	ACCGTGAATA	TTGAACATAA	GATCATGGTG	450
	CCTCCTGATA	TCTCAGGTAC	AATTTCCGAC	ATAAAGAGCG	GAAACTTTAC	500
	GGTAGTAGAC	ACAATCTGTA	CTCTGACTGA	TGGGACCGAA	TTGCAGATGA	550
	TGCAGAGGTG	GCCTGTTTCA	AGACCCAGAC	CTGTGAAGGC	AAAACCTTACT	600
	CCAACCAGGC	CTCTGGTTAC	AGGAATGAGA	ATCCTTGATG	GGCTTTTCCC	650
20	TGTGGCAAAA	GGCGGAACAG	CTGCAATCCC	CGGACCTTTC	GGATCGGGAA	700
	AGACCGTAAC	TCAGTAGTCG	CTTGCAAAAT	GGAGTGATAC	CGAAATTGTG	750
	GTCTACATCG	GTTGTGGTGA	CGGTGGAAC	GAAATGGCAG	ATGTTCTGAG	800
	CGAATTCCCT	GAACTCGAAG	ATCCGCAGAC	CGGGCGCCCA	CTTATGGAGC	850
	GTAATGTTCT	TATCGCTAAC	ACTTCAAACA	TGCCTGTGGC	CGCAAGAGAA	900
25	GCATCTGTGT	ATACCGGAAT	CACCATTGCA	GAATACTACC	GTGACATGGG	950
	ATTAGATGTA	TCCCTTATGG	CAGACTCCAC	CTCAAGGTGG	GCAGAAGCCA	1000
	TGAGAGAAAT	CTCTTCCCGT	CTGGAAGAAA	TGCCTGGTGA	AGAAGGTTAC	1050
	CCAGCATACC	TGTCTGCAAG	ACTGGCCGAA	TTCTACGAGC	GTGCCGGGGT	1100
	TGCGGAGAGT	CTTTGCGGGC	AAACAGGTTT	CATTACTGTT	ATTGGAGCAG	1150
30	TATCTCCACC	TGGCGGTGAC	TTCTCAGAGC	CTGTTACACA	GAATACCCTG	1200
	CGTATCGTAA	AAGTGTTCTG	GGCTCTCGAT	GCCAAACTAT	CTCAGAGGCG	1250
	TCACTTCCCG	GCCATCAACT	GGCTGAACAG	TTACAGTCTG	TATAAGGACA	1300
	GTCTTAATGA	CTGGTTTTCG	GATAATGTGG	CTCCTGATTA	TGTGCCTTTG	1350
	AGGGAAAGAG	CAATGGAAAT	GCTCCAGACA	GAATCTGAAC	TGCAGGAAAT	1400
35	CGTGCAGCTT	GTAGGTTCCG	ATGCTCTGCC	AGACGACCAG	CAGCTTCTGC	1450
	TTGAAATCAC	CCGTATGCTT	AGGGAAATTT	TCCTGCAGCA	GAATGCATTC	1500
	CACCCAGTAG	ATGCATACAG	CCCGTTTCGAT	CAGCAGTACA	AGATCCTTAA	1550
	GGCAATCATG	AAATGGGGAG	ACGCTGCGAT	GGATGCCTTG	AAATCAGGTG	1600
	TTCCCGTAAC	TGAAATTATC	AAGCTTGAAT	CCAAAAATGT	GCTTGCTAAG	1650
40	GTCAAGTACG	AAGAGAAGTT	TGATGAGTCT	ATGAATGCTG	TCCTGGCACA	1700
	GATGGATAAA	GAGTTTGCAT	CCCTGAGAGG	TAGGTAA		1737

45 2) INFORMATION FOR SEQ ID NO: 714

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1785 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Methanosarcina jannaschii*

(C) ACCESSION NUMBER: extracted from U67477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

60

	ATGAAAAGAG	AGGTTGAGAA	TATGCCAGTT	GTTGGTAAGA	TTATTAAAAAT	50
	CGCAGGGCCT	GTTGTAGTTG	CAGAGGGAAT	GAAAGGAGCT	CAGATGTATG	100
	AGGTCGTTAA	AGTAGGAGAA	GAGAAATTGA	CTGGAGAAAT	CATTCAGTTG	150
	CACGATGATA	AAGCAGTTAT	TCAGGTTTAT	GAAGAAACAT	CTGGAATTAA	200
5	ACCAGGAGAG	CCAGTTGTTG	GTACTGGAGC	TCCATTGTCT	GTTGAATTAG	250
	GGCCAGGGAT	GTTAAGAGCT	ATGTATGATG	GTATTCAGAG	GCCTTTAACA	300
	GCAATTGAAG	AGAAAACAGG	TTCAATCTTT	ATCCCAAGAG	GAGTTGATGT	350
	CCCTGCATTA	CCAAGAGATA	TAAAATGGGA	ATTTAAACCA	GTGGTAAATG	400
	AAGGAGATTA	TGTTGAAGAA	GGAGACATAA	TTGGAACGTG	TGATGAAACT	450
10	CCTTCAATAG	TTCATAAAAT	CTTAGTTCCA	ATTGGTGTTA	AAGGAAAAAT	500
	TGTTGAAATA	AAAGAGGGTA	AATTTACAGT	TGAAGAGACA	GTTGCAGTTG	550
	TAGAAACAGA	AAATGGAGAA	AGGAAAGAAA	TTACAATGAT	GCAAAAATGG	600
	CCAGTAAGAA	AACCAAGACC	ATATAAAGAG	AAACTACCTC	CAGAAATTCC	650
	ATTAATTACA	GGGCAAAGAG	TTGAAGACAC	TTTCTTTACA	TTAGCAAAAG	700
15	GAGGAACAGC	AGCAATTCCA	GGTCCATTCT	GTTTCAGGAA	AACGGTTACT	750
	CAGCATCAGT	TGGCAAAGTG	GTCTGACGCT	GATGTCGTTG	TTTATATCGG	800
	ATGTGGAGAA	AGAGGAAACG	AGATGACAGA	GGTTATTGAA	GAGTTCCCAC	850
	ACTTAGAAGA	TATTAGAACT	GGAAACAAAT	TAATGGATAG	AACTGTATTA	900
	ATAGCCAACA	CATCAACAT	GCCTGTCGCT	GCAAGGGAAG	CATCTGTCTA	950
20	TACAGGAATT	ACAATTGCAG	AGTACTTCAG	AGATATGGGT	TATGGAGTTT	1000
	TATTAACAGC	AGATTCAACA	TCAAGATGGG	CAGAGGCAAT	GAGAGAAATT	1050
	TCAGGTAGAT	TGGAAGAAAT	GCCAGGGGAA	GAAGGGTATC	CAGCATACTT	1100
	AGCTTCAAGA	TTGGCTCAGT	TCTATGAAAG	AGCTGGAAGA	GTTATAACCT	1150
	TAGGGAAAGA	TAACAGACAA	GGATTCGTTT	GTATCGTTGG	AGCTGTTTCA	1200
25	CCACCAGGAG	GGGACTTCTC	AGAACCAGTT	ACATCAAACA	CACTAAGGAT	1250
	AGTTAAGGTA	TTCTGGGCGT	TAGATGCAAA	CTTGGCAAGA	AGAAGACACT	1300
	TCCCAGCTAT	CAACTGGTTG	CAGAGTTATT	CATTATACAT	TGATGATGTT	1350
	ACAGAGTGGT	GGAACACAAA	TACTGGTCCA	GATTGGAGAC	AATTAAGAGA	1400
	TGAAGCAATG	AGCTTATTAC	AAAAAGAGGC	AGAGTTGCAA	GAGATTGTTC	1450
30	AGTTAGTTGG	GCCTGATGCA	TTGCCAGATA	GGGAGAGAGT	TATTTTGTAG	1500
	GTTGCAAGAA	TGTTGAGGGA	GGATTTCTTA	CAGCAAGATG	CGTTTGTATG	1550
	GGTAGATACC	TACTGTCTCT	CAATGAAACA	GTACTTAATG	TTAAAGATAA	1600
	TTATGACATT	CTACCAAGAA	GCATTGAAGG	CAGTTGAAAG	AGGAGTTGAA	1650
	CCAGCTAAGA	TTTTAGGAGT	TTCAGTTAAG	CAAGATATTG	CAAGAATGAA	1700
35	ATACATCCCA	CACGATGAGT	TTATAAATGT	TAAATCAAAA	GAAATAATGG	1750
	AGAAAATTAA	GAATGAATTA	GGTTCATTAA	ACTAA		1785

40 2) INFORMATION FOR SEQ ID NO: 715

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1354 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*
 (B) STRAIN: W83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

55	GTAGCGAGGT	GATCAAGGTG	ATCGGCAAAA	ATGCTTATGT	GCAGGTTTTTC	50
	GAAAGTACTC	GCGGTATGCA	CGTAGGAGAT	GAGGCAGAGT	TTACCGGCAG	100
	TATGCTTGAG	GTAACGCTCG	GCCCCGGTAT	GCTTTTCAAG	AACTACGACG	150
	GTCTGCAACA	CGACTTGGAC	AAGATGGACG	GGATCTTCCT	CAAACGAGGC	200
60	GATTATACTC	CCGCTCTCGA	TGACGACAAG	CTGTGGGACT	TCAAGCCTTT	250

	GGCCAATGTG	AACGACAATG	TGATCGCAGG	CTCATGGCTC	GGAGAGGTGA	300
	CGGAAAATTT	CCAACCGCAC	AAGATCATGG	TACCTTTCGT	TTTCGAAGGC	350
	AATTACAAGG	TGAAGAGTCT	GGCCAAAGCC	GGTTCGTACA	AAGTGAACGA	400
	TGTGATCGCT	GTGGTAACGG	ATCAGGACGG	GAAAGACCAC	AATGTAACCA	450
5	TGGTGCAGAA	ATGGCCGGTG	AAACGTGCTA	TCACTTGCTA	TCGCGAGAAG	500
	CCGCGTCCTT	TCAAACCTGCT	CGAAACGGGT	ATCCGTATCA	TCGACACTTT	550
	CAACCCCATC	GTAGAGGGTG	GTACGGGATT	TATCCCCGGT	CCTTTCGGTA	600
	CGGGAAAGAC	GGTGCTCCAG	CATGCTATCT	CGAAGCAGGC	GGAAGCCGAT	650
	ATCGTGATCA	TTGCAGCCTG	TGGCGAGCGT	GCAAACGAGG	TTGTGGAGAT	700
10	CTTTGCGGAA	TTCCCCCACC	TGAATGACCC	CCACACGGGA	CGTAAATTGA	750
	TGGAACGTAC	CATTATTATT	GCTAATACGT	CGAATATGCC	TGTGGCTTCG	800
	CGTGAGGCAT	CCGTATATAC	GGCCATGACG	ATAGCCGAGT	ACTATCGCTC	850
	CATGGGCCCTT	CGCGTGCTGA	TGATGGCAGA	CTCCACTTCG	CGTTGGGCAC	900
	AGGCTCTCGG	TGAGATGTCT	AACCGTCTGG	AAGAGCTTCC	CGGACCGGAT	950
15	GCTTTTCCGA	TGGACTTGTC	AGCTATCGTA	GCCAACTTCT	ACGCTCGTGC	1000
	AGGATACGTT	TACCTGAACA	ACGGTTTCGGC	CGGTTTCGGTA	ACGTTTCATCG	1050
	GTACGGTATC	TCCCGCCGGT	GGTAACCTCA	AAGAGCCTGT	GACGGAAAAC	1100
	ACCAAGAAAG	TGGCTCGCTG	CTTCTATGCT	TTGGAGCAGA	ATCGTGCCGA	1150
	CCGCAAACGT	TATCCGGCTG	TAAACCCCAT	CGATAGTTAC	TCGAAGTACA	1200
20	TCGAATATCC	CGAATTCGAG	AGCTATATAT	CGAACCACAT	CAGTTTACTC	1250
	ATTATATTCA	ACAGAAAGTTG	GCAGATATAT	GGATCAAATC	TTACAGCAGA	1300
	CTGGACTACT	AAGGTGAATG	AGCTGAAGAT	GCGCTTGCAT	CAGGGTAAAG	1350
	AAAT					1354

25

2) INFORMATION FOR SEQ ID NO: 716

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1788 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: Type 4
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

	TTTGACTCAA	GGGAAGATTA	TAAAGTATC	GGGACCTCTA	GTTATTGCAT	50
	CAGGTATGCA	GGAGGCTAAT	ATTCAAGATA	TTTGCCGTGT	AGGTAAGCTA	100
45	GGGTTAATCG	GTGAAATTAT	TGAAATGAGA	AGAGATCAGG	CATCTATCCA	150
	AGTCTATGAA	GAAACATCTG	GTCTTGGTCC	GGGAGAACCT	GTTGTTACAA	200
	CTGGAGAACC	TCTCTCGGTT	GAATTAGGGC	CAGGATTGAT	TTCTCAAATG	250
	TTTGATGGCA	TACAACGCCC	ATTAGATCGA	TTTAAATTGG	CTACTCATAA	300
	TGATTTTCTA	GTTTCGTGGGG	TAGAAGTTCC	AAGTTTGGAT	AGAGATATTA	350
50	AGTGGCATTT	TGATTCCACT	ATAGCAATTG	GTCAAAAAGT	GAGTACGGGT	400
	GATATTCTTG	GAAGTGTCAA	GGAAACCGAG	GTAGTTAATC	ATAAAATTAT	450
	GGTTCCTTAT	GGAGTATCTG	GAGAAGTCGT	TTCTATTGCA	TCTGGCGATT	500
	TTACAATTGA	TGAAGTTGTA	TATGAAATAA	AAAAATTGGA	CGGTAGTTTC	550
	TATAAAGGAA	CGCTTATGCA	AAAATGGCCT	GTCCGCAAGG	CGCGTCCTGT	600
55	TTCTAAACGT	TTAATTCCAG	AAGAACCATT	AATCACAGGT	CAACGAGTTA	650
	TTGATGCATT	CTTTCCAGTA	ACCAAAGGGG	GAGCTGCAGC	AGTTCCTGGA	700
	CCGTTTGGAG	CAGGAAAGAC	AGTTGTACAA	CACCAAGTAG	CTAAATTTGC	750
	CAATGTTGAT	ATTGTTATTT	ATGTCGGTTG	TGGAGAACGT	GGAAATGAAA	800
	TGACGGATGT	ACTGAATGAG	TTTCCTGAGT	TGATTGACCC	TAATACCGGA	850
60	CAATCAATTA	TGCAACGGAC	AGTTCTGATT	GCTAATACTT	CAAATATGCC	900

TGTTCGCTGCT CGTGAGGCTT CAATTTATAC AGGAATTACC ATGGCTGAGT 950
 ATTTTCGTGA TATGGGCTAC TCTGTCGCCA TTATGGCTGA TTCAACTTCA 1000
 CGTTGGGCAG AAGCGCTACG TGAAATGTCA GGACGTCTAG AAGAAATGCC 1050
 TGGTGATGAG GGTATCCTG CTTATCTGGG AAGTCGTATC GCTGAATATT 1100
 5 ATGAAAGAGC AGGACGTTCT CAGGTTCTAG GGCTTCCAGA ACGTGAAGGA 1150
 ACGATTACTG CTATTGGAGC TGTATCGCCA CCTGGTGGAG ATATTTTCAGA 1200
 ACCAGTTACT CAAAACACTT TACGGATTGT GAAAGTTTTT TGGGGGCTTG 1250
 ATGCTCCGTT GGCACAGCGA CGTCATTTTC CTGCAATTAA CTGGCTTACA 1300
 TCTTATTCAC TATATAAAGA CAGTGTGGGC ACTTATATAG ATGGTAAAGA 1350
 10 GAAGACAGAT TGAATAGTA AAATAACTCG TGCGATGAAC TACTTACAAC 1400
 GGAATCTAG TTTAGAGGAA ATTGTTTCGTC TTGTTGGAAT TGATTCTCTG 1450
 TCTGATAATG AACGACTAAC GATGGAAATT GCTAAACAAA TTCGAGAAGA 1500
 TTATTTGCAA CAGAACGCTT TTGATTCGGT AGATACATTC ACTTCGTTTG 1550
 CAAAACAAGA AGCAATGCTA AGTAATATTC TCACTTTTGC TGATCAGGCA 1600
 15 AATCATGCTT TAGAGTTGGG TTCTTACTTT ACAGAGATTA TGGAAGGTAC 1650
 CGTGGCAGTT CGAGACCGTA TGGCGAGAAG TAAATATGTT TCAGAAGATA 1700
 GATTAGATGA AATCAAAAT ATATCAAATG AGATTACACA TCAAATTCAT 1750
 TTGATATTAG AAACAGGAGG TCTATAAATG AGTGTTAT 1788

20

2) INFORMATION FOR SEQ ID NO: 717

- (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

CGATCCTGGT GTGCTCGGCC GCTGACGGCC CGATGCCGCA AACGCGTGAG 50
 CACATCCTGC TGGCGCGTCA GGTGCGGTGTG CCGTACATCA TCGTGTTCCT 100
 40 GAACAAGTGC GACATGGTGG ACGACGCGGA GCTGCTCGAG CTGGTCGAAA 150
 TGGAAGTGCG CGAAGTGTG TCGAAGTACG ACTTCCCGGG CGACGACACG 200
 CCGATCATCA AGGGTTCGGC GAAGCTGGCG CTGGAAGGCG ACAAGGGCGA 250
 GCTGGGCGAA GTGGCGATCA TGAACCTGGC CGACGCGCTG GACACGTACA 300
 TCCCGACGCC GGAGCGTGCG GTCGACGGCG CGTTCCTGAT GCCGGTGGAA 350
 45 GACGTGTTCT CGATCTCGGG CCGTGGTACG GTGGTGACGG GTCGTGTCGA 400
 GCGCGGCGTG ATCAAGGTTG GCGAGGAAAT CGAAATCGTC GGTATCAAGG 450
 CGACGGCGAA GACGACCTGC ACGGGCGTGG AAATGTTCCG CAAGCTGCTG 500
 GACCAGGGTC AGGCGGGCGA CAACGTCGGT ATCCTGCTGC GCGGCACAAA 550
 GCGTGAAGAC GTGGAGCGCG GCCAGGTTCT GGCGAAGCCG GGTTCGATCA 600
 50 CGCCGCACAC GCACTTCACG GCAGAAGTGT ACGTGCTGAG CAAGGACGAA 650
 GGCGGCCGCC ACACGCCGTT CTTCAACAAC TACCGTCCGC AGTTCTACTT 700
 CCGTACGACG GACGTGACGG GCTCGATCGA GCTGCCGAAG GACAAGGAAA 750
 TGGTGATGCC GGGCGACAAC GTGTCGATCA CCGTGAAGCT GATCGCGCCG 800
 ATCGCGATGG AAGAAGGTCT GCG 823

55

2) INFORMATION FOR SEQ ID NO: 718

- 60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia pseudomallei*
 (B) STRAIN: 1026B

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

15	GCGATCCTGG	TGTGCTCGGC	CGCTGACGGC	CCGATGCCGC	AAACGCGTGA	50
	GCACATCCTG	CTGGCGCGTC	AGGTCGGTGT	GCCGTACATC	ATCGTGTTCC	100
	TGAACAAGTG	CGACATGGTG	GACGACGCGG	AGCTGCTCGA	GCTGGTCGAA	150
	ATGGAAGTGC	GCGAACTGCT	GTCGAAGTAC	GACTTCCC GG	GCGACGACAC	200
	GCCGATCATC	AAGGGTTCGG	CGAAGCTGGC	GCTGGAAGGC	GACAAGGGCG	250
	AGCTGGGCGA	AGTGGCGATC	ATGAACCTGG	CCGACGCGCT	GGACACGTAC	300
20	ATCCCGACGC	CGGAGCGTGC	GGTCGATGGC	GCGTTCCTGA	TGCCGGTGGA	350
	AGACGTGTTT	TCGATCTCGG	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	400
	AGCGCGGCGT	GATCAAGGTT	GGCGAGGAAA	TCGAAATCGT	CGGTATCAAG	450
	GCGACGGCGA	AGACGACCTG	CACGGGCGTG	GAAATGTTCC	GCAAGCTGCT	500
	GGATCAGGGT	CAGGCGGGCG	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	550
25	AGCGTGAAGA	CGTGGAGCGC	GGCCAGGTTT	TGGCGAAGCC	GGGTTTCGATC	600
	ACGCCGCACA	CGCACTTCAC	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	650
	AGGCGGCCGC	CACACGCCGT	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	700
	TCCGTACGAC	GGACGTGACG	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	750
	ATGGTGATGC	CGGGCGACAA	CGTGTGATC	ACGGTGAAGC	TGATCGCGCC	800
30	GATCGCGATG	GAAGAAGGTC	TGCG			824

2) INFORMATION FOR SEQ ID NO: 719

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

50

55	TGTATCAGCA	GCAGATGGTC	CAATGCCACA	AACAAGAGAA	CATATACTAC	50
	TAGGATCAAG	AGTTGGTATC	CAATATATCG	TAGTATTCTT	AAATAAAGCA	100
	GATATGGTAG	ACGATCCAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTAAG	150
	AGAATTATTA	AGCGAATATG	ACTTCCCAGG	AGACGATATT	CCAGTAATAA	200
	CAGGATCAGC	ATTAAAAGCA	TTAGAAAATC	CAACAGATGA	AGAAGCAATT	250
	AAGCCAATCA	TGGATTTAAT	GGAAGCAGTA	GATAGCTATA	TCCCAACTCC	300
	AGAAAGAGCA	ACAGATAAGC	CATTCTTAAT	GCCAATCGAA	GATGTATTCA	350
	CAATTACAGG	AAGAGGAACA	GTTGCAACAG	GAAGAGTTGA	AGCTGGAGTA	400
	CTTCATGTAG	GAGATGAAGT	AGAAATCGTT	GGATTAACAG	AAGAAAAGAA	450
60	GAAAGTTGTA	GTAAGTGGAA	TCGAAATGTT	CAGAAAGTTA	TTGGATGAAG	500

```

5  CACAAGCTGG AGATAACATC GGAGCATTAT TAAGAGGAGT TCAAAGAACT 550
   GATATTGAAA GAGGTCAAGT TTTATCAAAA CCAAATTCAG TACACCCTCA 600
   CACTAAATTT GTAGGTCAAG TATACGTACT TAAAAAAGAA GAAGGTGGAA 650
   GACATACTCC ATTCTTTGAT GGATACAGAC CACAATTCTA TTTCAGAACA 700
   ACAGACGTTA CAGGRTCAAT CAAGTTACCA GATGGAATGG AAATGGTAAT 750
   GCCTGGAGAT CACATTGATA TGAATGTTGA ATTAATCACT CCAATCGCAA 800

```

10 2) INFORMATION FOR SEQ ID NO: 720

(i) SEQUENCE CHARACTERISTICS:

```

15  (A) LENGTH: 799 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Clostridium innocuum
    (B) STRAIN: ATCC 14501

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

```

25  GGTGCTATCC TGGTTGTTGC TGCATCTGAT GGTCCCTATGC CTCAGACTCG 50
    TGAGCACATC CTGCTTGCTC GTCAGGTAGG TGTTCCCTTAC ATCGTTGTAT 100
    TCCTGAACAA ATGCGACATG GTTGATGACG AAGAACTGAT CGACCTTGTT 150
    GAAATGGAAG TACGTGAGCT GTTAAGCGAG TACGGATTCTG ACGGAGATAA 200
30  CGCTCCGGTT ATCCGTGGTT CTGCACTGAA GGCTCTGGAA GGTGACGACA 250
    AATACGTTGG CGCTATCAAA GAACGTGATGG ATGCAGTTGA TGAATTCATC 300
    CCAGATCCAA CTCGTGAAAC TGACAAACCA TTCCTGATGT CTGTAGAAGA 350
    CGTTATGACA ATCACAGGAC GTGGTACAGT TGCTACAGGA CGTGTTGAGC 400
    GTGGGGTAGT AAAACTGGGA GAAGAAGTTG AAATCGTTGG TATCAAGGAT 450
35  ACTCAGAAAA CTGTTGTTAC CGGACTGGAA ATGTTCCGTA AGCAGCTGGA 500
    CTTTCGAGAA TCCGGAGACA ACATCGGTGC TCTGCTGCGT GGTATCAACC 550
    GTGACCAGAT TCAGCGTGGA CAGGTTCTTG CTAAACCAGG ATCCGTACAT 600
    CCACACACAA AGTTCAAGGC TCAGGTTTAT GTATTAACAA AAGAAGAAGG 650
    TGGACGTCAC ACTCCATTCTG TTTCTAATC CCGTCCTCAG TTCTACTTCC 700
40  GTACAACTGA CGTAACTGGT GTTATTACAT TACCGGAAGG AACTGAAATG 750
    GTTATGCCTG GTGACAACGT TGAAATGAAC GTTGAGCTGA TTGCTCCAA 799

```

45 2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:

```

50  (A) LENGTH: 789 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Clostridium novyi
    (B) STRAIN: ATCC 19402

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

60

```

TTGTATCAGC AGCAGATGGT CCAATGCCAC AAACAAGAGA ACACATCCTA      50
TTAGCATCAA GAGTAGGAGT TAACCACATA GTAGTATTCT TAAACAAAGC      100
AGACCAAGTA GATGATCCAG AATTACTAGA ATTAGTAGAA ATGGAAGTAA      150
GAGAATTATT AAGCGAATAC GGATTTGACG GAGACGAATG TCCAGTAGTA      200
5 GTAGGATCAG CATTA AAAAGC AATCGAAGAA GGGGATGACC AATGCATCCT      250
AGACTTAATG AAAGCTGTAG ATGAATATAT CCCAACTCCA GAAAGAGCAA      300
CAGATCAACC ATTCTTAATG CCTGTAGAAG ATGTATTTAC AATTACAGGA      350
AGAGGAACAG TTGCAACAGG AAGAGTTGAA AGAGGAGTAC TACACGTAGG      400
AGATGAAGTA CAAATCGTAG GAATGAAAGA AGAAATCGGA AAGACAACAA      450
10 TCACAGGAGT AGAAATGTTT AGAAAGATGT TAGATGAAGC AATGGCTGGA      500
GATAACATCG GAGCATTATT AAGAGGAGTA CAAAGAGACG AAATCGAAAG      550
AGGTCAAGTA CTAGCAAAAC CAGGTTTCAGT AACACCTCAC AAAAAATTCTG      600
TAGGTCAAGT TTACGTATTA AAGAAAGAAG AAGGTGGAAG ACACACTCCA      650
TTCTTTAACG GATACAGACC ACAATTCTAC TTCAGAACAA CAGACGTAAC      700
15 AGGATCAATC GCTTTACCAG AAGGAGTAGA AATGGTAATG CCAGGAGACC      750
ATATAGACAT GAACGTAGAA TTAATCACAC CAGTAGCAA      789

```

20 2) INFORMATION FOR SEQ ID NO: 722

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 798 bases
(B) TYPE: Nucleic acid
25 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Clostridium septicum
(B) STRAIN: ATCC 12464

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

```

35 GTTCAGCAGC AGACGGTCCA ATGCCACAAA CAAGAGAACA TATACTACTA      50
GCATCAAGAG TTGGTGTGTA CTATATCGTA GTATTCTTAA ACAAGGCAGA      100
TATGGTAGAT GACGAAGAAT TATTAGAATT AGTAGAAATG GAAGTTAGAG      150
AATTATTATC AGAATACAAC TTCCCAGGAG ATGATATTCC AGTAATCAAG      200
40 GGATCAGCTT TAGTAGCATT AGAAAACCCA ACAGATGAAA AATCAATCGC      250
TCCAATCTTA GAATTAATGG AAGCAGTAGA TAGCTACATT CCAACACCAG      300
AAAGAGCAAC AGATAAGCCA TTCTTAATGC CAGTAGAAGA TGTATTACAA      350
ATAACTGGTA GAGGAACAGT TGCAACAGGA AGAGTTGAAA GAGGAGTTCT      400
TCATGTAGGA GACGAAGTAG AAATCGTTGG ATTATCAGAA GAAAGCAGAA      450
45 AAGTAGTAGT AACAGGAATA GAAATGTTCA GAAAGTTACT AGACGAAGCA      500
CAAGCTGGAG ATAATGTTGG AGTACTTTTA AGAGGTGTTT AAAGAACAGA      550
TATCGAAAGA GGTCAAGTAT TAGCAAAGAC TGGATCAGTT AAGCCACACA      600
GCAAGTTCGT AGGTCAAGTA TACGTACTTA AGAAAGAAGA AGGTGGAAGA      650
CATACTCCAT TCTTCGATGG ATACAGACCA CAATTCTACT TCAGAACAAC      700
50 AGACGTTACT GGATCAATCA AATTACCAGA CGGAATGGAA ATGGTTATGC      750
CAGGAGACCA CATTGATATG AACGTTGAAT TAATCACTCA AGTAGCAA      798

```

55 2) INFORMATION FOR SEQ ID NO: 723

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 799 bases
(B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Double

```

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

```

10 GTTCAGCAGC AGATGGTCCA ATGCCTCAAA CAAGAGAACA CATACTACTA      50
   GCTTCAAGAG TTGGTGTTGA CTACATAGTT GTTTCTTAA ACAAGGCAGA      100
   TATGGTAGAT GACGAAGAAT TATTAGAATT AGTTGAAATG GAAGTAAGAG      150
   AATTATTATC AGAATACAAC TTCCCAGGAG ATGATATTCG AGTAATAAAG      200
15 GGTTCAGCTT TACAAGCATT AGAAAACCCA ACAGATGAAA AAGCAATCGC      250
   TCCAATCCTT GAGTTAATGG AAGCTGTAGA TAGCTACATT CCAACTCCAG      300
   AAAGAGCAAC AGATAAGCCA TTCTTAATGC CAGTAGAAGA TGTATTCACA      350
   ATCACTGGTA GAGGAACAGT TGCTACAGGA AGAGTTGAAA GAGGAGTTCT      400
   TCACGTAGGA GACGAAGTAG AAATCGTTGG ATTATCAGAA GACAGCAGAA      450
20 AAGTAGTAGT AACAGGAATA GAAATGTTCA GAAAGTTACT AGACGAAGCG      500
   CAAGCTGGAG ACAACGTAGG AGTTCTTTTA AGAGGAGTTC AAAGAAGTGA      550
   CATCGAAAGA GGTCAAGTTT TAGCAAAAGT TGGATCAGTT AAGCCACACA      600
   AGAAATTTGT AGGTCAAGTA TACGTACTTA AAAAAGAAGA AGGTGGAAGA      650
   CATACTCCAT TCTTCGATGG ATACAGACCA CAATTCTACT TCAGAACAAC      700
25 AGAYGTTACT GGTTCATCA AGTTACCAGA TGGAAATGGAA ATGGTTATGC      750
   CAGGAGACCA CATTGATATG AACGTTGAAT TAATCACTCA AGTAGCTAT      799

```

30 2) INFORMATION FOR SEQ ID NO: 724

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium tetani*
 (B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

```

45 TAGTAAGTGC AGCAGATGGT CCAATGCCAC AAACAAGAGA ACACATACTA      50
   TTAGCATCCA GAGTTGGAGT TGAGCACATA GTAGTATTCT TAAATAAAGC      100
   AGACCAAGTA GATGACGCAG AGTTAATCGA ATTAGTAGAA ATGGAAGTAA      150
   GGGAATTAAT GAACGAATAC GGATTCCTCAG GAGATGACGC ACCAGTAGTA      200
50 GTAGGATCCG CATTAAAAGC ATTAGAAAAT CCAGAAGATG ATGCAGCAAC      250
   ACAATGCATA ATGGACTTAA TGGCAGCAGT AGATGAATAT ATACCAACAC      300
   CAGAAAGAGC AACAGATAAG CCATTCTTAA TGCCAGTAGA AGATATCTTC      350
   ACAATCACAG GAAGAGGAAC AGTTGCAACA GGAAGAGTAG AAAGAGGAAT      400
   TCTAAAAGTA GGAGACGAAA TAGAAATCGT AGGATTAAGT GATGAAAGCA      450
55 AGAAATCAGT AATCACAGGA ATAGAAATGT TCAGAAAACCT ATTAGATGAA      500
   GCACAAGCAG GAGATAACAT CGGAGCATTA TTAAGAGGTG TTCAAAGAGA      550
   TGAAATCCAA AGAGGTCAAG TATTAGCAGC AACAGGATCA GTAAAACCAC      600
   ATAAGAGTTT TACAGGTCAA GTATATGTAT TAAAGAAAGA AGAAGGAGGA      650
   AGACACACTC CATTCTTTAA CGGATACAGA CCACAATTCT ACTTTAGAAC      700
60 AACAGACGTA ACAGGTTCAA TCGCACTACC AGAAGGAGTA GAAATGGTAA      750

```

TGCCAGGAGA CCACATAGAC ATGAAGGTAG AATTAATAAC AAGAGTAGCA 800
A 801

5

2) INFORMATION FOR SEQ ID NO: 725

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 633 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
(B) STRAIN: ATCC 43197

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

TATGCCTCAA ACTCGTGAAC ACATCTTGTT ATCTCGTAAC GTTGGTGTTT 50
CTTACATCGT TGTATTCTTA AACAAAATGG ATATGGTTGA TGATGAAGAA 100
TTACTAGAAT TAGTTGAAAT GGAAGTTCGT GACTTATTGT CAGAATACGA 150
25 CTTCCCAGGC GACGACACTC CAGTTATCGC TGGTTCAGCT TTGAAAGCTT 200
TAGAAGGCGA TGCTTCATAC GAAGAAAAAA TCCTAGAATT AATGGCTGCT 250
GTTGATGAAT ATATCCCAAC ACCAGTTCGT GATACTGACA AACCATTTCAT 300
GATGCCAGTC GAAGATGTAT TCTCAATCAC TGGTCGTGGA ACTGTTGCAA 350
CTGGTCGTGT TGAACGTGGA CAAGTTCGCG TTGGTGACGA AGTTGAAATC 400
30 GTTGGTATTG CTGAAGCAAC TGCTAAAACA ACTGTTACAG GTGTTGAAAT 450
GTTCCGTAAT TTGTTAGATT ACGCTGAAGC AGGCGATAAC ATTGGTGCAT 500
TGTTACGTGG TGTTGCACGT GAAGACATCC AACGTGGACA AGTATTGGCT 550
AAACCAGCTT CAATCACTCC ACATACAAAA TTCTCTGCAG AAGTTTACGT 600
TTTAACTAAA GAAGAAGGCG GACGTCATAC TCC 633

35

2) INFORMATION FOR SEQ ID NO: 726

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
45 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Enterococcus sulfureus*
(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

CACGTGAACA CATCTTGTTA TCTCGTAACG TAGGTGTTCC TTACATCGTT 50
55 GTATTCTTAA ACAAATGGA TATGGTTGAT GACGAAGAAT TATTAGAATT 100
AGTAGAAATG GAAGTTCGTG ACTTATTATC AGAATACGAT TTCCCAGGCG 150
ATGACACTCC AGTTGTTGCA GGTCTGCTT TGAAAGCTTT AGAAGGCGAC 200
GCTTCTTACG AAGAAAAAAT CATGGAATTA ATGGCTGCAG TTGACGAGTA 250
CATCCCAACT CCAACTCGTG ACACTGACAA ACCATTTCATG ATGCCAGTTG 300
60 AGGATGTATT CTCAATCACT GGACGTGGTA CTGTTGCTAC AGGTCGTGTT 350

GAACGTGGAC AAGTTCGCGT TGGTGACGTT GTAGATATCG TTGGTATCGC 400
 TGACGAAACT GCTCAAACAA CTGTAACAGG TGTTGAAATG TTCCGTAAAT 450
 TATTAGACTA CGCTGAAGCA GCGGATAACA TCGGTGCTTT ATTACGTGGT 500
 GTTGCTCGTG AAGACATCCA ACGTGGACAA GTTTTAGCTA AACCAGCTTC 550
 5 AATCACTCCA CATACAAAT TCTCTGCTGA AGTATACGTA TTAAGCAAAG 600
 AAGAAGGTGG ACGTCATACT CCA 623

10 2) INFORMATION FOR SEQ ID NO: 727

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus garvieae*
 (B) STRAIN: ATCC 49156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

25 CGGTCCTATG CCTCAAACCTC GTGAACACAT CTTGTTATCA CGTAACGTTG 50
 GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT GGTTGATGAC 100
 GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA 150
 ATATGACTTC CCAGGCGACG ATGTTCCCTGT AATCGCTGGT TCTGCTTTGA 200
 30 AAGCTCTTGA AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG 250
 GCTGCAGTTG ACGAATACGT TCCAACCTCCA GAACGTGATA CTGACAAACC 300
 ATTCATGATG CCAGTCGAAG ACGTATTCTC AATCACTGGA CGTGGTACTG 350
 TTGCTACAGG CCGTGTTGAA CGTGGACAAG TTCGCGTTGG TGATGAAGTA 400
 GAAATCGTTG GTATTGCTGA CGAAACTGCT AAAACAACTG TAACAGGTGT 450
 35 TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG 500
 GTGCATTGCT ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA 550
 TTGGCTAAAG CTGGTACAAT CACACCTCAT ACAAATTCA AAGCTGAAGT 600
 TTATGTTTTG ACAAAGAAG AAGGTGGACG TCACACTCCA TTCTTC 646

40 2) INFORMATION FOR SEQ ID NO: 728

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma pirum*
 (B) STRAIN: ATCC 25960D

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

GAGCAATTTT AGTTGTTTCT GCAACTGATG GTCCAATGCC TCAAACCTCGT 50
 GAACATATCT TATTAGCACG CCAAGTTGGT GTTCCTAAAA TGGTTGTTTT 100
 CTTAAACAAA TGTGATGTTG CTTCTGATCC AGAAATGCAA GAATTAGTTG 150
 60 CTGAAGAAGT AAAAGACTTA TTAAAATCTT ATGGTTTGA TGGTGACAAT 200

```

ACTCCAATTA TTCGTGGTTC AGCATTAGAA GCATTAAATG GTAAACCTGA 250
ATGAGAAGAA AAAATTAAAG AATTAATGAA GGCAGTGGAT GACACTATTC 300
CTGATCCAGT TCGTGATACT GAAAAGCCAT TCTTGTTACC AATTGAAGAC 350
GTAATGACAA TTACAGGTCG TGGTACTGTT GTTACAGGTC GTGTAGAACG 400
5 TGGTACTCTA AAATTAAATG ATGAAGTTGA AATTGTTGGT TTAGGTGAAA 450
CATTTAAATC TGTGTAAACA GGTATTGAAA TGTTCGTAA AGAATTAGAT 500
GAAGCTCGTG CTGGTGACAA TGCTGGTATT TTACTIONCGTG GTGTTGACCG 550
TGGTCAAGTA CAACGTGGTC AAGTTCTTGC TAAACCAGGT TCTATTACTC 600
CTCATACTAA ATTTAAAGCT GAAATTTATG CTTTGAAAAA AGAAGAAGGT 650
10 GGTTCGTCATA CTGCTTTCTT AAACGGTTAT CGTCCTCAAT TCTATTTTCA 700
AACAACGTGAT GTTACAGGTT CTATTAAATT AAAAGATGGA ACTGAAATGG 750
TTATGCCTGG TGACAATACT GAAATCACTG TAGAATTAAT TTCACCAATT 800
GCTTGTAATA AGGAAGTAAG TTT 823

```

15

2) INFORMATION FOR SEQ ID NO: 729

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 826 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Mycoplasma salivarium
        (B) STRAIN: ATCC 23064

```

30

~~(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729~~

```

GGAGCAATCT TAGTTGTTGC TGCAACTGAT GGTGCGATGC CTCAAACTCG 50
TGAACACGTT TTACTTGCAA AACAAGTTGG TGTTCCTAAA ATCGTTGTTT 100
35 TCTTAAACAA AATCGATATG TTCAAGCCAG AAGAAAAGAGC CGAAATGGTT 150
GAAATGGTTG AAATGGACAT TCGTGACTTA TTAAACAAAT ACGACTTTGA 200
TGGTGACAAT ACTCCTATTA TTGCTGGTTC AGCATTAAAA GCATTACAAG 250
GTGATCCAGA ATATGAAAAG AATATTCTAG AACTTATGGA TGCAGTAGAC 300
ACATACATTG ATGAACCTAC TCGTGATAAA GATAAACCAT TCTTAATGGC 350
40 TGTAGAAGAC GTATTTACAA TTACTGGTTC TGGAACTGTT GCTACTGGTA 400
GAGTAGAACG TGGTACATTA CATCTAAATG ATGAAGTTGA AATCGTTGGT 450
CTACGTCCAA CAATTAAAC TGTGTACTT GGAATTGAAA TGTTCGTAA 500
AAATTTAAAA GAAGCTCAAG CTGGAGATAA TGCAGGACTT TTACTACGTG 550
GAATTGATAG AGATCAAGTA GAACGTGGAC AAGTTTGGC CAAACCAAAA 600
45 AGTATTATTC CTCACACAGA ATTTGAAGCT GCTGTGTATG TTCTAAAAGC 650
TGAAGAAGGT GGACGTCACA CTCCATTCTT TGAACACTAT AAACCACAAT 700
TTTACTTTTC TACAACCGAC GTTACTGGTG GAATTAAATT CAAACCTGGA 750
CGTGAAATGG TTATGCCTGG CGAAAATGTT GAATTTACAG TTACTTTAAT 800
TGCTCCTATT GCAGTTGAAG AAGGAA 826
50

```

2) INFORMATION FOR SEQ ID NO: 730

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 810 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60

```


(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria polysaccharea*

(B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

```

10 TGGTATGTTT CGCAGCYGAY GGYCCTATGC CTCAAACTCG CGAACACATC 50
CTGYTGGCTC GCCAAGTAGG YGTACCTTAC ATCATCGTRT TCATGAACAA 100
ATGCGACATG GTTGACGATG CCGAGCTGTT GGAAGTGGTT GAAATGGAAA 150
TCCGYGACCT GYTGTTCMAGC TACGACTTCC CMGGCGACGA CTGCCCCAATC 200
GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGYGAYGCTG GTTACGAAGA 250
GAAAATCTTC GAAATGGCTG CTGCTTTGGA CAGCTACATC CCAACTCCTG 300
15 AGCGTGCTGT GGACAAACCK TTCYTGYTGC CTATCGAAGA CGTRTTCTCT 350
ATCTCTGGYC GYGGTACMGT AGTAACYGGY CGTGTAGAGC GCGGTRTCAT 400
CCACGTTGGT GACGAGATYG AAATCGTAGG TCTGAAAGAA ACCCAAAAAA 450
CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGTCAA 500
GCWGGTGACA ACGTAGGCGT ATTGYTGCGT GGTACCAARC GTGAAGACGT 550
20 AGAGCGTGGT CAAGTATTGG CYAAACCAGG YACCATYACT CCSCACACCA 600
AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG TGGTCGYCAC 650
ACTCCATTCT TCGCYAACTA CCGYCCMCAA TTCTACTTCC GTACYACTGA 700
CGTAACYGGT GCAGTTACTT TGGAAGAAGG TGTAGAAATG GTAATGCCAG 750
GTGAGAACGT AACCATTACY GTAGAAGTGA TTGCGCCTAT CGCTAGGAAG 800
25 AAGGTCTGCG 810

```

2) INFORMATION FOR SEQ ID NO: 731

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Enteritidis

(B) STRAIN: ATCC 13076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

```

45 CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC GTGAGCACAT 50
CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG TTCCTGAACA 100
AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT TGAAATGGAA 150
GTTCGYGAAC TGCTGTCTCA GTACGACTTC CCGGGCGACG ACACTCCGAT 200
50 CGTTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA GAGTGGGAAG 250
CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT CCCGGAACCA 300
GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG ACGTATTCTC 350
CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA CGCGGTATCA 400
TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA GACTCAGAAG 450
55 TCTAACCTGTA CTGGCGTTGA AATGTTCCGC AACTGCTGG ACGAAGGCCG 500
TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAA CGTGAAGAAA 550
TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA GCCGCACACC 600
AAGTTCGAAT CTGAAGTGTA CATTTCTGTCC AAAGATGAAG GCGGCCGTCA 650
CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG 700
60 ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT GGTAAATGCCG 750

```

GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA TCGCAATGGA 800
CGACGGTCTG CGT 813

5

2) INFORMATION FOR SEQ ID NO: 732

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Gallinarum
(B) STRAIN: ATCC 9184

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732

CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC GTGAGCACAT 50
CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG TTCCTGAACA 100
25 AATGCGACAT GGTGTGATGAC GAAGAGCTGC TGGAACTGGT TGAAATGGAA 150
GTTTCGYGAAC TGCTGTCTCA GTACGACTTC CCGGGCGACG ACACTCCGAT 200
CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA GAGTGGGAAG 250
CGAAAATCAT CGAACTGGCT GGCTTCTCTG ATTCTTACAT CCCGGAACCA 300
GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG ACGTATTCTC 350
30 CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA CGCGGTATCA 400
TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA GACTCAGAAG 450
TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG ACGAAGGCCG 500
TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA CGTGAAGAAA 550
TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA GCCGCACACC 600
35 AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG GCGGCCGTCA 650
CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG 700
ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT GGTAATGCCG 750
GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA TCGCAATGGA 800
CGACGGTCTG CG 812

40

2) INFORMATION FOR SEQ ID NO: 733

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi B
(B) STRAIN: ATCC 8759

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733

60 TGTTTGTGTC TGCGACTGAC GGYCCGATGC CGCAGACCCG TGAGCACATC 50

```

CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA 100
ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG 150
TTCGYGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC 200
GTTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC 250
5 GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG 300
AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC 350
ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAAGAAC GCGGTATCAT 400
CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT 450
10 CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT 500
GCTGCTGCGT GGTATCAAAC GTGAAGAAAT 550
CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA 600
AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT 650
ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA 700
CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG 750
15 GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCAATGGAC 800
GACGGTCTGC GTTT 814

```

20 2) INFORMATION FOR SEQ ID NO: 734

(i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 828 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

```

----- (A) ORGANISM: Salmonella choleraesuis subsp. choleraesuis
          serotype Virchow
          (B) STRAIN: ATCC 51955

```

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734

```

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
40 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 200
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATT 300
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAAGAAC 400
45 GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG 650
50 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
GTACTACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
CGCAATGGAC GACGGTCTGC GTTTCGCA 828

```

55

2) INFORMATION FOR SEQ ID NO: 735

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 825 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCTTTC	ATCATCGTAT	100
15	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGACTTCC	CTGGTGATGA	200
	CCTGCCAGTT	GTTCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCTTGCTGC	CAATCGAAGA	350
20	CGTATTCTCC	ATCTCCGGYC	GTGGTACYGT	AGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTACTGG	CTAAACCAGG	TTCAATCAAG	600
25	CCACACACCA	AATTCGACTC	AGAAGTTTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTAACCCTGA	TTCACCCAAT	800
30	CGCGATGGAC	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 736

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736

	TATTAGTTTG	TTCAGCAACA	GATGGACCAA	TGCCACAAAC	AAGAGAGCAT	50
50	ATACTATTAT	CAAGACAAGT	TGGAGTACCA	TATATAGTAG	TATTCTTAAA	100
	CAAATGTGAC	ATGGTAGATG	ATGAAGAGTT	ATTAGAGTTA	GTAGAGATGG	150
	AAGTAAGAGA	TTTATTAACA	GAATATGATT	TCCCAGGAGA	TGACACTCCA	200
	ATAGTAAGAG	GTTTCAGCATT	AATGGCATT	GAAGATCCAA	AGAGYGAGTG	250
	GGGAGATAAG	ATAGTAGAAT	TATTCGAGCA	AATAGATGAG	TATATACCAG	300
55	CTCCAGAGAG	AGATACAGAT	AAACCATCT	TAATGCCAGT	AGAGGACGTA	350
	TTCTCAATCA	CAGGAAGAGG	AACAGTTGCA	ACAGGAAGAG	TGGAAAGAGG	400
	AGTACTAAAA	GTACAAGACG	AAGTAGAKTT	AGTAGGATTA	ACAGAAGCAC	450
	CAAGAAAAGT	AGTAGTAACA	GGAGTAGAGA	TGTTTCAGAAA	ATTATTAGAC	500
	CAAGCACAAAG	CAGGGGATAA	TATAGGAGCA	TTATTAAGAG	GAGTACAAAG	550
60	AAACGAGATA	GAAAGAGGAC	AAGTACTAGC	AAAGACTGGA	TCAGTAAAGG	600

CACACACAAA	GTTTACAGCA	GAAGTATATG	TACTTAAAAA	AGAAGARGGT	650
GGAAGACATA	CACCATTCCT	TGATGGATAT	AGACCACAAT	TCTATTTTCAG	700
AACAACAGAC	GTAACAGGAG	CTTGTAAGTT	ACCAGAAGGA	ATAGAGATGG	750
TAATGCCTGG	AGATAACGTA	ACAATGGAAG	TAGACTTAAT	AAACTCAA	798

5

2) INFORMATION FOR SEQ ID NO: 737

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 411 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Burkholderia pseudomallei*
 - (B) STRAIN: 1026B
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737

GTCAACATGA	TGGAGCTCAT	CAACAACATC	GCGAAGGAGC	ACGGCGGTTA	50
CTCCGTGTTT	GCGGGCGTGG	GCGAGCGTAC	CCGTGAAGGG	AACGACTTCT	100
ACCACGAAAT	GAAGGACTCG	AACGTTCTCG	ACAAGGTCGC	GCTGGTGTAC	150
GGCCAGATGA	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTGG	CGCTGACGGG	200
CCTCACGATG	GCCGAGCACT	TCCGTGACGA	AGGCCTCGAC	GTGCTGTTCT	250
TCGTCGACAA	CATCTACCGT	TTCACGCTGG	CCGGTACCGA	AGTGTCGGCG	300
CTGCTCGGCC	GTATGCCGTC	GGCAGTGGGC	TATCAGCCGA	CGCTGGCTGA	350
AGAAATGGGC	AAGCTGCAAG	AGCGCATCAC	GTGACGAAG	AAGGGCTCGA	400
TCACGTCGGT	T				411

35

2) INFORMATION FOR SEQ ID NO: 738

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium bifermentans*
 - (B) STRAIN: ATCC 638
- 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738

TACAAGAGCT	TATTAACAAT	ATAGCTACTC	AACACGGTGG	TATATCAGTA	50
TTCGCAGGTG	TTGGAGAGAG	AACAAGAGAA	GGTAACGACT	TATTCCATGA	100
GATGAGCGAT	ACAGGAGTTA	TAAATAAAAC	AGCTCTAGTA	TTCGGACAAA	150
TGAATGAGCC	ACCTGGAGCA	AGAATGAGAG	TTGCTTTAAC	TGGTCTTACA	200
ATGGCTGAAT	ACTTCAGAGA	TCAACAAGGG	CAAGACGTTT	TATTATTCGT	250
AGATAATATA	TTCCGTTTCA	CTCAAGCAGG	ATCTGAGGTT	TCTGCACTTC	300
TTGGACGTAC	TCCATCAGCA	GTTGGATACC	AACCAACATT	AGCAACAGAG	350
ATGGGTAGAT	TACAAGAGAG	AATAACATCT	ACAAATAAAG	GGTC	394

60

2) INFORMATION FOR SEQ ID NO: 739

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium beijerincki* (deposited as *Clostridium butyricum*)
- (B) STRAIN: ATCC 8260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739

20	TTAATAAACA ACATAGCTAA ACAACATGGT GGTTTATCAG TATTTACTGG	50
	AGTTGGTGAA AGATCAAGAG AAGGTAATGA CTTATATCAT GAAATGAGAG	100
	AGTCAGGAGT TATTGATAAG ACAGCATTAG TATTTGGACA AATGAATGAG	150
	CCACCGGGTG CCAGAATGAG AGTTGCATTA ACAGGTCTTA CTATGGCAGA	200
	GTATTTTAGA GATAAAGGTC AAGATGTGTT ACTATTCATA GATAACATAT	250
25	TCAGATATAC TCAAGCAGGT TCAGAGGTTT CAGCATTACT TGGAAGAACA	300
	CCTTCAGCGG TTGGATATCA GCCAACACTT GCAACTGAAA TGGGTGCACT	350
	TCAGGAAAGA ATTACATCAA CAGTTAATGG TTCTATTACG TCAG	394

2) INFORMATION FOR SEQ ID NO: 740

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740

50	TTATAAACAA TATTGCTAAG CAACATGGTG GTATTTCTGT ATTTTCAGGA	50
	GTAGGAGAAA GAACAAGAGA AGGTAACGAC CTTTATGGCG AAATGAGTGA	100
	GTCTGGAGTT ATAAATAAAA CAGCTCTAGT ATTTGGTCAA ATGAATGAAC	150
	CACCTGGAGC GAGAATGAGA GTTGCTTTAA CTGGACTTAC AATGGCAGAA	200
	CATTTTAGAG ATGAGCAAGG ACAAGACGTT TTA CTTTTCG TTGATAATAT	250
	ATTCCGTTTC ACACAAGCTG GTTCAGAAGT TTCAGCACTT CTAGGACGTA	300
	TGCCATCAGC TGTTGGTTAT CAGCCAACAT TAGCTACTGA AATGGGTGCA	350
55	CTTCAAGAGA GAATAACATC AACTAAGAAA GGTTCAATAA CAT	393

2) INFORMATION FOR SEQ ID NO: 741

(i) SEQUENCE CHARACTERISTICS:

625

- (A) LENGTH: 398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: *Clostridium ramosum*
- (B) STRAIN: ATCC 25582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741

15	TTGATTCAAG AATTCATTAA TAACATTGCT ACAGAACATG GTGGTTTATC	50
	AGTTTTTGCT GGAGTTGGTG AACGTAGCCG TGAAGGTAAT GATTTATATT	100
	ATGAAATGAA GGAAAGTGGT GTTTTATCTA AAACAACACT AGTATTTGGA	150
	CAGATGAATG AACCCCCAGG AGCTCGTTTA AGAGTTGCTT TAACGGGTCT	200
	TACTATGGCA GAAGAATTCC GTGATGAACA AGGTCAGGAT GTCTTATTAT	250
	TCATCGATAA TATTTTCCGT TTTACTCAAG CTGGATCTGA AGTATCTGCC	300
20	TTACTTGGAC GGGTACCATC ACAAGCTGGG TATCAGCCAA CTTTAGCAAC	350
	CGAAATGGGT GCTTTACAAG AACGGATTAC ATCAACTAAA AAAGGATC	398

25 2) INFORMATION FOR SEQ ID NO: 742

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 380 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
- (B) STRAIN: ATCC 12964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742

40	TAGCTAAGGA ACACGGTGGA CTTTCAGTAT TCACAGGTGT TGGAGAAAGA	50
	TCAAGAGAAG GTAATGATTT ATATTACGAA ATGAAAGAAT CAGGAGTTAT	100
	AGACAAGACA GCTCTAGTGT TTGGACAAAT GAATGAATCT CCAGGAGCTA	150
	GAATGAGAGT ATCTTTAACA GGATTAACATA TGGCTGAATA TTTCAGAGAT	200
45	CAAGGTCAAG ATGTGCTTTT ATTCATAGAT AACATATTTA GATTTACTCA	250
	AGCTGGATCA GAAGTATCGG CTTTACTTGG AAGAATACCA TCAGCAGTTG	300
	GTTATCAACC AACACTAGCA ACTGAAATGG GTGCACTTCA AGAAAGAATT	350
	ACTTCAACTA AAAATGGATC AATAACTTCA	380

50

2) INFORMATION FOR SEQ ID NO: 743

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 389 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium tertium*

(B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743

5 TTAATAAATA ATATAGCAAA AGAGCATGGT GGTCTTTCTG TATTTACAGG 50
 AGTTGGAGAA AGGTCAAGAG AAGGTAACGA CTTATATTAT GAAATGAAAG 100
 10 AGTCAGGGGT TATAGATAAG ACAGCTTTAG TATTTGGACA AATGAATGAA 150
 TCACCAGGAG CAAGAATGAG AGTTTCATTA ACTGGATTAA CTATGGCTGA 200
 ATATTTTAGA GATCAAGGTC AAGACGTTCT TTTATTTATA GATAATATAT 250
 TTAGATTTAC TCAAGCGGGA TCAGAAGTTT CTGCGTTATT AGGAAGAATT 300
 CCTTCAGCAG TTGGATATCA ACCAACTCTT GCAACTGAAA TGGGAGCACT 350
 15 TCAAGAAAGA ATAACATCAA CAAAGAATGG ATCAATCAC 389

2) INFORMATION FOR SEQ ID NO: 744

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 843 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Comamonas acidovorans*

(B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744

35 TTCCCCCGCA CGCATGCCCA AGGTGTTCTGA TGCCCTGAAG CTCGACGGCT 50
 CGGCCCTGAC GCTGGAAGTG CAGCAACTGC TGGGTGACGG CGTTGTGCGT 100
 ACCATCGCCC TGGGTTTCGTC CGACGGTCTG CGTCGCGGCC TGATGGTGTC 150
 CAACACCGGC AACCCCATCA CCGTGCCCGT GGGCAAGGCG ACGCTGGGTC 200
 GCATCATGGA CGTGCTGGGC AATCCCATCG ACGAACGTGG TCCCGTGGAT 250
 40 CAGGCGCTGA CGGCTCCCAT CCACCGCAAG GCACCGGCTT ATGACGAGCT 300
 GTCGCCTTCG CAGGAACTGC TGGAACCGG CATCAAGGTG ATCGACCTGA 350
 TCTCGCCCTT CGCCAAGGGC GGCAAGGTGG GTCTGTTCTG TGGCGCCGGT 400
 GTGGGCAAGA CCGTGAACAT GATGGAACAT ATCAACAACA TCGCCAAGGG 450
 CCACGGTGGT CTGTGCGGTGT TCGCCGGTGT GGGTGAACGT ACCCGCGAAG 500
 45 GCAATGACTT CTATCACGAA ATGTCGGACG CCGGCGTGGT CAACCAGGAG 550
 TCGCTGAACG ACTCCAAGGT GGCCATGGTC TACGGCCAGA TGAACGAACC 600
 CCCGGGCAAC CGTCTGCGCG TGCGCTGAC CGGCCTGACC ATGGCCGAAG 650
 CCTTCCGTGA CGAAGGCAAG GACGTGCTGT TCTTCGTGGA CAACATCTAC 700
 CGCTACACGC TGGCCGGTAC CGAAGTGTCC GCTCTGCTGG GTCGCATGCC 750
 50 TTCCGCCGTG GGCTACCAGC CCACGCTGGC CGAGGAAATG GGCCGCCTGC 800
 AAGAGCGCAT CACCTCGACC AAGGTCGGTT CGATCACTTC CAC 843

2) INFORMATION FOR SEQ ID NO: 745

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis

(B) STRAIN: ATCC 13884

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745

	GCCGTACCAC	GCGTGACGA	AGCCCTTGAG	GTACAGAATG	GTAATGAAGT	50
	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTGGG	CGGCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCTGAT	GGTCTGCGCC	GCGGTCTGGA	TGTAAAAGAC	150
15	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCAAC	CGGTGACAT	GAAAGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CGTCCTATGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGCGGT	GCGGGTG TAG	400
20	GTAAAACTGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGACGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
25	ACTGCTGTTT	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCCGCGCT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAAC	800
	CGGTTCTATC	ACCTCCGTA				819

30

2) INFORMATION FOR SEQ ID NO: 746

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria canis*
(B) STRAIN: ATCC 14687

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746

	GCGATTCTAT	TCCGCGCGTA	TATGATGCTC	TTAAACTAGT	GGATAGAGAA	50
	CTGACGCTTG	AAGTACAACA	ACAGTTGGGT	GATGGTGTCG	TTCGTACTAT	100
50	TGCGATGGGT	AGTTCCGACG	GCCTCAAACG	AGGTTTGCGC	GTAGTTAACA	150
	CCGGTGCTCC	AATTACAGTG	CCTGTGGGCA	AAGCAACATT	AGGCCGTATT	200
	ATGGACGTAT	TAGGTAATCC	GGTTGATGAA	GCTGGTCCGA	TTGGCTCCGA	250
	GCAAACCCGA	GCAATCCACC	AACCTGCTCC	TAAGTTCGAC	GAGCTTTCCTA	300
	GCGCCACAGA	GATTTTGGAA	ACAGGTATTA	AAGTAATTGA	TTTGCTTTGC	350
55	CCGTTTGCCA	AAGGCGGTAA	AGTAGGTTTG	TTTGGTGGTG	CGGGAGTGGG	400
	CAAAACCGTA	AATATGATGG	AGTTGATTAA	CAACATCGCG	AAAGCACACA	450
	GCGGTTTGTC	TGTATTTGCC	GGTGTGGGTG	AACGGACGCG	TGAAGGTAAT	500
	GACTTTTATC	ATGAGATGAA	AGATTCCAAT	GTATTAGATA	AAGTAGCCAT	550
	GGTTTACGGT	CAGATGAACG	AGCCTCCCGG	TAACCGTTTG	CGCGTTGCGC	600
60	TAAGTGGCTT	GTCTATGGCC	GAATTCTTCC	GTGACGAGAA	AGATGAAAAC	650

GGTAAAGGCC	GTGATGTATT	GTTCTTTGTA	GACAATATTT	ACCGCTATAC	700
CCTAGCCGGT	ACAGAAGTAT	CTGCATTGCT	TGGCCGTATG	CCTTCGGCAG	750
TAGGTTATCA	GCCGACGTTG	GCAGAGGAAA	TGGGCCGCTT	GCAAGAGCGT	800
ATTACYTCAM	CCCAAACAGG	CTCT			824

5

2) INFORMATION FOR SEQ ID NO: 747

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Neisseria cinerea*
 (B) STRAIN: ATCC 14685
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747

CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
25 TCTGACTCTG	GAGGTTCAAC	AGCTTCTGGG	CGACGGCGTT	GTCCGTACTA	100
TTGCAATGGG	TAGTTCAGAC	GGCCTTAAAC	GCGGTATGTC	TGTAAGCAAT	150
ACTGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
ACAAAAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCGA	CGAGTTGTCT	300
30 TCAGCTACCG	AATTGTTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
TCCGTTTGCT	AAAGGCGGTA	AAGTAGGTCT	GTTGCGGTGGT	GCCGGTGTGG	400
GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
AGCGGTCTGT	CCGTGTTTCG	AGGTGTGGGT	GAGCGTACCC	GTGAAGGTAA	500
CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
35 TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600
TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
CGGTAAAGGC	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
CTTTGGCCGG	TACTGAAGTA	TCTGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
40 TATTACCTCT	ACCCAAACCG	GTTCCATTAC	T		831

2) INFORMATION FOR SEQ ID NO: 748

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 862 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Neisseria cuniculi*
 (B) STRAIN: ATCC 14688
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748

60 CCGTGGCCAA	GTACCACAAA	TTTATGACGC	ACTGAGTGTT	GATGGCACCG	50
---------------	------------	------------	------------	------------	----

AAACAACCTT GGAAGTTCAA CAGCAGTTGG GTGATGGCGT GGTGCGTACC 100
 ATTGCGATGG GTTCAACCGA AGGCTTGAAG CGTGGTTTGA CTGTATCTAA 150
 CTCTGGTGCA CCGATTTCTG TGCCAGTGGG TCAAGCGACT TTGGGTCGTA 200
 TTATGGATGT GTTGGGTCGT CCAATCGACG AGGCAGGTCC TGTAATGCT 250
 5 CAAGAAAAAT GGTC AATTCA CCGTGAAGCA CCAAGCTATG ATGAGCAATC 300
 AAACTCAACT GAGCTGCTAG AAACAGGCAT CAAAGTAATT GATTTGCTTT 350
 GCCCATTTGC TAAAGGTGGT AAAGTTGGCT TGTTCGGTGG TGCAGGTGTG 400
 GGTAAAACCG TGAATATGAT GGAGCTGATT AATAATATCG CTCTGAAGCA 450
 TTCAGGTCTT TCTGTTTTTG CAGGTGTTGG TGAGCGTACT CGTGAGGGTA 500
 10 ACGATTTTTTA TCACGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAC 550
 TTCACCAAGT CAAAAGTAGC GATGGTTTAT GGTGAGATGA ATGAGCCACC 600
 AGGAAACCGT TTGCGTGTTG CATTGACAGG CTTGACGATG GCAGAATATT 650
 TCCGTGACGA AAAAGATGAA GCAACAGGCA AAGGGCGTGA TGTTCTATTG 700
 TTCGTTGATA ACATCTATCG TTACACACTG GCTGGTACGG AAGTGTCAGC 750
 15 ACTTCTAGGT CGTATGCCAT CAGCAGTAGG TTATCAACCG ACTCTGGCTG 800
 AAGAAATGGG TGC GTTCAA GAGCGTATTA CCTCAACGCA ATCGGGTTCC 850
 ATCACTTCGG GG 862

20 2) INFORMATION FOR SEQ ID NO: 749
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749
 GGAAGTCCCA CGTGACGCTA TCCGCGATGT TTTTGATGCA TTAAAATTAG 50
 TTGAAAATGA CCTAACCTTA GAAGTTCAAC AACTTTTGGG GGATGGTGTA 100
 GTGCGTACCA TTGCGATGGG TAGTTCAGAT GGATTAAAGC GTGGTATGGC 150
 40 TGTGAATAAT ACCGGAGCTC CGATTACTGT TCCTGTTGGC CGTGAAACTT 200
 TGGGTCGTAT CATGGATGTA TTGGGTAATC CGGTTGATGA GGCAGGTCCG 250
 GTAAATGCAT CCAATACACG TGCGATCCAT CAAGAGGCTC CTAAGTTTGA 300
 TGAGCTTTCT TCAACAACGG AATTATTAGA AACTGGCATT AAGGTTATCG 350
 ACTTGTTATG TCCGTTTGCC AAAGGTGGTA AAGTAGGTCT GTTTGGTGGT 400
 45 GCGGGTGTAG GTAAAACCGT AAATATGATG GAGTTAATTA ACAACATTGC 450
 CAAGGCACAT AGCGGTTTGT CTGTGTTTGC AGGCGTGGGT GAACGTACTC 500
 GTGAAGGTAA TGACTTCTAT CACGAGATGA AAGATTCCAA CGTATTGGAC 550
 AAAGTGGCAA TGGTTTACGG TCAGATGAAC GAACCTCCAG GCAACCGTCT 600
 GCGCGTTGCT TTGACCGGTT TGACTATGGC CGAATACTTC CGTGACGAAA 650
 50 AAGACGAAAA CGGTAAAGGT CGCGACGTAT TGTTCCTTCGT GGACAACATT 700
 TACCGTTACA CTTTGCCCGG TACGGAAGTA TCCGCATTGC TGGGTCGTAT 750
 GCCTTCAGCA GTAGGTTACC AACCGACATT GGCTGAAGAA ATGGGTCGTT 800
 TGCAAGAGCG TATTACCTCT ACCCAGACAG GCTCTATTAC TTCC 844

55 2) INFORMATION FOR SEQ ID NO: 750
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria flavescens*
 (B) STRAIN: ATCC 13120

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750

	CGCGACGCTA	TTCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
15	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACCGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGCCGTAT	200
	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAACGTCTC	CGAAATTCTGA	TGAGTTGTCT	300
	TCAACTACCG	AATTGTTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
20	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGCCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	TCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
25	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGATGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGTCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAGGAGCG	800
30	TATTACTTCT	ACGCAAACCG	GTTCCATTAC	TTCC		834

2) INFORMATION FOR SEQ ID NO: 751

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 31426

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751

	CGCGACATGA	TTCCGCGCGT	TTACGACGCT	TTGAAATTAG	ACGAAAACGG	50
50	TCTGACTTTG	GAAGTCCAAC	AGCTTTTGGG	TGATGGCGTA	GTCCGTACCA	100
	TCGCTATGGG	CAGCTCGGAC	GGTTTGAAAC	GCGGCATGAC	TGTGAGCAAT	150
	ACTGGTTCGC	CCATTACTGT	GCCGGTAGGT	AAAGGTACGT	TGGGACGCAT	200
	TGTCGATGTA	TTGGGAACTC	CTGTTGACGA	GGCAGGTCCA	ATTGATACCG	250
	ACAAGAGTCG	TGCCATCCAC	CAAGCCGCTC	CTAAGTTTGA	CGAACTGTCT	300
55	TCCACAACCG	AATTGCTCGA	AACGGGCATT	AAAGTGATTG	ACTTGCTGTG	350
	TCCGTTTGCC	AAAGGCGGTA	AAGTAGGTCT	GTTCGGCGGT	GCCGGTGTGG	400
	GTAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGCTTGT	CCGTGTTCTC	AGGCGTGGGT	GAGCGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
60	TGGTGTATGG	CCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600

	TTGACCGGTT	TGACTATGGC	TGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGTGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
5	TATTACCTCT	ACCCAAACCG	GTTCCATTAC	TTCC		834

2) INFORMATION FOR SEQ ID NO: 752

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
- (B) STRAIN: ATCC 27628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752

25	ACATGATTCC	GCGCGTTTAC	GACGCTTTGA	AATTAGACGA	AAACGGTCTG	50
	ACTTTGGAAG	TCCAACAGCT	TTTGGGTGAT	GGCGTAGTCC	GTACCATCGC	100
	TATGGGCAGC	TCGGACGGTT	TGAAACGCGG	CATGACTGTG	AGCAATACTG	150
	GTTGCCCCAT	TACTGTGCCG	GTAGGTAAAG	GTACGTTGGG	ACGCATTGTC	200
	GATGTATTGG	GAACGCCTGT	TGACGAGGCA	GGTCCAATTG	ATACCGACAA	250
30	GAGTCGTGCC	ATCCACCAAG	CCGCTCCTAA	GTTTGACGAA	CTGTCTTCCA	300
	CAACCGAATT	GCTCGAAACG	GGCATTAAAG	TGATTGACTT	GCTGTGTCCG	350
	TTTGCCAAAG	GCGGTAAAGT	AGGTCTGTTC	GGCGGTGCCG	GTGTGGGTAA	400
	AACCGTGAAC	ATGATGGAAT	TGATCAACAA	CATCGCCAAA	GCGCACAGCG	450
	GCTTGTCGGT	GTTCTCAGGC	GTAGGTGAGC	GTACCCGCGA	AGGTAACGAC	500
35	TTCTACCACG	AGATGAAAGA	TTCCAACGTA	TTGGATAAAG	TAGCCATGGT	550
	GTATGGCCAA	ATGAACGAAC	CTCCAGGCAA	CCGTCTGCGC	GTTGCTTTGA	600
	CCGGTTTGAC	TATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	CGAAAACGGT	650
	AAAGGTCGTG	ACGTATTGTT	CTTCGTTGAC	AACATCTACC	GTTACACTCT	700
	GGCCGGTACC	GAAGTATCCG	CACTGTTGGG	CCGTATGCCT	TCTGCAGTGG	750
40	GTTACCAACC	GACATTGGCT	GAAGAAATGG	GTCGTTTGCA	AGAGCGTATT	800
	ACCTCTACCC	AAACCGGTTC	CATTA			825

45 2) INFORMATION FOR SEQ ID NO: 753

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria lactamica*
- (B) STRAIN: ATCC 23970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753

```

5  GATGCGATTTC CGCATGTTTA CGATGCCCTG AAATTGGACG AGAACGGTCT 50
   GACCCTGGAA GTCCAACAGC TTTTGGGTGA CGGCGTTGTC CGTACTATTG 100
   CAATGGGTAG TTCAGACGGC CTGAAACGCG GCATGTCTGT CAGCAATACC 150
   GGTGCGCCAA TCACTGTGCC GGTAGGTAAA GGTACGTTGG GCCGTATTGT 200
   CGACGTATTG GGTACACCTG TTGACGAAGC AGGTCCGATC GATACCGACA 250
   AGAGCCGCGC CATCCACCAA ACCGCCCCGA AATTCGACGA GTTGTCTTCA 300
   ACTACCGAAT TGTGGAAC CCGCATTAAG GTGATCGATT TGCTGTGTCC 350
   GTTTGCTAAG GCGCGTAAAG TAGGTCTGTT CGGTGGTGCC GGTGTGGGCA 400
   AAACCGTGAA CATGATGGAA TTGATCAACA ACATCGCCAA AGCGCACAGC 450
10 GGTCTGTCCG TGTTTGCAGG CGTGGGCGAG CGTACCCGCG AAGGTAACGA 500
   CTTCTACCAC GAGATGAAAG ATTCCAACGT ATTGGATAAA GTAGCCATGG 550
   TGTATGGTCA GATGAACGAA CCTCCGGGCA ACCGTCTGCG CGTTGCTTTG 600
   ACCGGTTTGA CGATGGCCGA ATACTTCCGC GACGAAAAAG ACGAAAACGG 650
   CAAAGGCCGC GACGTATTGT TCTTCGTGGA CAACATCTAC CGTTACACCC 700
15 TGGCCGGTAC CGAAGTATCC GCACTGTTGG GCCGTATGCC TTCCGCAGTG 750
   GGTTACCAAC CGACATTGGC TGAAGAAATG GGTCTGTTGC AAGAGCGTAT 800
   TACCTCTACC CAAACCGGTT CCATTACTTC C 831

```

20

2) INFORMATION FOR SEQ ID NO: 754

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 836 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: 2241C

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754

```

40 CCACGCGACA TGATTCCGCG CGTTTACGAC GCTTTGAAAT TAGACGAAAA 50
   CGGTCTGACT TTGGAAGTCC AACAGCTTTT GGGCGACGGC GTAGTCCGTA 100
   CCATTGCGAT GGGCAGCTCG GACGGTTTGA AACCGGCGCAT GACTGTGAGC 150
   AATACCGGTG CGCCCATTAC TGTGCCGGTA GGTAAAGGTA CGTTGGGACG 200
   CATTGTGCGT GTATTGGGAA CGCCTGTTGA CGAGGCAGGT CCAATCGATA 250
   CCGACAAGAG CCGTGCCATC CACCAAGCCG CTCCTAAGTT TGACGAAC TG 300
   TCTTCCACAA CCGAATTGCT CGAAACGGGC ATTAAAGTGA TTGACTTGCT 350
   GTGTCCGTTT GCCAAAGGCG GTAAAGTAGG TCTGTTCGGC GGTGCCGGTG 400
45 TGGGTAAAAC CGTGAACATG ATGGAATTGA TCAACAACAT CGCCAAAGCG 450
   CACAGCGGCT TGTCCGTGTT CGCAGGCGTG GGTGAGCGTA CCCGCGAAGG 500
   TAACGACTTC TACCACGAGA TGAAAGATTC CAACGTATTG GATAAAGTGG 550
   CAATGGTTTA CGGTCAGATG AACGAACCTC CGGGCAACCG TTTGCGCGTC 600
   GCATTGACCG GTTTGACCAT GCGGAATAC TTCCGTGACG AAAAAGACGA 650
50 AAACGGCAAA GGCCGCGACG TATTGTTCTT CGTGACAAC ATCTACCGTT 700
   AACTCTAGC TGGTACCGAA GTATCCGCAT TGTGCGGCCG TATGCCGTCT 750
   GCAGTGGGCT ACCAACCGAC ATTGGCAGAA GAAATGGGTC GTTTGCAGGA 800
   GCGTATTACC TCTACCCAAA CCGGTTCTAT TACTTC 836

```

55

2) INFORMATION FOR SEQ ID NO: 755

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 837 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755

	CCGCGTGATG	CCATTCCGCG	TGTTTACGAC	GCCCTGAAAT	TGGATGCAAA	50
	CGGCCTGACT	TTGGAAGTGC	AACAGCTTCT	GGGTGACGGC	GTAGTTCGTA	100
15	CTATTGCAAT	GGGTAGTTCG	GATGGTTTGA	AACGCGGCAT	GA CTGTAAAGC	150
	AATACAGGTG	CGCCGATTAC	AGTACCGGTA	GGTAAAGGTA	CTTTGGGACG	200
	TATTGTTCGAT	GTATTGGGTA	CGCCTGTTGA	CGAAGCAGGT	CCGATTGATA	250
	CCGACAAACA	CCGTGCCATC	CATCAGACAG	CTCCGAAATT	TGATGAACTG	300
	TCTGCGACTA	CTGAGCTGCT	GGAACCGGC	ATTAAAGTGA	TTGACTTGCT	350
20	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCGGT	GGTGCCGGTG	400
	TAGGCAAAAC	CGTCAACATG	ATGGAATTAA	TTAACAACAT	CGCCAAAGCA	450
	CATAGCGGTT	TGTCCGTGTT	TGCAGGTGTG	GGTGAGCGTA	CCCGTGAAGG	500
	TAATGACTTC	TACCACGAGA	TGAAAGATTG	CAACGTATTG	GACAAAGTGG	550
	CGATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGTAACCG	TCTGCGTGTA	600
25	GCCTTGACCG	GTTTGACGAT	GGCCGAATAC	TTCCGTGATG	AAAAAGACGA	650
	AAGCGGCAAA	GGCCGTGACG	TATTGTTCTT	CGTGGACAAT	ATCTACCGTT	700
	ACACCCTGGC	CGGTACCGAA	GTATCCGCAT	TGTTGGGTGCG	TATGCCTTCA	750
	GCAGTAGGTT	ACCAACCGAC	ATTGGCTGAA	GAAATGGGTC	GTTTGCAAGA	800
30	GCGTATTACC	TCTACCCAAA	CAGGCTCCAT	TACCTCC		837

2) INFORMATION FOR SEQ ID NO: 756

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756

	CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
50	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACTGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAAGTCTC	CGAAATTCGA	CGAGTTGTCT	300
55	TCAACTACCG	AATTGCTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGTCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
60	TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600

```

TTGACCGGTT TGA CTATGGC CGAATACTTC CGTGACGAAA AAGACGAAAA 650
CGGTAAAGGT CGCGACGTAT TGTTCCTTCGT TGACAACATC TACCGTTACA 700
CTCTGGCCGG TACCGAAGTA TCTGCACTGT TGGGCCGTAT GCCTTCTGCA 750
GTGGGTTACC AACCGACATT GGCTGAAGAA ATGGGTCGTT TGCAAGAGCG 800
5 TATTACCTCT ACCCAAAGTGT GTTCCATTAC TTCC 834

```

2) INFORMATION FOR SEQ ID NO: 757

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
- (B) STRAIN: ATCC 51223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757

```

25 CCCGTGATGC TATTCCCATG TATACGATGC CCTGAAATTG GTAGATAACG 50
ATCTGACCCT GGAAGTGCAA CAACTTTTAG GTGATGGTGT GGTTCGTACC 100
ATTGCAATGG GTAGTTCAGA CGGCCTAAAA CGTGGTATGG CTGTTAACAA 150
TACCGGCGCT CCGATTACTG TTCCGGTGGG GAAAGCCACC TTGGGACGTA 200
TTATGGATGT GTTGGGTAAT CCGGTTGATG AAGCAGGTCC TGTGTATCA 250
30 GAAGAAACTC GCGCTATTCA TCAAGCTGCC CCTAAATTTG ACGAACTGTC 300
TTCAGCAACT GAGTTGTTGG AAACAGGCAT TAAAGTAATT GACTTGCTGT 350
GCCCCGTTTG CAAAGGTGGT AAAGTAGGTT TGTGTTGGTGG TGCCGGCGTG 400
GGTAAAACCG TAAATATGAT GGAGTTGATC AACACATCG CGAAGGCACA 450
TAGTGGTTTG TCTGTATTCG CCGGTGTAGG TGAGCGTACC CGTGAAGGTA 500
35 ACGACTTCTA CCATGAAATG AAAGACTCTA ACGTATTGGA TAAAGTAGCC 550
ATGGTTTATG GCCAGATGAA TGAACCTCCG GGTAACCGTT TGCGCGTTGC 600
TTTGACTGGT TTGACTATGG CCGAATATTT CCGTGACGAG AAAGATGAAA 650
ACGGCAAAGG TCGTGACGTC TTGTTCTTTG TGGATAATAT CTATCGCTAT 700
ACTCTGGCCG GTACTGAAGT GTCTGCACTG TTAGGTCGTA TGCCGTCTGC 750
40 AGTAGGTTAT CAGCCTACAT TGGCAGAAGA AATGGGTCGC TTGCAGGAGC 800
GTATTACTTC TACTCAAACA GGTTCGATTA CTT 833

```

2) INFORMATION FOR SEQ ID NO: 758

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria animalis*
- (B) STRAIN: ATCC 19573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758

5 CGCGATGCCA TTCCTCACGT TTACGATGCC CTGAAATTGG ACGACACCGG 50
 TCTGACTTTG GAAGTACAAC AACTTCTGGG CGACGGTGTG GTACGTACCA 100
 TTGCAATGGG TAGTTCAGAC GGCTTGAAAC GGGGTTTGTC TGTGAGCAAT 150
 ACCGGTTCTC CGATTGCCGT TCCTGTCGGT AAAGCGACTT TGGGTCGTAT 200
 TATGGACGTA TTGGGCAATC CGGTTGATGA AGCCGGTCCG GTTGCTACCG 250
 AAGAGAAACG TGCTATTCAC CAAGCCGCAC CGAAGTTTGA TGAATTGTCA 300
 TCAGCTACCG AGTTGTTGGA AACCGGTATT AAAGTAATCG ACTTGCTGTG 350
 TCCGTTTGCA AAAGGCGGTA AAGTAGGTCT GTTCGGCGGT GCCGGTGTGG 400
 GCAAAACCGT AAACATGATG GAATTGATCA ACAACATCGC CAAAGCACAC 450
 10 AGCGGTCTGT CTGTGTTTGC CGGTGTAGGT GAACGTACCC GCGAAGGTAA 500
 CGACTTCTAC CACGAGATGA AAGATTCCAA CGTGTGGAT AAAGTAGCCA 550
 TGGTGTACCG TCAGATGAAT GAGCCGCCGG GCAACCGCTT GCGCGTGGCT 600
 TTGACCGGCC TGAATATGGC CGAATACTTC GTGACGAAA AGACGAAAAC 650
 GGCAAAGGTC GTGACGTATT GTTCTTCGTG GACAACATTT ACCGCTACAC 700
 15 ACTGGCCGGT ACCGAAGTAT CAGCATTGTT GGGCCGTATG CCGTCTGCAG 750
 TAGGTTATCA GCCGACATTG GCAGAGGAAA TGGGTCGCTT GCAAGAGCGT 800
 ATTACCTCTA CCCAAACCGG TTCGATTACC TCT 833

20

2) INFORMATION FOR SEQ ID NO: 759

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759

40 AGCGTCCCTA AAGTATACGA CGCTCTTGAG GTTATGAATG GTAAAGAAAA 50
 ACTGGTGTCTG GAAGTTCAGC AACAGTTAGG CGGTGGTATC GTTCGTTGTA 100
 TCGCAATGGG TACATCAGAC GGTTTAAGCC GTGGCTTAAA AGTTGAAGAT 150
 TTAGGCCACC CAATTGAAGT ACCAGTAGGT AAAGCAACAC TGGGACGTAT 200
 CATGAACGTT CTGGGTACAC CTATTGATAT GAAAGGTGAT ATTGCAACTG 250
 AAGAACGTTG GTCTATTACAC CGTGAAGCAC CAACCTACGA AGAGTTATCA 300
 AACTCACAAAG AACTGCTTGA AACCAGGTATC AAAGTAATGG ACTTAATCTG 350
 TCCGTTTGCT AAAGGTGGTA AAGTAGGTCT GTTCGGTGGT GCGGGTGTGG 400
 45 GTAAACAGT TAACATGATG GAATTGATCC GTAATATCGC GATCGAGCAC 450
 TCAGGTTACT CTGTATTGTC TGGTGTGGT GAGCGTACTC GTGAGGGTAA 500
 CGACTTCTAT CATGAAATGA CAGATTCTAA CGTTCCTGAC AAAGTATCGT 550
 TAGTTTATGG TCAGATGAAT GAGCCACCAG GAAACCGTCT GCGTGTAGCA 600
 CTGACTGGTC TGACTATGGC TGAAAAATTC CGTGATGAAG GCCGTGACGT 650
 50 ACTGTTATTC GTCGATAACA TTTATCGTTA CACCTTAGCC GGTACAGAAG 700
 TATCAGCACT GTTAGGTCGT ATGCCATCAG CGGTAGGTTA CCAGCCAACA 750
 TTGGCTGAAG AGATGGGTGT TCTGCAAGAA CGTATCACTT CAACCAAAC 800
 AGGTTCAATC ACCTCTGTA 819

55

2) INFORMATION FOR SEQ ID NO: 760

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 819 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Enteritidis

10 (B) STRAIN: ATCC 13076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
15	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
20	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCCGC	AAGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CAGTGTTTGC	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
25	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	AGTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
30	CGTTTCTATC	ACCTCCGTA				819

2) INFORMATION FOR SEQ ID NO: 761

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761

50	ACCAAAAGTG	TACAACGCC	TTGAGGTAGA	AGGTACAAC	GAAAAGTTAG	50
	TGCTGGAAGT	TCAGCAACAG	TTGGGCGGTG	GTGTTGTTCG	TTGTATCGCA	100
	ATGGGCTCTT	CCGATGGTCT	GAGCCGTGGG	TTGAAAGTAA	CCAACCTAGA	150
	ACACCCGATC	GAAGTACCGG	TTGGTAAAGC	GACCCTTGGC	CGTATCATGA	200
	ACGTATTGGG	TGAACCAATC	GACATGAAAG	GTCCTATCGG	TGAAGAAGAG	250
55	CGTTGGGCAA	TCCATCGCGA	AGCGCCTTCT	TATGAAGAGC	TTGCTAGCTC	300
	ACAAGATCTG	TTAGAAACCG	GTATCAAGGT	TATGGACCTG	ATTTGTCCGT	350
	TTGCTAAGGG	CGGTAAAGTC	GGTCTGTTTC	GTGGTGCGGG	TGTAGGTAAA	400
	ACAGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	AGCACTCTGG	450
	GTATTCTGTA	TTTGCCGGTG	TAGGTGAGCG	TACCCGTGAG	GGTAATGACT	500
60	TCTACCATGA	AATGACTGAC	TCCAACGTTT	TGGACAAAGT	ATCCTTGGTT	550

TACGGCCAGA TGAATGAGCC ACCAGGTAAC CGTCTACGCG TTGCACTGAC 600
 CGGCCTGACC ATGGCCGAGA AATTCCGTGA TGAAGGTCGT GACGTACTGC 650
 TGTTTATCGA TAATATCTAT CGTTATACCC TAGCTGGTAC GGAAGTATCC 700
 GCATTGCTGG GTCGTATGCC ATCAGCGGTA GGTATCAGC CAACACTGGC 750
 5 TGAAGAGATG GGTGTGTTGC AGGAACGTAT TACTTCCACT AAGACGGGTT 800
 CAATCACCTC TG 812

10 2) INFORMATION FOR SEQ ID NO: 762

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762

25 CGACGTGATC GAGCCCTTCT TCGTCGACGT GATGCGCTCT TGCAGCTTGC 50
 CCATTTCTTC AGCCAGCGTC GGCTGATAGC CCACTGCCGA CGGCATACGG 100
 CCGAGCAGCG CCGACACTTC GGTACCGGCC AGCGTGAAAC GGATAGATGTT 150
 GTCGACGAAG AACAGCACGT CGAGGCCTTC GTCACGGAAG TGCTCGGCCA 200
 30 TCGTGAGGCC CGTCAGCGCC ACAGCGAGAC GGTTGCCCGG CGGCTCGTTC 250
 ATCTGGCCGT ACACCAGCGC GACCTTGTCT AGAACGTTCT AGTCCTTCAT 300
 TTCGTGGTAG AAGTCGTTCC CTTACGGGT ACGCTCGCCC ACGCCCGCGA 350
 ACACGGAGTA ACCGCCGTGC TCCTTCGCGA TGTTGTTGAT GAGCTCCATC 400
 ATGTTGAC 408
 35

2) INFORMATION FOR SEQ ID NO: 763

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium sordellii*
 50 (B) STRAIN: ATCC 9714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763

55 GAACCTATAA ACAACATAGC TACTCAACAT GGTGGTATAT CAGTATTCGC 50
 AGGTGTTGGA GAGAGAACAA GAGAAGGTAA CGACCTTTAC GGAGAAATGA 100
 GTGAGTCTGG AGTTATAAAC AAGACAGCTC TAGTATTCGG ACAAATGAAT 150
 GAGCCACCTG GAGCAAGAAT GAGAGTTGCT TTAAGTGGTC TTACAATGGC 200
 TGAATATTTT AGAGATCAAG AAGGACAAGA CGTTTTATTA TTCGTAGATA 250
 ATATATTCCG TTTCACTCAA GCAGGATCTG AGGTTTCTGC ACTTCTTGGA 300
 60 CGTACTCCAT CAGCAGTTGG ATACCAACCA ACATTAGCTA CAGAGATGGG 350

TAGATTACAA GAGAGAATAA CATCTACAAA TAAAGGGTCT ATAACATCAG 400

5 2) INFORMATION FOR SEQ ID NO: 764

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium novyi*
(B) STRAIN: ATCC 19402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764

TTAATTCAAG	AATTAATCAA	CAATATAGCG	AAGGAACACG	GTGGATTATC	50
TGTATTTACA	GGAGTTGGAG	AAAGAACAAG	AGAAGGTAAT	GACCTTTACT	100
ATGAAATGAA	AGAATCTGGT	GTTATAAATA	AAACAGCACT	AGTATTTGGT	150
CAAATGAATG	AGCCACCTGG	AGCAAGAATG	AGAGTTGCTC	TTACAGGACT	200
TACTATGGCA	GAATATTTCA	GGGATCAAGG	ACAAAACGTA	CTTTTATTCA	250
TAGACAACAT	ATTTAGATTTC	ACTCAAGCAG	GTTCAGAGGT	GTCAGCTTTA	300
CTTGGAAGAA	TACCTAGTGC	CGTTGGATAC	CAACCAACAC	TAGCAACAGA	350
AATGGGTGCG	CTTCAAGAAA	GAATAACATC	TACAAAGCAT	GGTTCTATAA	400
CATCA					405

2) INFORMATION FOR SEQ ID NO: 765

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
(B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765

AATTAATAAA	TAACATAGCT	AAAGAACATG	GTGGATTATC	AGTGTTTACT	50
GGAGTTGGAG	AAAGATCTAG	AGAAGGTAAT	GATCTTTATC	ATGAAATGAG	100
AGAATCAGGC	GTTATAGATA	AAACCGCATT	AGTATTTGGT	CAAATGAATG	150
AGCCACCTGG	TGCTAGAATG	AGAGTTGCAT	TAACAGGGTT	AACTATGGCT	200
GAATATTTTA	GAGATAAAGG	TCAAGATGTA	TTACTATTTA	TAGATAATAT	250
ATTTAGATTT	ACTCAAGCTG	GATCAGAAGT	TTCAGCATT	CTTGGAAGAA	300
TACCATCAGC	AGTTGGTTAC	CAACCAACTT	TAGCAACTGA	AATGGGTGCA	350
CTTCAAGAGA	GAATTACATC	AACTAAGAAT	GGTTCTATAA	CAT	393

60 2) INFORMATION FOR SEQ ID NO: 766

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium histolyticum*
 (B) STRAIN: ATCC 19401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766

15	AGGAACTTAT	AAATAATATT	GCAAAACAAT	ATGGAGGTCT	ATCTGTATTT	50
	ACAGGTGTTG	GTGAAAGAAC	AAGAGAAGGT	AATGACCTAT	ATAATGAAAT	100
	GAAAGATTCT	GGGGTTATAG	AGAAAACCTGC	ACTAGTATTT	GGACAGATGA	150
	ATGAACCACC	AGGAGCGAGA	ATGAGAGTAG	CATTGACAGG	ACTTACTATG	200
20	GCAGAAATATT	TTAGAGATCA	AGGGCAAGAT	GTACTTTTAT	TTATAGATAA	250
	TATATTTTGA	TTTACGCAGG	CTGGTTCTGA	AGTTTCTGCA	TTGTTAGGAA	300
	GAATTCCTAAG	TGCAGTTGGA	TATCAACCAA	CCCTTGCAAC	TGAAATGGGT	350
	GCATTACAAG	AAAGAATAAC	ATCCACAAAA	AATGGATCAA	TTACTTCAG	399

2) INFORMATION FOR SEQ ID NO: 767

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767

45	CATGATGGAA	CTGATCCGTA	ACATCGCCAT	CGAGCACAGC	GGTTATTCCG	50
	TGTTTCGCCG	TGTGGGTGAG	CGTACTCGTG	AGGGTAACGA	CTTCTACCAC	100
	GAGATGAAGG	ACTCCAACGT	TCTGGACAAA	GTGGCACTGG	TCTACGGTCA	150
	GATGAACGAG	CCGCCGGGTA	ACCGTCTGCG	CGTAGCACTG	ACTGGCCTGA	200
	CCATGGCCGA	GAAGTTCCGT	GACGAAGGTA	ACGACGTTCT	GTTGTTCGTC	250
	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	ACTGAAGTAT	CCGCACTGCT	300
	GGGCCGTATG	CCTTCGGCAG	TAGGTTACCA	GCCGACCCTG	GCTGAAGAGA	350
50	TGGGCGTTCT	GCAAGAACGT	ATCACTTCGA	CCAAGGAAGG		390

2) INFORMATION FOR SEQ ID NO: 768

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Absidia corymbifera*
(B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768

```

10 AGGTCTTGTT CGTGGCAAAA GGTCATTGAC ACTGGTGCTC CTATCACCAT      50
   TCCTGTTGGT AACGAAGTCC TTGGTCGTAT CATTAAACGTC ATTGGTGAGC      100
   CCATTGATGA GCGTGGTCCY ATCAAGTCCA AGGCCACTCG TGCTATCCAC      150
   GCTGATGCTC CCGAGTTCGT TGATCAATCC CCCACTCCCG AGATTCTCGA      200
   GACTGGTATC AAGGTTGTCT ATTTGCTTGC TCCCTATGCT CGTGGTGGTA      250
15 AGATTGGTCT TTTCCGGTGGT GCCGGTGTCT GCAAGACTGT CTTGATTCAA      300
   GAATTGATCA ACAACATTGC CAAGGCTCAC GGTGGTTACT CTATCTTCTG      350
   TGGTGTCTGGT GAACGTACTC GTGAAGGCAA CGATTGTGAC CACGAAATGA      400
   TTTCCACTGG TGTCATCAAG CTTGAAGGTG AATCCAAGTG TGCTCTTGTC      450
   TTTGGTCAAA TGAACGAACC CCCCAGGAGCT CGTGCCCGTG TTGCCCTTGAC      500
20 TGGTTTGACC ATTGCCGAAT ACTTCCGTGA TGAGGAAGGT CAAGATGTGT      550
   TGCTCTTCAT TGACAACATT TTCCGTTTCA CTCAAGCCGG TTCTGAAGTG      600
   TCCGCTTTGC TTGGTCTGAT TCCCTCTGCT GTCGGTTACC AACCCACTCT      650
   YTCCACTGAT ATGGGTGGTA TGCAAGAGCG TATTACTACC ACCAAGAACG      700
   GTTCCATTAC CTCCGTGCAA GCTGTCTACG TCCCTGCTGA CGATTTGACT      750
25 GATCCTGCTC CTGCTACTAC TTTTGCTCAC TTGGACGCCA CCACTGTGTT      800
   GTCTCGTTCC ATTGCTGAGT TGGGTATCTA CCCTGCTGTC GATCCCCTTG      850
   ACTCCAAGTC CCGTATCTTG GATCCCCGTA TCGTTGGTGA TGAGCACTAC      900
   TCTGTTGCCA CTGGTGTCCA ACAAATCCTT CAAAACCTACA AGTCGCTTCA      950
   AGA
30

```

2) INFORMATION FOR SEQ ID NO: 769

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1343 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Alternaria alternata*
(B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769

```

50 CGCGGTTCCA AGGCCACCGA CACCGGTGCC CCCATCAAGA TTCCCGTTGG      50
   TCACGGTACC CTTGGTCGTA TCATGAACGT CACTGGTGAC CCCATTGACG      100
   AGCGTGGTCC CATCAAGGCC ACCAAGTACG CTCCCATCCA CGCCGACCCC      150
   CCGGAGTTCA CCGAGCAATC CACCTCCGCT GAGGTCCTCG TTACCGGTAT      200
   CAAGGTTGTC GACCTGTTGG CTCCTTACGC TCGTGGTGGA AAGATTGGTC      250
   TCTTCGGAGG TGCTGGTGTC GGAAAGACTG TCTTCATTCA GGAGCTGATT      300
55 GTAAGGAGAC ACACTGTCTA CTGGCTGAGC ATTAGCTAAC GGCAGGCAGA      350
   ACAACATCGC CAAGGCCAC GGTGGTTTCT CTGTCTTCAC TGGTGTCTGGT      400
   GAGCGTACCC GTGAGGGTAA CGATCTGTAC CACGAGATGC AGGAGACTTC      450
   CGTCATTGAG CTTGACGGTG ACTCCAAGGT CGCCCTCGTC TTCGGTCAGA      500
   TGAACGAGCC CCGGGGTGCC CGTGCCCGTG TCGCTCTTAC TGGTCTTACT      550
60 GTTGCTGAGT AAGTCTTGAA TTCACTGTGT TGACAACGTC GTGGCTAATG      600

```

	GGAAAAAAGA	TACTTCCGTG	ACGAAGAGGG	ACAGGATGTG	CTTCTCTTCA	650
	TCGACAGTAA	GTGCTTGTAC	GAACTGCCTG	TGAGACATAC	ACTGACTTCG	700
	GCAATAGACA	TTTTCCGTTT	CACCCAGGCC	GGTCCGAGG	TGTCCGCTCT	750
	TCTTGGTCGT	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCACC	CTCGCCATTG	800
5	ACATGGGTGT	CATGCAGGAG	CGTATTACCA	CCACCACCAA	GGGTTCATC	850
	ACCTCCGTCC	AGGCCGTCTA	CGTGCCCGCT	GACGATTGTA	CTGACCCTGC	900
	CCCCGCCACC	ACCTTCGCCC	ATTTGGACGC	CACCACTGTC	TTGTCCCGTG	950
	GTATCTCCGA	GTTGGGTATC	TACCCCGCCG	TCGACCCTCT	TGACTCCAAG	1000
	TCCCGTATGT	TGGACCCCCG	TGTCATTGGT	CAGGACCACT	ACGACACCGC	1050
10	CACCCGCGTT	CAGCAGATTG	TCCAGGAGTA	CAAGTCGCTC	CAGGATATCA	1100
	TTGCCATTCT	CGGTATGGAC	GAGTTGTCGG	AAGCTGACAA	GCTTACCGTC	1150
	GAGCGTGCCC	GTAAGATCCA	GCGTTTCTTG	AGCCAGCCTT	TCGCTGTCGC	1200
	CCAGGCTTTC	ACTGGTATTG	AGGGCAAGCT	TGTCGACCTC	AAGGACACCA	1250
	TCCGATCATT	CAAGGCTATC	TTGACTGGTG	AGGGTGACGA	CCTTCCCGAG	1300
15	GGTGAGTCTC	GACTATCTCC	GCATTCATAG	CGTATAACTG	ACA	1343

2) INFORMATION FOR SEQ ID NO: 770

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 25 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 30 (A) ORGANISM: *Aspergillus flavus*
 - (B) STRAIN: ATCC 26947
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770

35	TTCAGGAGTT	GATTGTATGT	TCACCTGCAA	CATAAGACTT	CCCATTCTCC	50
	ACTCTTTTCT	AACTCTTCAC	AGAACAACAT	TGCCAAGGCT	CACGGTGGTT	100
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGATCTG	150
	TACCACGAAA	TGCAGGAGAC	TGGTGTCATT	CAGCTCGAGG	GTGAATCTAA	200
	GGTCGCCCTT	GTCTTCGGTC	AGATGAACGA	GCCCCCAGGT	GCCCCGTGCCC	250
40	GTGTGCGCCT	TACCGGTCTG	ACCATCGCCG	AGTACTTCCG	TGACGAGGAA	300
	GGTCAGGATG	TGCTGCTCTT	CATTGACAAC	ATTTTCCGTT	TCACCCAGGC	350
	CGGTTCTGAG	GTGTCTGCCC	TTCTTGGTG	TATCCCCTCC	GCTGTCGGTT	400
	ACCAGCCCAC	TCTGGCCGTC	GACATGGGTG	GTATGCAGGA	GCGTATTACC	450
45	ACCACCACCA	AGGGTTCCAT	TACCTCCGTC			480

2) INFORMATION FOR SEQ ID NO: 771

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1174 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 55 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 60 (A) ORGANISM: *Mucor circinelloides*
 - (B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771

```

5   CTCGAACAAG AYAACCTTGCC YGCCATTTTG AACGCCCTTG AAGTCAAGGA      50
   YCACTCTGGT GGACGTCTCG TYCTCGAAGT CTCTCAACAT TTGGGTGAGA      100
   ACACGTGTCG TACTATTGCT ATGGATGGTA CTGAAGGTAA GTTATGTYCA      150
   TCCCANNGGA TACAGTCARA CAGMAATGTC TAGTGGTTAT AGCAGYAGCA      200
   GATGATTGAC CAATATGTTA GGTCTTGTC GGTGGTCAAA AGGTTGTTGA      250
   CACTGGTGCT CCCATTACCA TCCCCGTTGG TAAGGAAGTC CTTGGTCGTA      300
10  TCATCAACGT TATTGGTGAA CCCATTGATG AACGTGGTCC CATTGACGCC      350
   AAGACTCACC GTCCTATTCA CGCTGAAGCT CCCGAATTCG TTGATCAATC      400
   CCCCCTCCC GAAATCCTCG AGACTGGTAT CAAGGTYGTC GATTTGTTGG      450
   CTCCTTATGC TCGTGGTGGT AAGATTGGTC TCTTCGGTGG TGCTGGTGTC      500
   GGTAAAGACTG TCTTGATTCA AGAATTGATT AACAACATYG CCAAGGCTCA      550
15  CGGTGGTTAC TCTATCTTCT GTGGTGTCGG TGAACGTACT CGTGAGGGTA      600
   ACGATTTGTA CCATGAAATG ATTGAAACCG GTGTCATTCA ATTGGAAGGC      650
   GAGTCCAAGT GTGCTCTCGT CTTTGGTCAA ATGAACGAAC CCCAGGTGC      700
   TCGTGCCCGT GTCGCTTTGA CTGGTTTGAC TATTGCTGAA TACTTCCGTG      750
   ATGATGAGGG TCAAGATGTC TTGCTTTTCA TTGATAACAT TTTCAGATTC      800
20  ACTCAAGCTG GTTCTGAGGT ATCTGCCCTT TTGGGTCGTA TTCCTTCCGC      850
   TGTCGGTTAC CAACCCACTC TTTCCACYGA TATGGGTGGT ATGCAAGAGC      900
   GTATTACTAC CACCAAGAAC GGTTCCATTA CCTCCGTCCA AGCTGTCTAC      950
   GTCCCTGCTG ATGATTTGAC CGATCCTGCT CCTGCCACCA CTTTGTGCTCA     1000
   CTTGGATGCC ACCACTGTCT TGTCTCGTTC CATCGCTGAA TTGGGTATCT     1050
25  AYCCCGCTGT CGATCCTCTT GATTCCAAGT CTCGTATCCT CGATCCCCGT     1100
   ATTGTCGGTG ATGAGCACTA CAAGGTTGCC ACTGAAGTTC AACAAATCCT     1150
   CCAAACACTAC AAGTCTCTCC AAGA                                     1174

```

30

2) INFORMATION FOR SEQ ID NO: 772

(i) SEQUENCE CHARACTERISTICS:

```

35  (A) LENGTH: 467 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Piedraia hortai
   (B) STRAIN: ATCC 24292

```

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772

```

   AGGAGCTTAT CAACAACATC GCCAAGGCTC ACGGTGGTTA CTCCGTCTTC      50
   ACTGGTGTCG GTGAGCGTAC TCGTGAGGGT AACGATTTGT ACCACGAGAT      100
   GCAAGAGACT TCCGTCAATC AGCTTGACSG CGAGTCCAAG GTCGCTCTCG      150
50  TGTTCCGGTCA GATGAACGAG CCCCCGGGTG CCCGTGCCCC TGTTGCCCTG      200
   ACTGGTCTTA CCATCGCTGA GTACTTCCGT GATGCCGAGG GTCAGGATGG      250
   TAAGTTCTAT AACTCTTGTC GCAAAGGTTT CATTCTGGTC GCTAACTTGC      300
   TCAGTGCTCC TGTTTCATCGA CAACATTTTC CGTTTCACCC AGGCTGGTAT      350
   GGAGGTGTCT GCCCTCCTCG GTCGTATTCC TTCTGCCGTC GGTTACCAAC      400
55  CTACTCTCGC CGTCGACATG GGTGGTATGC AAGAGCGTAT TACCACTACC      450
   AAGAAGGGAT CCATTAC                                     467

```

60 2) INFORMATION FOR SEQ ID NO: 773

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
 (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773

```

15 TTGCCAAGGC CCACGGTGGT TACTCTGTCT TCACTGGTGT CGGTGAGCGT      50
   ACCCGTGAGG GTAACGATCT GTACCACGAA ATGCAGGAAA CCTCCGTCAT      100
   TCAGCTTGAT GGCAGAGTCCA AGGTCGCGCT TGTCTTCGGT CAGATGAACG      150
   AGCCCCCTGG TGCCCGTGCT CGTGTCGCTC TTACTGGTCT TACCGTTGCC      200
20 GAGTACTTCC GTGATGAGGA GGGTCAGGAT GGTAAGTTAT ATCGTTTTTA      250
   TTATCTTCTT TGCCACCACC CCTCTACGAA TCCATGCCTC CGTTGGTGAA      300
   GGCATCGTTT GTAGGGCGGG TCGGAGTTTG CGGCAATTTC TGCCGTCGGC      350
   TTGAAGCCGC GGATGCCCGA TGTTTGACGC GTATCGATGC TAACAACAAT      400
   GACAACAGTG CTTCTCTTCA TTGACAACAT TTTCCGATTC ACCCAGGCCG      450
25 GTTCCGAGGT GTCTGCCCTT CTCGGTCGTA TTCCCTCTGC CGTCGGTTAC      500
   CAGCCCACTC TTGCCGTAGA CATGGGTGCC ATGCAGGAAC GTATTACCAC      550
   CACCAAGAAG GGTTCGATTA CCTCCGTC      578

```

2) INFORMATION FOR SEQ ID NO: 774

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhizopus oryzae*
 (B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774

```

50 AACTTACCYG CTATCTTGAA CGCTCTCGAA GTCCAAGATC ACTCTGGTGG      50
   ACGTCTTGTC CTTGAAGTTC GCTCAACACT TGGGTGAAAA TACTGTCCGT      100
   ACTATTGCTA TGGATGGTAC TGAAGGTAAG CTATACTATA ACCGTKTTAT      150
   CCGAGTATGA TATTAAGTTG AAAAAAGGTC TCGTYCGTGG TCAAAAGGTT      200
   ATTGACACTG GTGCTCCCAT TACCATTCCCT GYTGGTAAGG AAGTTCTCGG      250
   TCGTATCATT AACGTCATTG GTGAACCCAT CGATGAACGT GGTCCATCA      300
   ACGCCAAGAG CCAACGTCCC ATTCACGCCG AAGCTCCCGA ATTTCGTTGAC      350
   CAATCTCCTA CTCCCGAAAT TCTTGAAACT GGTATCAAGG TTGTCGACTT      400
55 GTTGGCTCCT TATGCTCGTG GTGGTAAGAT TGGTCTTTTC GGTGGTGCTG      450
   GTGTCGGTAA GACTGTGTTG ATTCAAGAAT TGATTAACAA CATCGCCAAG      500
   GCTCACGGTG GTTACTCTAT TTTCTGTGGT GTCGGTGAAC GTACTCGTGA      550
   AGGTAACGAT CTTTACCACG AAATGATTGA AACTGGTGTC ATCAAGCTCG      600
   ATGGTGACTC CAAGTGTGCT CTTGTCTTTG GTCAAATGAA CGAACCCCA      650
60 GGAGCTCGTG CCCGTGTTGC CTTGACTGGT TTGACCATTG CTGAATACTT      700

```

CCGTGATGAT GAAGGTCAAG ATGTGTTGCT TTTCATTGAT AACATTTTCC 750
 GTTTCACCCA AGCTGGTTCW GAAGTATCTG CCCTTTTGGG TCGTATTCCC 800
 TCCGCTGTCG GTTACCAACC CACTCTTTCT ACTGATATGG GTGGTATGCA 850
 AGAACGTATT ACAACCACCA AGAACGGTTC CATTACATCC GTCCAAGCTG 900
 5 TCTACGTCCC TGCTGATGAT TTGACCGATC CTGCTCCCGC CACCACTTTT 950
 GCTCACTTGG ATGCCACCAC TGTCTTGTCT CGTTCCATTG CCGAATTGGG 1000
 TATTTACCCT GCCGTCGATC CTCTTGAYTC CAAGTCTCGT ATCTTGGATC 1050
 CTCGTATCGT TGGTGACGAA CACTACAAGG TCGCTACCGA AGTTCAACAA 1100
 ATCCTTCAAA ACTACAAGTC TCT 1123
 10

2) INFORMATION FOR SEQ ID NO: 775

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Scopulariopsis koningii*
 25 (B) STRAIN: ATCC 38745
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775

30 ATTCAGGAGC TCATCAACAA CATTGCCAAG GCTCACGGTG GTTACTCTGT 50
 GTTCACTGGT GTCGGTGAGC GTACCCGTGA GGGTAACGAT CTGTACCACG 100
 AAATGCAGGA GACTTCGGTC ATTACAGCTCG AGGGCGAGTC CAAGGTCGCG 150
 CTTGTGTTTCG GTCAGATGAA CGAGCCCCC GGTGCCCGTG CCCGTGTCGC 200
 CCTTACCGGT CTGACCGTTG CCGAGTACTT CCGTGACGAG GAGGGCCAGG 250
 ATGGTGAGTA ACCGACGAAG TCTGAGATCT TGTCGGGCAT TATTCTAACG 300
 35 ACAACTAGTG CTTCTCTTCA TCGACAACAT TTTCCGCTTC ACCCAGGCCG 350
 GTTCCGAGGT GTCCGCGCTT CTCGGCCGTA TCCCCTCTGC CGTCGGTTAC 400
 CAGCCCACCC TGGCCGTCGA CATGGGAGGT ATGCAGGAGC GTATTACCAC 450
 GACTCAGAAG GGCTCGATTA CCTCGGT 477
 40

2) INFORMATION FOR SEQ ID NO: 776

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 610 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 50 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776

60 TCCGGAGTTG ATTGTAAGTC ATTTGAAACC CAGCCCCAAG AAACAGAAGC 50
 TAGGCGAAAA TTGGACAATT GAGCAATTTA GCCATTGGAG AAAAGAAATT 100
 TCGAGTATTA ATTGTTTTTA TAGAACAACA TTGCCAAGGC TCACGGTGGT 150

```

TACTCTGTCT TCACTGGTGT CGGAGAGCGT ACCCGTGAAG GAAACGATCT 200
CTACCATGAA ATGCAGGAGA CCGGTGTCAT TCAGCTTGAT GGCGAGTCCA 250
AGGTCGCCCT GGTCTTCGGC CAGATGAACG AGCCCCCAGG TGCCCGTGCC 300
CGTGTTCGCTC TTACTGGTTT GACCATTGCT GAGTACTTCC GTGATGAGGA 350
5 AGGTCAAGAC GGTGAGTTTY TTATGGATAA AARATTTTTT TTTTTTTTTT 400
TTTTTTMAAR AAATTCATGT TCTAACAAAG TATATCCTAG TGCTTCTCTT 450
CATCGACAAC ATTTTCCGTT TCACTCAGGC TGGTTCCGAA GTGTCTGCCC 500
TGCTTGGTTCG TATCCCATCT GCCGTCGGTT ACCAACCAC TCTTGCCGTC 550
GACATGGGTG GTATGCAGGA ACGTATTACC ACCACCAAGA AGGGATCCAT 600
10 TACCTCCGTC 610

```

2) INFORMATION FOR SEQ ID NO: 777

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 25 (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777

```

30 GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG 50
GTGAAAATTG GACAATTGAA CAATTTAGCC CTTGGAGAAA AGAAATTTTCG 100
AGTATTAATT ATTTTATAG AACAACATTG CCAAGGCTCA CGGTGGTTAC 150
TCTGTCTTCA CTGGTGTTCG AGAGCGTACC CGTGAAGGAA ACGATCTCTA 200
CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG 250
35 TCGCCCTGGT CTTCGGCCAG ATGAACGAGC CCCAGGTGC CCGTGCCCGT 300
GTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG 350
TCAAGACGGT GAGTTTCTTA TGGATGAAAG ATTTTTTTTT TTCAAGAAAT 400
TCATGTTCTA ACAAAGTGTA TTCTAGTGCT TCTCTTCATC GACAACATTT 450
TCCGTTTCAC TCAGGCTGGT TCCGAAGTGT CTGCCCTGCT TGGTCGTATC 500
40 CCATCTGCCG TCGGTTACCA ACCCACTCTT GCCGTCGACA TGGGTGGTAT 550
GCAGGAACGT ATTACCACCA CCAAGAAGGG ATCCATTACC TCC 593

```

45 2) INFORMATION FOR SEQ ID NO: 778

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1141 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778
- 60

	CCGTGGTCAA	GAAGTTATTG	ACACTGGTGC	CCCAATTACC	ATTCCTGTTG	50
	GTCGTGGTAC	TCTTGGTAGA	ATTATCAACG	TCATTGGTGA	ACCAATTGAC	100
	GAACGTGGCC	CTATCAAGGC	TTCTAAGTAT	GCTCCTATCC	ATACTGAACC	150
	ACCAACCTTT	GCTGAACAAT	CTACTTCTGC	TGAAGTTCTT	GAAACCGGTA	200
5	TCAAGGTTGT	CGATCTTCTT	GCTCCTTACG	CCCGTGGTGG	TAAGATTGGT	250
	CTTTTCGGTG	GTGCTGGTGT	CGGTAAGACT	GTCTTCATTG	AAGAACTTAT	300
	TAACAACATT	GCCAAGGCTC	ACGGTGGTTT	CTCTGTCTTC	ACTGGTGTCG	350
	GTGAAAGAAC	CCGTGAAGGT	AACGATCTTT	ACCGTGAAAT	GAAGGAAACT	400
	GGTGTCATCA	ACCTCGAAGG	TGACTCCAAG	GTCGCTCTCG	TTTTTCGGTCA	450
10	AATGAACGAA	CCTCCAGGTG	CCCGTGCCCG	TGTCGCTTTG	ACTGGTCTTA	500
	CCATTGCCGA	ATACTTCCGT	GATGAAGAAG	GACAAGATGT	CTTGCTTTTC	550
	GTTGACAACA	TTTTTCAGATT	CACCCAAGCC	GGTTCTGAAG	TCTCTGCTCT	600
	TTTGGGTTCG	ATTCCATCTG	CCGTCGGTTA	CCAACCTACC	CTTGCTACCG	650
	ATATGGGTGC	CCTCCAAGAA	CGGTATTACCA	CCACCCAAAA	GGGTTCGGTC	700
15	ACATCTGTCC	AAGCCGTCTA	TGTCCCAGCA	GACGATTTGA	CTGATCCTGC	750
	CCCAGCCACC	ACTTTCGCTC	ACTTGGACGC	CACCACTGTC	TTGTCTCGTT	800
	CCATTTCCGA	ATTGGGTATC	TACCCAGCTG	TCGATCCTCT	CGATTCCAAG	850
	TCTCGTCTTT	TGGATCCTGA	AGTTATTGGA	CACGAACACT	ACGAAGTTGC	900
	CACTCAAGTT	CAACAAACCC	TCCAAGCTTA	CAAGTCTCTC	CAAGATATCA	950
20	TTGCCATTTT	GGGTATGGAT	GAATTGTCTG	AAGCTGATAA	GCTTACTGTC	1000
	GAACGTGGCC	GTAAGATCCA	AAGATTCCTT	TCCCAACCAT	TCGCTGTTGC	1050
	CGAAGTTTTT	ACTGGTATCG	AAGGTCGTCT	CGTTCCATTG	AAGGAAACCG	1100
	TCAGATCTTT	CAAGGAAATC	CTTGAAGGTA	AGTACGATCA	C	1141

25

2) INFORMATION FOR SEQ ID NO: 779

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 22864

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779

	GCTGAAGGCC	GAACGTGAGC	GTGGTATCAC	CATCGATATC	GCGCTCTGGA	50
	AGTTCGAGAC	TCCCAAGTAC	TTCGTCACCG	TCATCGATGC	CCCTGGTCAT	100
45	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	CTGATTGTGC	150
	TATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTCGAGGCC	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CATGCTCTGC	TCGCCTACAC	CCTGGGCGTG	250
	AAGCAGCTTA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AATGGTCTGA	300
	GGATCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAAC TTC	ATCAAGAAGG	350
50	TCGGATACAA	CCCCAAGTCC	GTTCCATTCT	TGCCCCATCT	CGGCTTCAAC	400
	GGTGACAACA	TGATCGACGT	CTCCACCAAT	GCCCCCTGGT	ACAAGGGCTG	450
	GGAAAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTTGAGG	500
	CTATCGACTC	CATCGACCCT	CCTGCTCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCACTCC	AGGATGTCTA	CAAGATTTCT	GGTATCGGCA	CGGTGCCCCG	600
55	CGGTCTGTGT	GAGACTGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTTG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAA	700
	CAGCTCGCCG	AGGGCGTTCC	GGGTGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
	CGTCTCCGTG	AAGGAGGTTT	GTCGTGGAAA	CGTTGCTGGT	GACTCCAAGA	800
	ACGACCCCCC	CAAGGGTGCC	GACTCCTTCA	ACGCCCAGGT	CATCGTCCTC	850
60	AACCACCTTG	GTCAGGTCGG	TGCTGGCTAC	GCCCCGGTCT	TGGATTGCCA	900

CACTGCCCAC	ATTGCCTGCA	AGTTCTCTGA	GCTCCTCGAG	AAGATCGATC	950
GTCGTACCGG	CAAGTCCATG	GAAAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
GATGCTGCCA	TCGTGAAGAT	GGTTCCCAGC	AAGCCTATGT	GCGTTGAGGC	1050
TTTCACCGAC	TACCCTCCTC	TTGGTCGTTT	CGCCGTCCGT	GAC	1093

5

2) INFORMATION FOR SEQ ID NO: 780

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cunninghamella bertholletiae*
- (B) STRAIN: ATCC 42115

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780

25	TACTTGTA	AA TGGTCT	CAAG ATCGTT	ACAA CGAAATT	GTT AAGGAAG	TTT	50
	CTTCCTTC	AT CAAGAAG	ATT GGTACAA	TC CTAAAT	CCGT TCCTTT	CGTY	100
	CCTATCTC	TG GTTGGC	ACGG TGATAA	CATG TTGGAAG	CTT CTACCA	AACAT	150
	GCCTTGGT	AC AAGGGAT	GGA CCAAGGA	AAC TAAAGCT	GGT TCTTCC	ACTG	200
	GTAAGACT	CT CTTAGA	AGCC ATTGAC	AGCA TTGAAC	CTCC TACCCG	TCCT	250
	TCTGACA	AGC CTTTAC	GTCT TCTTT	ACAA GATGTT	TACA AGATTG	GTGG	300
30	TATTGGT	ACT GTCCCT	GTTG GTCGTG	TGA AACTGG	TGC ATCAAG	GCTG	350
	GTATGGT	TGT TACYTT	CGCT CCCGCT	AACG TCACCA	CTGA AGTTAA	GTCC	400
	GTTGAA	ATGC ATCAG	AACA ATTAGA	ACAA GGTGTT	CCCTG GTGACA	ACGT	450
	TGGTTT	CAAC GTCA	AGACG TTTCCG	TAA GGATAT	CCGT CGTGGT	AACG	500
	TCTGTT	CCGA CTCCA	AGAAC GACCCC	GCTA AGGAAT	CTGC TTCCTT	CAAC	550
35	GCTCAAG	TTA TCGTCT	TGAA CCACC	TGGT CAAATT	GGTG CTGGTT	TATGC	600
	CCCAGTT	CTT GACTGT	CACA CTGCT	CACAT TGCTTG	TAAG TTCGCT	GAAAT	650
	TATTAGA	AAAA GATCG	ATCGT CGTTCC	GTA AGAAAC	TCGA AGATG	CTCCT	700
	AAATTCG	TTA AATCT	GGTGA CTCTG	CTATC GTTAAG	ATGG TTCCTT	TCCAA	750
	GC						752

40

2) INFORMATION FOR SEQ ID NO: 781

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Curvularia lunata*
- (B) STRAIN: ATCC 26425

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781

60	CAAGTGGT	TCT GAGGAC	CGTT ACCA	GAAAT CATCA	AGGAG ACCTC	CAACT	50
	TCATCA	AAGAA GGT	CGGCTAC	AACCCCA	AGC ACGTT	CCCTT	100

	TCCGGTTTCA	ACGGAGACAA	CATGATTGAG	GCCTCCACCA	ACTGCCCCCTG	150
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	200
	TCCTTGAGGC	CATCGACGCC	ATCGACCCTC	CTGTCCGTCC	TACCGACAAG	250
	CCCCTCCGCC	TTCCCCCTCCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	300
5	GGTCCCCGTC	GGTCGTGTCTG	AGACCGGTAT	CATCAAGCCC	GGTATGGTCG	350
	TCACCTTCGC	CCCCGCTGGT	GTCACCACCG	AAGTCAAGTC	CGTCGAGATG	400
	CACCACGAGC	AGCTTACTGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	450
	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTGCGCGGTG	500
	ACTCCAAGAA	CGACCCCCCC	AAGGGTTGCG	AGTCCTTCAA	CGCCCAGGTC	550
10	ATCGTCCTCA	ACCACCCTGG	TCAGGTCGGT	GCCGGTTACG	CCCCAGTCCT	600
	TGACTGCCAC	ACTGCCCACA	TTGCCTGCAA	GTTCTCCGAG	CTCCTCGAGA	650
	AGATCGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCCCC	CAAGTTCATC	700
	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGA			728

15

2) INFORMATION FOR SEQ ID NO: 782

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1145 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

30

--(xi)--SEQUENCE DESCRIPTION: SEQ ID NO: 782

	TGAAGTCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACTC	CCAAGTAAGG	CTCAACAGAC	ACAACAAGCA	AATGCATACT	100
35	CGCTAACCTA	TTCACCCACC	ACAGGTACAA	CGTCACCGTC	ATTGACGCCC	150
	CCGGTCACCG	TGATTTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGCGCCA	TTCTCATCAT	TGCCGCCGGT	ACTGGTGAGT	TCGAGGCCGG	250
	TATCTCCAAG	GACGGTCAGA	CCCGTGAGCA	CGCTCTTCTC	GCCTACACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	350
40	TGGTCTGAGG	CCCGTTACCA	GGAGATCATC	AAGGAGACCT	CCGGTTTCAT	400
	CAAGAAGGTC	GGCTTCAACC	CCAAGCACGT	TCCCTTCGTG	CCCATCTCCG	450
	GTTTCAACGG	TGACAACATG	ATCGACGTCT	CCACCAACTG	CCCCTGGTAC	500
	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGCCATCG	ACCCCCCAC	TCGTCCCACC	GACAAGCCCC	600
45	TCCGTCTTCC	CCTYCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGCACGGTT	650
	CCCGTCGGTC	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTCAC	700
	CTTCGCCCCC	GCTGGTGTCA	CCACTGAGGT	CAAGTCCGTC	GAGATGCACC	750
	ACGAGCAGCT	TCCCCGAGGT	CTCCCCGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTCT	CCGTCAAGGA	GATCCGTCTG	GGCAACGTCG	CCGGTGACTC	850
50	CAAGAACGAC	CCCCCAAGG	GTCGCGACAG	CTTCAACGCC	CAGGTCATCG	900
	TCCTCAACCA	CCCCGGTCAG	GTCGGCGCCG	GCTACGCGCC	CGTCCTCGAC	950
	TGCCACACTG	CTCACATTGC	TTGCAAGTTC	TCTGAGCTCC	TCGAGAAGAT	1000
	CGACCGCCGT	ACCGGCAAGT	CCATTGAGGC	CAGCCCCAAG	TTCATCAAGT	1050
	CTGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	TATGTGCGTT	1100
55	GAGGCCTTCA	CCGACTACCC	CCCTCTTGGA	CGTTTCGCCG	TCCGT	1145

2) INFORMATION FOR SEQ ID NO: 783

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783

```

15 GCTCAAGGCT GAGCGTGAGC GTGGTATCAC CATTGACATC GCCCTCTGGA      50
   AGTTCGAGAC CCCCAAGTAC ATGGTCACCG TCATCGGTAT GCTTTATCTG      100
   TTTCCCATTT ATAGTTGCGA CAAGTAACTA ATAAAAAGTA GATGCCCCCG      150
   GACACCGTGA CTTCATCAAG AACATGATTA CTGGTACCTC CCAGGCCGAC      200
   TGCGCTATTC TCATCATTGC TGCCGGTACT GGTGAGTTTC AGGCTGGTAT      250
20 CTCCAAGGAT GCCCAGACTC GTGAGCACGC CCTGCTCGCT TTCACCCTCG      300
   GTGTCAAGCA GCTCATCGTT GCCATCAACA AGATGGACAC CACCAACTGG      350
   TCTGAGTCCC GTTTCGGTGA AATCATCAAG GAAGTCACCA ACTTCATCAA      400
   GAAGGTCGGC TACGACCCCA AGGGTGTCCTT ATTCGTCCCA ATCTCTGGCT      450
   TCAACGGTGA CAACATGATT GAGCCCTCCA CCAACTGCCC ATGGTACAAG      500
25 GGATGGAACA AGGAGACCAA GGCCGGTGCC AAATCCTCTG GTAAGACCCT      550
   CCTTGAGGCC ATCGATGCCA TTGACATGCC CACTCGTCCC ACCGACAAGC      600
   CTCTCCGTCT CCCACTCCAG GATGTCTACA AGATCTCTGG TATCGGAACA      650
   GTACCAAGTC GTCGTGTTGA GACTGGTATC ATCAAGCCTG GTATGGTTGT      700
   CACTTTCGCC CCCGCCAACG TCACCACTGA AGTCAAGTCC GTCGAAATGC      750
30 ACCACCAGCA GCTCGTTCAG GGTGTTCCCG GTGACAACGT TGGCTTCAAC      800
   GTCAAGAACG TCTCTGTCAA GGAAGTCCGC CGTGGTAACG TTGCCGGTGA      850
   TTCCAAGAAC GACCCACCAT CTGGCTGCGC CTCTTTCAAG GCCCAGGTCA      900
   TCGTCCTCAA CCACCCCGGC CAGATCGGTG CTGGTTACGC CCCAGTCCTC      950
   GACTGCCACA CTGCCCACAT TGCTTGCAAG TTCTCTGAGC TTCTTGAGAA      1000
35 GATTGACCGC CGTACTGGTA AATCCGTCGA AACCAGCCCT AAGTTCGTCA      1050
   AGTCTGGTGA TGCCGCTATT GCCACCATGG TTCCATCCAA GCCCATGTGC      1100
   GTTGAGGCTT TCACTGACTA CCCACCACTT GGTGCTTTTC CCGTCCGTGA      1150
C

```

2) INFORMATION FOR SEQ ID NO: 784

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
 (B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784

```

CCAAGTGGTC TCAAGATCGT TACAACGAAA TTGTCAAGGA AGTTTCCGGT      50
TTCATCAAGA AGATCGGTTT CAACCCCAAG TCCGTTCCCT TCGTTCCCAT      100
60 TTCTGGCTGG CACGGTGATA ACATGTTGGA TGAATCCACC AACATGCCCT      150

```

	GGTTCAAGGG	ATGGAACAAG	GAGACCAAGG	CCGGTTCCAA	GA CTGGTAAG	200
	ACTCTCCTCG	AAGCCATCGA	TGCCATTGAG	CCCCCTGTCC	GTCCTTCTGA	250
	CAAGCCTCTC	CGTCTTCCTC	TTCAAGATGT	CTACAAGATT	GGTGGTATTG	300
	GTACAGTTCC	CGTCGGTCGT	GTTGAAACTG	GTACTATCAA	GGCTGGTATG	350
5	GTTGTCAACT	TCGCTCCCGC	TGCTGTCACC	ACTGAAGTTA	AGTCCGTTGA	400
	AATGCATCAC	GAAACCCTCT	CTGAAGGTCT	CCCCGGTGAC	AACGTTGGTT	450
	TCAACGTCAA	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	500
	TCCGACTCCA	AGAACGATCC	CGCTAAGGAA	TCTGCCTCTT	TCACTGCTCA	550
	AGTTATTATC	TTGAACCATC	CCGGTCAAAT	CTCTGCTGGT	TACGCACCAG	600
10	TTCTCGATTG	TCACACTGCT	CACATCGCCT	GTAAGTTCTC	TGAACTCATT	650
	GAGAAGATTG	ATCGTCGTTT	CGGTAAGTAC	CTGCATCTGT	CAGAATTGAA	700
	GGTCCGCCGT	TATAGCAAAG	GCTGGGTTTA	AATGTTGGGG	TTTGTCTGAT	750
	CTATAATGAT	GATTGCTCCT	TCAATTTTGT	ACATAATTTG	ATGATCTGAA	800
	TTGTGTTGCT	AACGTCGCAT	TTGCTTCTTT	TGCTTCTTTT	GCATGTAGGT	850
15	AAGAAGATTG	AAGATGCTCC	CAAAGTAAGT	ATTACGATTG	ATGGACAATT	900
	AAAATAGAAT	ACTAACAATT	ATTGTTTATA	GTTCTGCAAG	TCTGGTGACT	950
	CTGCTATCGT	CAAGATGGTT	CCCTCCAAG			979

20

2) INFORMATION FOR SEQ ID NO: 785

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 1099 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phialaphora verrucosa*
- (B) STRAIN: ATCC 38561

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785

	GGACAAGCTG	AAGGCCGAAC	GTGAGCGTGG	TATCACCATC	GATATCGCGC	50
	TCTGGAAGTT	CGAGACTCCC	AAATACTTCG	TCACCGTCAT	TGATGCCCCCT	100
	GGTCATCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	150
40	TTGTGCCATC	CTCATCATTG	CCGCCGGTAC	CGGTGAGTTC	GAAGCCGGTA	200
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTCCTCGC	CTACACCCTA	250
	GGTGTGAAGC	AGCTTATCGT	CGCCATCAAC	AAGATGGACA	CCGCCAAATG	300
	GTCCGAGGAT	CGGTTCAACG	AAATCATCAA	GGAGACTTCC	AACTTCATCA	350
	AGAAGGTCGG	ATACAACCCC	AAGTCCGTCC	CGTTCGTGCC	CATCTCCGGT	400
45	TTCAACGGTG	ACAACATGAT	CGACGTCTCC	TCCAACGCCC	CCTGGTACAA	450
	GGGTTGGGAG	AAGGAGACCA	AGGCCGGCAA	GGCCACTGGC	AAGACCCTCC	500
	TCGAGGCCAT	CGACGCGATT	GACCCTCCTA	CTCGTCCCAC	CGACAAGCCC	550
	CTCCGTCTCC	CTCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGCACGGT	600
	GCCCGTTGGT	CGTGTTGAGA	CCGGTACCAT	CAAAGCCGGT	ATGGTCGTCA	650
50	CCTTCGCTCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	700
	CACGAACAGC	TCGCCGAAGG	TGTTCCAGGT	GACAATGTCT	GCTTCAACGT	750
	CAAGAACGTC	TCCGTCAAGG	AGGTTCTGTC	TGGAAACGTT	GCCGGTGACT	800
	CCAAGAATGA	CCCCCCCCAAG	GGTGCCGACT	CCTTCAACGC	TCAGGTCATC	850
	GTCCTCAACC	ACCCTGGTCA	GGTCGGTGCC	GGCTACGCCC	CGGTCTTGGA	900
55	TTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTC	CTCGAGAAGA	950
	TCGATCGTCG	TACCGGCAAG	TCCATGGAAA	ACAACCCCAA	GTTTATCAAG	1000
	TCTGGTGATG	CTGCCATCGT	GAAGATGGTT	CCCAGCAAGC	CTATGTGCGT	1050
	TGAGGCCTTC	ACCGACTATC	CTCCTCTTGG	TCGTTTCGCC	GTCCGTGAC	1099

60

2) INFORMATION FOR SEQ ID NO: 786

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saksenaea vasiformis*
 (B) STRAIN: ATCC 60625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786

	ACCACCAAGT	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	50
	CGGYTTCATC	AAGAAGGTCG	GCTTCAACCC	CAAGCACGTT	CCCTTCGTGC	100
20	CCATCTCCGG	TTTCAACGGT	GACAACATGA	TCGACGTCTC	CACCAACTGC	150
	CCCTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACCGGCAA	200
	GACCMTCCTC	GAGGCCATTG	ACGCCATCGA	CCCCCYAGY	CGTCCCACCG	250
	ACAAGCCCCT	YCGTCTTCCC	CTMCAGGATG	TYTACAAGAT	TGGCGGTATT	300
	GGCAGCGTTC	CCGTCGGTCC	TGTYGAGACC	GGTRCCATCA	AGGGTGGCAT	350
25	GGTCGTCACC	TTCCCCCCCC	CTGGTGTCAC	CACTGAGGTC	AAGTCCGTCG	400
	AGATGCACCA	CGAGCAGCTC	GCCGAGGGTS	TCCCCGGTGA	CAACGTCGGC	450
	TTCAACGTCA	AGAACGTCTC	CGTCAAGGAG	ATCCGTCGTG	GCAACGTTGC	500
	CGGTGACTCC	AAGAACGACC	CCCCCAAGGG	CTGCGACAGC	TTCAACGCCC	550
	AGGTCATCGT	CCTCAACCAC	CCCGGTCAGG	TCGGCGCCGG	CTACGCGCCS	600
30	GTCCTSGACT	GCCACACTGC	TCACATTGCC	TGCAAGTTCT	CTGAGCTCCT	650
	CGAGAAGATC	GACCGCCGTT	CCGGCAAAGT	CATCGAGTCC	GGCCCCAAGT	700
	TCATCAAGTC	TGGTGACGCC	GCCATCGTCA	AGATGGTTCC	CTCCAAGCCC	750

2) INFORMATION FOR SEQ ID NO: 787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Syncephalastrum racemosum*
 (B) STRAIN: ATCC 32330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787

	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCTCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CACGTCACCG	TCATTGATGC	CCCCGGCCAT	100
	CGTGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CTGACTGCGG	150
55	TATCCTCATC	ATTGCCGCCG	GTA CTGGTGA	GTTCGAGGCT	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TTGCCTTCAC	CCTCGGTGTC	250
	CGTCAGCTGA	TCGTCCGCCAT	CAACAAGATG	GACTCGACCA	AGTACTCTGA	300
	GGCCCGTTAC	AACGAAATCG	TCAAGGAGGT	CTCCACCTTC	ATCAAGAAGA	350
	TCGGTTTCAA	CCCCAAGTCC	GTTCCCTTCG	TCCCCATCTC	TGGCTGGAAC	400
60	GGTGACAACA	TGTTGGAGGA	GTCCTCCAAC	ATGCCCTGGT	TCAAGGGCTG	450

	GAAGAAGGAG	ACCAAGGCTG	GCGAGAAGTC	CGGCAAGACC	CTCCTTGAGG	500
	CCATTGACAA	CATTGACCCC	CCGGTCCGTC	CCTCGGACAA	GCCCCCTCCGT	550
	CTTCCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATCGGCA	CAGTCCCCCGT	600
	CGGTCCGTGTC	GAGACTGGTG	TCATCAAGGC	TGGTATGGTC	GTGACCTTCG	650
5	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
	CAGTCCGTCG	AGGGTGTCCC	CGGTGACAAC	GTCGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTC	AAGGATATCC	GCCGTGGTAA	CGTCTGCTCT	GACTCCAAGA	800
	ACGACCCCCG	CAAGGAGTCT	GCCTCGTTCA	CCGCCCAGGT	CATCGTCCTG	850
	AACCACCCCCG	GTCAGATCGG	TGCCGGTTAC	GCCCCGGTTC	TTGACTGCCA	900
10	CACCGCTCAC	ATTGCCTGCA	AGTTCGCTGA	GCTCCTCGAG	AAGATCGACC	950
	GTCGTTCCCG	YAAGAAGCTC	GAAGAGTCCC	CCAAGTTCGT	CAAGTCGGGT	1000
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1050
	CTACACTGAG	TACCCCCCTC	TTGGCCGTTT	CGCC		1084

15

2) INFORMATION FOR SEQ ID NO: 788

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 1155 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
25	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Trichophyton tonsurans</i>
	(B) STRAIN: ATCC 56185

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788

	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	AATGTCACCG	TCATTGGTAT	GTTTTTCTTT	100
35	ACCTTTCCCC	TCCATCGTCT	TGCTGTGCCA	TAAC TAACGA	GAGTAGACGC	150
	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	200
	CTGACTGTGC	TATTCTCATC	ATTGCTGCCG	GTACTGGTGA	GTTCGAGGCT	250
	GGTATCTCCA	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TCGCCTTCAC	300
	CCTTGGTGTC	AAGCAGCTCA	TCGTTGCCAT	CAACAAGATG	GACACCACCA	350
40	ACTGGTCCGA	GGACCGTTTC	AAGGAAATCA	TCAAGGAAGT	CACCAACTTC	400
	ATCAAGAAGG	TTGGCTACGA	CCCCAAGGGT	GTTCCATTCG	TTCCAATCTC	450
	TGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCAGCAAC	TGCCCATGGT	500
	ACAAGGGATG	GAACAAGGAG	ACCAAGGCCG	GTGGTGCCAA	GACTGGCAAG	550
	ACCCTYCTCG	AGGCCATCGA	TGCCATCGAC	ATGCCAACCC	GTCTTACCGA	600
45	CAAGCCCCTY	CGTCTCCAC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	650
	GAAGTGTACC	AGTCGGTCGT	GTTGAGACCG	GTATCATCAA	GCCTGGTATG	700
	GTCGTCACCT	TCGCCCCCTG	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	750
	AATGCACCAC	CAGCAGCTTC	AGCAGGGTGT	CCCCGGTGAC	AACGTCGGCT	800
	TCAACGTCAA	GAACGTTTCC	GTCAAGGAAG	TCCGCCGTGG	TAACGTTGCC	850
50	GGTGACTCCA	AGAACGACCC	ACCATCCGGC	TGTGCCTCCT	TCAACGCCCA	900
	GGTCATCGTC	CTCAACCACC	CCGGCCAGAT	CGGTGCTGGT	TACGCCCCAG	950
	TCCTCGACTG	CCACACTGCT	CACATTGCTT	GCAAGTTCGC	TGAGCTCCTC	1000
	GAGAAGATTG	ACCGCCGTAC	CGGTAAATCC	GTCGAAGCCA	ACCCCAAGTT	1050
	CGTCAAGTCT	GGTGATGCCG	CTATCGCCAA	GATGGTTCCC	TCCAAGCCCA	1100
55	TGTGCGTTGA	GGCTTTCACT	GACTACCCCC	CACTTGGTCG	TTTCGCCGTC	1150
	CGTGA					1155

60 2) INFORMATION FOR SEQ ID NO: 789

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1138 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789

```

15 TCAAGGCCGA GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG      50
   TTCGAGACCC CCAAGTACAA TGTCACCGTC ATTGGTATGT TTCTCTTTAC      100
   CTTTCCCCTC CATCGTCTTG CTGTGCCATA ACTAACGAGA GTAGACGCCC      150
   CCGGTCACCG TGACTTCATC AAGAACATGA TCACTGGTAC CTCCCAGGCT      200
20 GACTGTGCTA TTCTCATCAT TGCTGCCGGT ACTGGTGAGT TCGAGGCTGG      250
   TATCTCCAAG GATGGCCAGA CCCGTGAGCA CGCTCTGCTC GCCTTCACCC      300
   TTGGTGTCAA GCAGCTCATC GTTGCCATCA ACAAGATGGA CACCACCAAC      350
   TGGTCCGAGG ACCGTTTCAA GGAAATCATC AAGGAAGTCA CCAACTTCAT      400
   CAAGAAGGTT GGCTACGACC CCAAGGGTGT TCCATTCTGT CCAATCTCTG      450
25 GTTTC AACGG TGACAACATG ATTGAGGCCT CCACCAACTG CCCATGGTAC      500
   AAGGGATGGA ACAAGGAGAC CAAGGCCGGT GGTGCCAAGA CTGGCAAGAC      550
   CCTCCTCGAG GCCATCGATG CCATCGACAT GCCAACCCGT CCTACCGACA      600
   AGCCCCTCCG TCTCCCACTC CAGGATGTCT ACAAGATCTC TGGTATCGGA      650
   ACTGTACCAG TCGGTCGTGT TGAGACCGGT ATCATCAAGC CCGGTATGGT      700
30 CGTCACCTTC GCCCCTGCCA ACGTCACCAC TGAAGTCAAG TCCGTCGAAA      750
   TGCACCACCA GCAGCTTCAG CAGGGTGTCC CCGGTGACAA CGTCGGCTTC      800
   AACGTCAAGA ACGTTTCCGT CAAGGAAGTC CGCCGTGGTA ACGTTGCCGG      850
   TGACTCCAAG AACGACCCAC CATCCGGCTG TGCCCTCCTTC AACGCCCAGG      900
   TCATCGTCTT CAACCACCCC GGCCAGATCG GTGCTGGTTA CGCCCCAGTC      950
35 CTCGACTGCC ACACTGCTCA CATTGCTTGC AAGTTCGCTG AGCTCCTCGA      1000
   GAAGATTGAC CGCCGTACCG GTAAATCCGT CGAAGCCAAC CCCAAGTTCTG      1050
   TCAAGTCTGG TGATGCCGCT ATCGCCAAGA TGGTTCCATC CAAGCCTATG      1100
   TGC GTTGAGG CTTTCACTGA CTACCCCCCA CTTGGTCTG      1138

```

40

2) INFORMATION FOR SEQ ID NO: 790

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790

```

60 CACCACCAAG TGGTCTGAGG AGCGTTACCA GGAAATCATC AAGGAGACCT      50
   CCAACTTCAT CAAGAAGGTC GGCTACAACC CCAAGCACGT TCCCTTCGTC      100
   CCCATCTCTG GTTTC AACGG AGACAACATG ATTGAGGCTT CCACCAACTG      150

```

	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACTGGTA	200
	AGACCCTTCT	CGAGGCCATC	GACGCCATCG	ACCCCCCTGT	CCGTCCTACC	250
	GACAAGCCCC	TCCGCCTTCC	CCTCCAGGAT	GTGTACAAGA	TTGGTGGTAT	300
	TGGCACGGTT	CCCGTCGGTC	GTGTCGAGAC	CGGTATCATC	AAGCCCCGTA	350
5	TGGTCGTCAC	CTTCGCCCCC	GCTGGTGTCA	CCACTGAAGT	CAAGTCCGTC	400
	GAGATGCACC	ACGAGCAGCT	TGCCGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
	CTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGTAACGTTG	500
	CCGGTGACTC	CAAGAACGAC	CCCCCAAGG	GTTGCGAGTC	CTTCAACGCC	550
	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCCG	GTTACGCACC	600
10	AGTCCTTGAC	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGCTCC	650
	TCGAGAAGAT	TGACCGCCGT	ACCGGAAAGT	CTGTTGAGAA	CTCCCCCAAG	700
	TTCATCAAGT	CCGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAG	748

15

2) INFORMATION FOR SEQ ID NO: 791

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 958 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: ATCC 14110
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791

	CGCTATTGTC	GTTGTTGCTG	CCTCCGACGG	TCAGATGTAG	GTGGAACATC	50
	TTGGGAAATA	CGTCGTAAAA	CACGGCGCTT	ACGTTTTCGC	GAATAGGCCC	100
	CAGACTCGTG	AGCATTGCT	GCTCGCCCGC	CAGGTGGTG	TCCAGAAGAT	150
35	CGTTGTCTTC	GTCAACAAAA	TCGATGCTAT	TGATGATCCG	GAGATGCTGG	200
	AACTGGTCGA	ACTCGAGATG	CGTGAGCTGC	TGAACAGCTA	CGGTTTCGAG	250
	GGTGAAGAGA	CTCCGATCAT	TTTCGGTTCC	GCTCTCTGTG	CTCTCGAAGG	300
	ACGCCGTGAC	GACATCGGTA	AAGACAGAAT	TGAGCAGCTT	ATGAACGCTG	350
	TCGACACCTG	GATCCCCACT	CCTCAGCGTG	ACCTCGACAA	ACCTTTCTTG	400
40	ATGTCTGTCTG	AGGAAGTGTT	CTCTATCGCC	GGCCGTGGTA	CCGTGGCTTC	450
	TGGTCGTGTC	GAGCGTGGTA	TCTTGAAGAA	GGACTCTGAG	GTTGAGATTG	500
	TTGGAGGCTC	CTTCGAACCC	AAGAAGACCA	AAGTCACCGA	CATTGAAACC	550
	TTCAAGAAGA	GCTGTGATGA	ATCGCGTGCT	GGTGACAAC	CTGGTCTCCT	600
	CCTGCGTGGT	ATCCGACGTG	AAGACGTCAA	GCCTGGTATG	GTCATTGCTG	650
45	TTCCCGGCAG	CACCAAAGCT	CACGACAAGT	TCCTCGTCTC	CATGTACGTC	700
	CTGACCGAGG	CGGAGGGTGG	TCGTCTGACT	GGCTTCGGTG	CCAACTACCG	750
	TCCCCAAGTC	TTCATCCGTA	CTGCAGGTAA	GTTCCCGCAC	ACCGTGTCCA	800
	GATCTTCCGA	GAGATTAGCG	ATATATGCTA	ATGATTCATC	AGACGAGGCT	850
	GCTGACCTCA	GCTTCCCTGA	CGGCGACCAA	TCTCGCAGAG	TTATGCCTGG	900
50	TGACAACGTC	GAGATGATCC	TGAAGACCCA	CCACCCTGTT	GCTGCTGAGG	950
	CTGGTCAA					958

55 2) INFORMATION FOR SEQ ID NO: 792

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 936 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792

```

10 CGTTGTCGCA GCTTCTGACG GTCAAATGTA ATTGAATGCC CGCCCAGACG      50
   GATGAAAGGA TTTGACGTTT CTAACATCAT TCTAGGCCTC AGACCAGAGA      100
   ACATTTGCTC CTTGCCCCGCC AGGTCGGTGT CCAGAAGCTG GTCGTTTTTCG      150
   TTAACAAGGT CGATGCCGTT GAGGACCCAG AGATGTTGGA GCTTGTCGAA      200
15 CTTGAAATGC GTGAACTCCT CAGCCACTAC GGTTTCGAGG GTGAGGAGAC      250
   CCCCATCATT TTTGGCTCTG CTCTCTGTGC CCTCGAGTCC CGTCGACCTG      300
   AGCTTGGTGT CGAGAAGATT GACGAGCTAT TGAACGCCGT CGACACCTGG      350
   ATCCCCACCC CCGAGCGCGC CACTGATAAG CCTTTCCTCA TGTCCATTGA      400
   GGAAGTGTTT TCTATCTCTG GTCGTGGTAC CGTCGTCTCC GGTCTGTGTTG      450
20 AGCGTGGTAT CCTCAAGAAG GATTCCGACG TCGAAATTGT TGGTGGCTCT      500
   ACCACCCCTA TCAAGACCAA GGTCACAGAT ATCGAAACCT TCAAGAAGTC      550
   CTGCGATGAA TCTCGAGCTG GTGACAACTC TGGTCTCCTT CTCCGAGGTA      600
   TCAAGCGTGA GGACTTGAAG CGTGGAATGG TTGTTGCTGC CCCCGGATCC      650
   ACCAAGGCTC ACACCGACTT CATGGTCTCC CTCTACGTCC TGACTGAGGC      700
25 TGAGGGTGGT CGTTCCAACG GCTTCACCCA CAAGTACCGC CCCCAAATGT      750
   TCATCCGTAC TGCTGGTATG TAACCCAAGT TTCCGCTATT TACTAAGTAG      800
   ATCATTGCTA ACTTGTATTT CCTTCCGTAG ACGAAGCCGC ATCTTTCAGC      850
   TGGCCTGGAG AAGACCAAGA CAAGAAGGCT ATGCCTGGTG ACAACGTCGA      900
   GATGATTTGC AAGACCCTCC ACCCCATTGC TGCCGA      936
30

```

2) INFORMATION FOR SEQ ID NO: 793

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793

45 TTATTGTTGC TGCTGGTACT

20

2) INFORMATION FOR SEQ ID NO: 794

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794

GACGACAAGT CGGTGAACTT

20

2) INFORMATION FOR SEQ ID NO: 795

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795

ACTTGCACGC GATGTGGCAG

20

2) INFORMATION FOR SEQ ID NO: 796

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796

GGTCCAATGC CWCAAACWAG A

21

2) INFORMATION FOR SEQ ID NO: 797

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797

CATTAAGAAT GGYTTATCTG TSKCTCT

27

2) INFORMATION FOR SEQ ID NO: 798

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798

TGGTTGTCCC AGCCGATCGT TT

22

2) INFORMATION FOR SEQ ID NO: 799

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799

ACCTGTGAAT ACAAGCAATC T

21

2) INFORMATION FOR SEQ ID NO: 800

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800

GATGAAATCT TCAACGAAGT TGAT

24

2) INFORMATION FOR SEQ ID NO: 801

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

658

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801

ACAACACCGA GAAGATCCCA

20

2) INFORMATION FOR SEQ ID NO: 802

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802

TTGCCATTTC TGGTTTCGTT

20

2) INFORMATION FOR SEQ ID NO: 803

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803

ACTTCAGTGG TAACACCAGC

20

2) INFORMATION FOR SEQ ID NO: 804

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804

CCTGGGACGG CCTCTGGCAT

20

10

2) INFORMATION FOR SEQ ID NO: 805

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

15 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805

25

CTCTTGTCCTCA TCTTAGCAGT

20

30 2) INFORMATION FOR SEQ ID NO: 806

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806

45 AGCATCACCA GACTTGATAA G

21

2) INFORMATION FOR SEQ ID NO: 807

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

55 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Cryptosporidium parvum*

660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807

AAAGTGGCTT CAAAGGTTGC

20

5

2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808

GCITTAIWRG CATTAGAARA YCCA

24

20

2) INFORMATION FOR SEQ ID NO: 809

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809

TCTTCCTGTW GCAACTGTTC CTCT

24

35

2) INFORMATION FOR SEQ ID NO: 810

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810

AGAGMWACAG ATAARSCATT CTTA

24

50

2) INFORMATION FOR SEQ ID NO: 811

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

661

55

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811

5

TRAARTAGAA TTGTGGTCTR TATCC

25

10 2) INFORMATION FOR SEQ ID NO: 812

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

15

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812

GTIACIGGIT CYTYRARRTT ICCICC

26

25

2) INFORMATION FOR SEQ ID NO: 813

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813

AATCYGTYGA AATGCAYCAC GA

22

40

2) INFORMATION FOR SEQ ID NO: 814

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814

GCIGGCACGT ACACIGCCTG

20

55

2) INFORMATION FOR SEQ ID NO: 815

60 (i) SEQUENCE CHARACTERISTICS:

662

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815

10 TGGTGCATYT CKACRGACTT

20

2) INFORMATION FOR SEQ ID NO: 816

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816

25

GCTACGACGA GATCAAGGGC

20

30 2) INFORMATION FOR SEQ ID NO: 817

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817

40

TGGAAGAAGG CCGAGGAGTT

20

45

2) INFORMATION FOR SEQ ID NO: 818

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818

55

AGCCGGGCTG GATCTTCTTC

20

60

2) INFORMATION FOR SEQ ID NO: 819

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819

TCGAGCTTCT GGAGGAAGAG

20

2) INFORMATION FOR SEQ ID NO: 820

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820

GAAGGAGGTG TCTGCTTACA C

21

2) INFORMATION FOR SEQ ID NO: 821

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821

GGCGCAAACG TCACCACATC A

21

2) INFORMATION FOR SEQ ID NO: 822

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid

664

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822

CGGCGGATGT CCTTAACAGA A

21

2) INFORMATION FOR SEQ ID NO: 823

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823

GAGCGGTATG AYGAGATTGT

20

2) INFORMATION FOR SEQ ID NO: 824

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824

GGCTTCTGCG GCACCATGCG

20

2) INFORMATION FOR SEQ ID NO: 825

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825

ATGAGCARCG SAACCATCGT TCAGTG

26

2) INFORMATION FOR SEQ ID NO: 826

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826

15 TCGATCGTGC CGACCATGTA GAACGC 26

2) INFORMATION FOR SEQ ID NO: 827

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Clostridium novyi*
 (B) STRAIN: ATCC 19402

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827

35 CACCAACTTG CTAAATGGGG AGATGCCCAG ATTGTTGTAT ATATAGGCTG 50
 TGGAGAACGT GGAAATGAAA TGACAGATGT TCTTAATGAG TTTCCAGAAC 100
 TTAAAGATCC TAAGACTGGC AAATCAATAA TGGAAAGAAC AGTTTTAATA 150
 GCAAATACTT CTAATATGCC AGTTGCAGCC CGTGAAGCTT GTATATATAC 200
 AGGAATCACA ATAGCAGAAT ATTTTAGAGA TATGGGATAT TCAGTAGCAC 250
 40 TTATGGCGGA TTCCACTTCA CGTTGGGCAG AGGCATTAAG AGAAATGTCT 300
 GGAAGACTTG AAGAAATGCC TGGTGATGAA GGTACCCAG CTTATTTAGG 350
 ATCAAGACTT GCTGATTTCT ATGAAAGAGC TGGAAAAGTT GTGTGTTTAG 400
 GAGACGATGA AAGAGAAGGT GCCATTACTG CAATAGGTGC TGTATC 446

45

2) INFORMATION FOR SEQ ID NO: 828

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: 9689

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828

```

5  CAGCATCAGC TTGCTAAATG GGCAGATGCA GATATAGTTG TATATATAGG      50
   CTGTGGCGAG CGTGGAAATG AAATGACAGA TGTTCTTCTT GAATTTCCCTG      100
   AATTAAAAGA CCCAAGAACA GGCGAGTCAC TTATGCAAAG AACTGTGCTT      150
   ATAGCAAATA CATCAGATAT GCCGGTTGCT GCACGTGAAG CTTCTATATA      200
   CACTGGTATT ACAATAGCTG AATATTTTAG AGATATGGGA TATAGTGTG      250
   CACTTATGGC AGACTCTACA TCAAGATGGG CTGAGGCTCT TAGAGAGATG      300
   AGTGGTCGTT TAGAGGAGAT GCCTGGTGAA GAAGGTTATC CTGCATACTT      350
10 AGGTTACAGT CTTGCTCAAT TCTATGAGAG AGCAGGAAAG GTAAATTGTC      400
   TAGGTATGGA TGAAAGAGAA GGAACACTTA CAGCAATTGG TGCAG          445

```

15 2) INFORMATION FOR SEQ ID NO: 829

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 445 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Clostridium septicum
   (B) STRAIN: ATCC 12464

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829

```

30 ATGCTATAGC TAAATGGGGA GACAGCGAAA TAGTTGTTTA CGTTGGATGT      50
   GGAGAACGTG GTAACGAAAT GACAGACGTT CTTAACGAAT TCCCAGAACT      100
   TATTGACCCA AAAACTGGGG AAAGTTTAAT GAAGAGAACA GTACTTATAG      150
   CTAATACTTC AAACATGCCA GTTGCTGCTA GAGAAGCTTG CATATACACA      200
35 GGTATTACAA TAGCTGAATA CTTCAGAGAT ATGGGATACT CAGTATCTAT      250
   AATGGCTGAT TCAACTTCAA GATGGGCAGA AGCATTAAGA GAAATGTCAG      300
   GTAGACTTGA AGAAATGCCA GGTGATGAAG GATATCCAGC GTACTTAGGA      350
   TCAAGACTTG CTGATTATTA CGAAAGAGCA GGTAAGGTTG TTTGTCTAGG      400
40 TAAAGATGGT AGAGAAGGTG CTGTAACAGC AATTGGAGCT GTATC          445

```

2) INFORMATION FOR SEQ ID NO: 830

45 (i) SEQUENCE CHARACTERISTICS:

```

   (A) LENGTH: 444 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

55 (A) ORGANISM: Clostridium botulinum
   (B) STRAIN: 20:3.1

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830

```

60 TCAAATTGCT AAATGGGGAG ATGCAGAAAT CGTTGTTTAC GTTGGATGCG      50
   GAGAACGTGG TAACGAAATG ACAGACGTTG TTAATGAGTT CCCAGAACTT      100

```


	ATTGACCCTA	AGACTGGCGA	AAGCTTAATG	AAGAGAACAG	TTCTTATAGC	150
	TAATACTTCA	AACATGCCAG	TTGCAGCGAG	AGAAGCTTCA	ATATATACAG	200
	GTATCACAAT	AGCTGAATAT	TTCAGAGATA	TGGGATATGC	AGTATCAATA	250
	ATGGCTGACT	CAACTTCAAG	ATGGGCTGAG	GCATTAAGAG	AAATGTCTGG	300
5	TAGACTTGAA	GAAATGCCTG	GTGATGAAGG	ATATCCAGCT	TACCTTGGAT	350
	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAGGTTGA	ATGTTTAGGT	400
	AATGATGGAA	GAATTGGTTC	TATAACAGCA	ATCGGTGCGG	TATC	444

10 2) INFORMATION FOR SEQ ID NO: 831

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 456 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
(B) STRAIN: ATCC 13124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831

25	TAGTTCAGCA	CCAAGTTGCT	AAATGGGGAG	ATACTGAGAT	AGTTGTTTAC	50
	GTTGGATGTG	GAGAACGTGG	TAACGAGATG	ACAGACGTTT	TTAACGAATT	100
	CCCAGAACTT	AAAGACCCTA	AACTGGGGGA	AAGCTTAATG	AAGAGAACAG	150
	TTCTTATTGC	TAATACATCT	AACATGCCAG	TTGCTGCCAG	AGAAGCATCA	200
30	ATATATACTG	GTATAACAAT	AGCAGAGTAT	TTCAGAGATA	TGGGATACTC	250
	AGTATCAATC	ATGGCTGACT	CAACTTCACG	TTGGGCAGAG	GCTTTAAGAG	300
	AAATGTCAGG	AAGACTTGAA	GAAATGCCAG	GAGACGAAGG	TTACCCAGCA	350
	TACTTAGGAT	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAAGTTGT	400
	AGCTTTAGGT	AAAGATGGAA	GAGAAGGAGC	TGTTACAGCT	ATCGGAGCAG	450
35	TATCCC					456

2) INFORMATION FOR SEQ ID NO: 832

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 444 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Clostridium tetani*
(B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832

	CCAAGTTGCA	AAATGGGCTG	ATGCTCAAAT	AGTTGTGTAC	ATAGGATGTG	50
55	GAGAACGTGG	AAATGAAATG	ACAGACGTTT	TAAATGAGTT	CCCAGAATTA	100
	AAGGATCCTA	AAACCGGGGA	ATCTTTAATG	AAAAGAAGCTG	TGTTAATAGC	150
	AAATACATCT	AATATGCCTG	TTGCAGCTAG	AGAAGCATCT	ATATATACTG	200
	GTATAACAAT	AGGGGAATAT	TTTAGAGATA	TGGGATATTC	AATAGCACTA	250
	ATGGCAGATT	CGACTTCTAG	ATGGGCAGAG	GCTCTAAGAG	AAATGTCTGG	300
60	AAGACTAGAG	GAGATGCCAG	GTGAAGAAGG	TTATCCAGCT	TATTTAGGAT	350

CTAGATTAGC	AGAGTTCTAT	GAAAGAGCAG	GTAATGTTAT	ATGTTTAGGT	400
CAGGATGGAA	GAGAAGGAGC	ATTAACAGCT	ATAGGAGCAG	TTTC	444

5

2) INFORMATION FOR SEQ ID NO: 833

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 1786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833

20

20	TGAACCAAGG	AAAAATAATA	ACCGTTTCGG	GACCTCTTGT	TGTGGCTTCT	50
	GGGATGCAAG	AAGCTAATAT	TCAAGATATT	TGTCGTGTGG	GACATCTTGG	100
	CTTAGTCGGA	GAAATTATTG	AAATGCGTCG	CGATCAAGCG	TCTATTCAGG	150
	TTTATGAGGA	AACATCAGGG	ATCGGTCCAG	GAGAACCAGT	AGTGACTACT	200
25	GGTTGTCCTT	TGTCGGTCGA	GTTAGGCCCG	GGCCTGATTT	CAGAAATGTT	250
	TGACGGTATT	CAGCGACCGC	TTGATCGTTT	TCAAAAAGCA	ACGGACAGCG	300
	ACTTTTTAAT	CCGTGGTGTG	GCTATCCCAA	GTCTTGATCG	AAAGGCTAAG	350
	TGGGCATTTA	TTCCCAAGCT	AAGTGTGTTG	CAAGAAGTAG	TTGCAGGTGA	400
	TATTTTAGGA	ACTGTGCAAG	AAACAGCTGT	CATTGAGCAC	CGTATCATGG	450
30	TTCCTTATAA	AGTTTCAGGG	ACCTTGGTGG	CTATTCATGC	AGGGGACTTC	500
	ACAGTAACAG	ATACAGTTTA	TGAAATTAAG	CAGGAAGACG	GTTCCATTTA	550
	CCAAGGTAGC	CTCATGCAGA	CTTGGCCAGT	TCGTCAAAGT	CGCCCTGTTG	600
	CTCAAAAGCT	TATCCAGTC	GAACCTTTGG	TTACAGGTCA	ACGGGTTATT	650
	GACACCTTTT	TCCCTGTTAC	AAAAGGTGGT	GCCGCTGCCG	TTCCTGGACC	700
35	ATTTGGGGCA	GGAAAAACAG	TTGTGCAGCA	TCAAATAGCT	AAATTTGCCA	750
	ACGTTGATAT	TGTTATTTAT	GTCCGTTGTG	GGGAACGCGG	CAACGAGATG	800
	ACCGACGTTT	TGAATGAGTT	TCCAGAGTTA	ATTGACCCAA	ATACAGGCCA	850
	GTCCATTATG	GAGCGCACGG	TGTTAATTGC	AAACACCTCT	AATATGCCAG	900
	TAGCAGCGCG	TGAAGCGTCG	ATTTACACAG	GTATTACCAT	TGCCGAATAT	950
40	TTCCGTGATA	TGGGCTATTC	TGTGGCTATC	ATGGCAGACT	CGACATCACG	1000
	TTGGGCAGAA	GCTCTGCGCG	AGATGTCAGG	ACGCCTACAA	GAAATGCCTG	1050
	GTGATGAAGG	CTACCCGGCT	TACTTAGGGA	GTCGTATTGC	CGAATATTAT	1100
	GAACGGGCTG	GTCGTGTTTC	GACCTTGGA	AGTCAAGAAC	GTGAGGGAAC	1150
	CATTACAGCC	ATCGGCGCGG	TTTCTCCTCC	TGGAGGGGAT	ATTTTCAGAGC	1200
45	CTGTCACTCA	AAACACCCTT	CGGATTGTCA	AAGTTTTCTG	GGGGCTCGAC	1250
	GCGCCTCTTG	CGCAACGGCG	TCACTTCCCA	GCGATTAAC	GGCTGACGTC	1300
	TTATTCAATTG	TATCAAGATG	ATGTAGGAAG	CTATATTGAC	CGTAAACAGC	1350
	AATCTAATTG	GTCCAACAAG	GTAACCTCGT	CCATGGCTAT	TTTGCAGCGT	1400
	GAAGCCAGTC	TAGAAGAAAT	TGTACGCTTG	GTGGGGCTTG	ATTCACTGTC	1450
50	TGAACAAGAT	CGTTTGACCA	TGGCTGTTGC	CCGGCAAATT	CGGGAGGATT	1500
	ATCTCCAGCA	AAATGCCTTT	GATTCGGTGG	ATACCTTTAC	TTCCTTTCCG	1550
	AAACAAGAGG	CCATGCTAAC	CAATATTTTG	ACCTTTAATG	AGGAAGCCAG	1600
	CAAAGCCCTT	TCTTTGGGAG	CTTATTTTAA	TGAGATTATG	GAAGGCACTG	1650
	CTCAGGTACG	CGATCGCATC	GCACGCAGCA	AATTTATCCC	AGAAGAAAAC	1700
55	TTAGAGCAGA	TTAAAGGGCT	TACTCAGAAG	GTTACCAAAG	AGATTACCA	1750
	CGTTTTAGCA	AAGGGAGGAA	TTTAGATGAG	CGTTCT		1786

60 2) INFORMATION FOR SEQ ID NO: 834

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834

15	TATCTCACGT	AAGTTTTTGC	GCGGCGGTTA	TATATCACTC	CAGGCCCTGG	50
	CTAAGTACGC	TAATACTGAC	GTTACTGTCT	ATGTGGGATG	TGGAGAGCGT	100
	GGAAACGAGA	TTGCCGAGGT	GCTTAAGGAG	TTCCCTGAGC	TGAAGACCAA	150
	GGTTGATGGC	AAGGAAGTGA	GCATTATGAA	ACGCACTTGC	TTGGTGGCCA	200
	ATACTTCAAA	CATGCCAGTG	GCCGCCAGGG	AGGCTAGTAT	CTACACTGGC	250
20	ATTACCCTAT	GTGAATACTT	CAGGGATATG	GGATACAACG	CCTGTGTGAT	300
	GGCGGATTCC	ACCAGTCGTT	GGGCTGAGGC	TTTGCCTGAG	ATATCAGGTC	350
	GTTTAGCTGA	GATGCCTGCT	GATTCAGGTT	ATCCCGCCTA	CCTTGCTTCT	400
	AGGCTTTCGG	CGTTCTATGA	CGGTGCTGGT	ACAGCTGAGT	GTATTGGAAC	450
25	ACCACTTCGT	GAAGGTTTCAG	TTACCATTGT	TGGTGTCTGT	TCTCCACCA	499

2) INFORMATION FOR SEQ ID NO: 835

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 464 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835

45	TTTCTCAAGC	TTTGAGTAAA	TATAGTAACT	CTGATGTTAT	TATTTACATT	50
	GGTTGTGGAG	AAAGAGGAAA	TGAAATGGCA	GAAGTTCTTA	CAGAATTCCT	100
	TGAGCTTTAT	ACTATGGTTG	ATGGAAAGAA	GGAGTCAATT	ATGCAAAGAA	150
	CTTGTTTAGT	AGCTAATACA	TCAAATATGC	CTGTCTGCTG	TAGAGAAGCT	200
	TCCATCTACA	CTGGTATTAC	ACTTTCTGAA	TACTTTAGAG	ATATGGGATG	250
	TAATGTTTCT	ATGATGGCAG	ATTCAACTTC	TCGTTGGGCT	GAAGCTCTTA	300
	GAGAAATTTT	TGGTAGATTA	GCTGAAATGC	CTGCAGATTC	GGGTTACCCA	350
50	GCATATTTAG	GCGCCAGACT	TGCTTCATTC	TATGAAAGAT	CAGGAAGAGT	400
	TAAATGTATG	GGTTCCTCC	ATAGAGAAGG	TACAGTAACA	ATTGTTGGTG	450
	CAGTTTCTCC	ACCT				464

55

2) INFORMATION FOR SEQ ID NO: 836

- 3) (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 446 bases

60

670

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836

5 GCCCTCTCCA AGTACTCCAA CTCCGATTGC GTCATCTATG TCGGCTGCGG 50
 CGAGCGCGGT AATGAGATGG CCGAGGTGCT CATGGAGTTC CCGACCCTGA 100
 CGACCGTGAT CGATGGCCGC GAGGAGTCGA TCATGAAGCG CACCTGCCTC 150
 GTGGCGAACA CCTCGAACAT GCCAGTCGCA GCCCCTGAGG CCTCTATTTA 200
 CACCGGCATC ACCCTGGCCG AGTACTACCG TGATATGGGC AAGCATATCG 250
 CCATGATGGC TGACTCGACG TCTCGCTGGG CCGAGGCGCT TCGTGAGATT 300
 TCGGGTCGTC TGGCGGAGAT GCCGGCGGAT GGTGGCTACC CCGCCTACCT 350
 20 CAGCGCTCGT CTCGCCTCCT TCTACGAGCG CGCCGGCCTC GTCACCTGCA 400
 TCGGCGGGCC GAAGCGCCAG GGCTCCGTCA CGATCGTCGG TGCCGT 446

25 2) INFORMATION FOR SEQ ID NO: 837

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837

40 TTAGTCAGGC CCTCTCCAAG TACTCCAAC CCGACTGCGT CATCTATGTC 50
 GGCTGCGGCG AGCGCGGTAA TGAGATGGCT GAGGTGCTCA TGGATTTCCT 100
 AACTCTGACG ACCGTGATCG ATGGTCGCGA GGAGTCCATC ATGAAGCGCA 150
 CCTGCCTCGT GGCAAACACT TCGAACATGC CAGTCGCAGC CCGCGAGGCC 200
 TCTATTTACA CCGGCATCAC CCTGGCCGAG TACTACCGTG ATATGGGCAA 250
 45 GCATATTGCC ATGATGGCCG ACTCGACATC TCGCTGGGCC GAGGCGCTTC 300
 GTGAGATTTT CCGTCGTCTG GCGGAGATGC CAGCCGATGG TGGCTACCCT 350
 GCCTACCTCA GCGCTCGTCT CGCCTCCTTC TACGAGCGCG CCGGCCTCGT 400
 CACCTGCATC GGCGGGCCGA AGCGCCAGGG CTCCGTACAG ATCGTCGGTG 450
 50 CTGTGT 456

2) INFORMATION FOR SEQ ID NO: 838

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

671

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tarentolae*
(B) STRAIN: MOU-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838

	AGGCCCTCTC	CAAGTACTCC	AACTCCGACT	GCGTCATCTA	CGTCGGCTGC	50
10	GGCGAGCGCG	GTAATGAGAT	GGCCGAGGTG	CTCATGGAGT	TCCCGACCCT	100
	GACGACTGTG	ATTGATGGCC	GTGAGGAGTC	GATCATGAAG	CGGACCTGCC	150
	TCGTGGCCAA	CACCTCCAAC	ATGCCAGTCG	CAGCCCGTGA	AGCCTCTATT	200
	TACACTGGTA	TCACCCTGGC	CGAATACTAC	CGTGATATGG	GCAAGCATAT	250
	CGCCATGATG	GCTGACTCGA	CGTCTCGCTG	GGCGGAGGCG	CTTCGTGAGA	300
15	TTTCGGGTCG	CCTGGCGGAG	ATGCCGGCTG	ATGGTGGGTA	CCCCGCCTAC	350
	CTTAGTGCTC	GTCTTGCCTC	CTTCTACGAG	CGTGCCGGCC	TCGTCACCTG	400
	CATCGGTGGG	CCGAAGCGCC	AGGGCTCCGT	CACGATCGTC	GGTGCCGTGT	450

20

2) INFORMATION FOR SEQ ID NO: 839

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*
(B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839

	GCACTCTCGA	AGTACTCGAA	CAGTGACGCT	GTTATTTACG	TGGGTTGTGG	50
	TGAGCGTGCG	AATGAGATGG	CGGAGGTGCT	CATGGACTTT	CCCACCCTCA	100
40	CCACCATTTAT	TGATGGACGT	GAGGAGTCTA	TCATGAAGCG	CACATGCCTG	150
	GTGGCAAATA	CTTCCAATAT	GCCTGTTGCT	GCTCGTGAGG	CATCTATTTA	200
	CACTGGTATC	ACCTTAGCTG	AGTATTATCG	GGATATGGGA	AAACACATCG	250
	CCATGATGGC	CGATTCAACC	TCCCGCTGGG	CTGAGGCTTT	GCGTGAGATT	300
	TCCGGTCGTC	TTGCTGAAAT	GCCTGCAGAT	GGAGGTTATC	CCGCGTACCT	350
45	CAGCGCCCGT	TTGGCCTCCT	TCTACGAGCG	TGCTGGCCGT	GTGACATGCA	400
	TCCGTGGGCC	GAAGCGTGAA	GGGTCTGTAA	CAATTGT		437

50 2) INFORMATION FOR SEQ ID NO: 840

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1052 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840

```

5  TGAAGGCTGA GCGCGAGCGC GGCATCACGA TCGACATCGC GCTCTGGAAG      50
   TTCGAGTCGC CCAAGTCTGT GTTCACGATC ATCGACGCCC CCGGCCACCG      100
   CGACTTCATC AAGAACATGA TCACGGGCAC GTCTCAGGCG GACGCCGCCG      150
   TCCTTGTCAT TGCGTCATCG CAGGGTGAGT TTGAGGCGGG CATCTCGAAG      200
10  GACGGCCAGA CACGCGAGCA CGCGCTGCTC GCCTTCACGC TCGGCGTGAA      250
   GCAGATGGTT GTGTGCTGCA ACAAGATGGA CGACAAGTCG GTGAACCTCG      300
   CCCAGGAGCG CTACGATGAG ATTGTGAAGG AGGTGTCGGC GTACCTGAAG      350
   AAGGTTGGGT ACAACGTGGA GAAGGTGCGC TTCATCCCCA TCTCCGGCTG      400
   GCAGGGCGAC AACATGATTG ACAAGTCGGA AAATATGCCG TGGTACAAGG      450
15  GCCCCACGCT GCTGGAGGCA CTCGACATGC TGGAGCCCCC GGTGCGCCCC      500
   AGCGACAAGC CGCTGCGCCT GCCGCTGCAG GACGTGTACA AGATCGGCGG      550
   TATCGGCACC GTGCCGGTCG GTCGCGTGGA GACGGGCACG ATGAAGCCCC      600
   GCGACGTGGT GACGTTTGCG CCCGCCAACG TGACGACGGA GGTGAAGTCG      650
   ATTGAGATGC ACCACGAGCA GCTGGCCGAG GCCACGCCCG GCGACAACGT      700
20  CGGCTTCAAC GTGAAGAACG TGTCCGTGAA GGACATCCGC CGTGGCAACG      750
   TGTGCGGCAA CTCGAAGAAC ACAAGTCGGA AGGAGGCGGC CGACTTCACG      800
   GCGCAGGTGA TCATCCTGAA CCACCCCGGC CAGATCGGCA ACGGCTATGC      850
   GCCGGTGCTC GACTGCCACA CCTGCCACAT CGCGTGCAAG TTCGCCGAGA      900
   TCGAGTCCAA GATCGACCGC CGCTCCGGCA AGGAGCTTGA GAAGAACCCC      950
25  AAGTCGATCA AGTCCGGTGA CGCCGCCATG GTGCGCATGG TGCCGCAGAA     1000
   GCCCATGTGC GTGGAGGTGT TCAACGACTA CGCTCCTCTT GGCCGCTTTG     1050
   CC                                                                1052

```

30 2) INFORMATION FOR SEQ ID NO: 841

(i) SEQUENCE CHARACTERISTICS:

```

35  (A) LENGTH: 1061 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: CGL-1

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841

```

50  TGAAGGCTGA GCGCGAGCGC GGCATCACGA TCGACATCGC GCTCTGGAAG      50
   TTCGAGTCGC CCAAGTCTGT GTTCACGATC ATCGACGCCC CCGGCCACCG      100
   CGACTTCATC AAGAACATGA TCACGGGCAC GTCTCAGGCG GATGCCGCCG      150
   TCCTTGTCAT TGCGTCATCG CAGGGTGAGT TTGAGGCGGG CATCTCGAAG      200
   GACGGCCAGA CACGCGAGCA CGCGCTGCTC GCCTTCACGC TCGGCGTGAA      250
   GCAGATGGTT GTGTGCTGCA ACAAGATGGA CGACAAGTCG GTGAACCTTG      300
   CCCAGGAGCG CTACGATGAG ATTGTGAAGG AGGTGTCGGC GTACCTGAAG      350
   AAGGTTGGGT ACAACGTGGA GAAGGTGCGC TTCATCCCCA TCTCCGGCTG      400
55  GCAGGGCGAC AACATGATTG ACAAGTCGGA AAATATGCCG TGGTACAAGG      450
   GCCCCACGCT GCTGGAGGCA CTCGACATGC TGGAGCCCCC GGTGCGCCCC      500
   AGCGACAAGC CGCTGCGCCT GCCGCTGCAG GATGTGTACA AGATCGGCGG      550
   TATCGGCACC GTGCCGGTCG GTCGCGTGGA GACGGGCACG ATGAAGCCCC      600
   GCGACGTGGT GACGTTTGCG CCCGCCAACG TGACGACGGA GGTGAAGTCG      650
60  ATTGAGATGC ACCACGAGCA GCTGGCCGAG GCCACGCCCG GCGACAACGT      700

```

	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
	TGTGCGGCAA	CTCGAAGAAC	GATCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTT	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
5	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
	CCGTGCGTGA	C				1061

10

2) INFORMATION FOR SEQ ID NO: 842

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1062 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
(B) STRAIN: PCU-1

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842

	GCTGAAGGCT	GAGCGCGAGC	GCGGCATCAC	GATCGACATC	GCGCTCTGGA	50
	AGTTCGAGTC	GCCCAAGTCT	GTGTTACAGA	TCATCGACGC	CCCCGGCCAC	100
30	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCTCAGG	CGGACGCCGC	150
	CGTCCTTGTC	ATTGCGTCAT	CGCAGGGTGA	GTTTGAGGCG	GGCATCTCGA	200
	AGGACGGCCA	GACACGCGAG	CACGCGCTGC	TCGCCTTCAC	GCTCGGCGTG	250
	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGT	CGGTGAACCT	300
	CGCCCAGGAG	CGCTACGATG	AGATTGTGAA	GGAGGTGTCTG	GCGTACCTGA	350
35	AGAAGGTTGG	GTACAACGTG	GAGAAGGTGC	GCTTCATCCC	CATCTCCGGC	400
	TGGCAGGGCG	ACAACATGAT	TGACAAGTCG	GAAAATATGC	CGTGGTACAA	450
	GGGCCCCACG	CTGCTGGAGG	CACTCGACAT	GCTGGAGCCC	CCGGTGCGCC	500
	CCAGCGACAA	GCCGCTGCGC	CTGCCGCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGTATCGGCA	CCGTGCGCGT	CGGTGCGCTG	GAGACGGGCA	CGATGAAGCC	600
40	CGGCGACGTG	GTGACGTTTG	CGCCCGCCAA	CGTGACGACG	GAGGTGAAGT	650
	CGATTGAGAT	GCACCACGAG	CAGCTGGCCG	AGGCCACGCC	CGGCGACAAC	700
	GTCGGCTTCA	ACGTGAAGAA	CGTGTCCGTG	AAGGACATCC	GCCGTGGCAA	750
	CGTGTGCGGC	AACTCGAAGA	ACGACCCCCC	AAAGGAGGCG	GCCGACTTCA	800
	CGGCGCAGGT	GATCATCCTG	AACCACCCCG	GCCAGATCGG	CAACGGCTAT	850
45	GCGCCGGTGC	TCGACTGCCA	CACCTGCCAC	ATCGCGTGCA	AGTTCGCCGA	900
	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	CAAGGAGCTT	GAGAAGAACC	950
	CCAAGTCGAT	CAAGTCCGGT	GACGCCGCCA	TGGTGCGCAT	GGTGCCGCAG	1000
	AAGCCCATGT	GCGTGGAGGT	GTTCAACGAC	TACGCTCCTC	TTGGCCGCTT	1050
	TGCCGTGCGT	GA				1062

50

2) INFORMATION FOR SEQ ID NO: 843

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1057 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bovis*

(B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843

```

10  TACATTGACA GCTGCATTGA CCAAGGTCTG TTCGATGGGT GGTCATGGCG      50
    AGTACACTCC TTATGAAGCA ATTGACCGTG CTCCTGAGGA GCGTAAACGT      100
    GGTATTACTA TAAATTTCGAC ACATGTTGAA TATGAGACTA AGAACCGTCA      150
    TTACGGTCAC GTGGACTGTC CAGGTCACCTC TGATTATGTG AAGAACATGA      200
    TATCTGGCGC TGCTCAGATG GATGGTGCCA TATTGGTTGT TTCTTGTGTT      250
    GACGGTCCCA TGCCTCAGAC TAAGGAGCAC GTGTTGCTTG CTAAGCAGAT      300
15  TGGTGTACCT CGTTTAGTTG TGTTTTTGAA CAAGCTTGAC ATGTTAGAGG      350
    ACTCTGAGCT ATTGGAGTTG GTGGAGTTAG AGGTTCTGTA GTTATTGAGT      400
    GAGTTTGGTT ACGACGGTGA CAACACGCCT ATCGTTCGTG GCAGTGCTAT      450
    AAAGGCATTG AACAGTAGTT CCGAGGCTGA CATTAAGCCA ATTCAGGATT      500
    TATTGGATGC GTGTGATGCC TTTTCTACTGA CTCCAGAACG TAAGGATGAC      550
20  ATGCCGCTCT TGGTTGCTAT TGACGATGTT CTTGCCATTC CTGGCAAGGG      600
    TACTGTTGTA ACCGGTAGGA TAGAGCAGGG CAAGATTCGT TGTGGTGACC      650
    GTATTGAGGT TTGCGCCGGT CCGAAGTCCG GCAAGAAGAC TGTGTGTGTT      700
    GGTCTTRARA TGTTCGCAA GAGTCTCAGT RAGGGTATTG CTGGTGACCA      750
    GATTGGTGTT TTGCTCAAGG GTGTGAAGCG CGACRAGGTA GAGCGCGGGT      800
25  TTGTATTGAT TCAACCCGGA AGTTACAAAT GTCACGGTGA ATTTGATGCT      850
    GACTTGTACG TGTTGACTAC GRAGGAAGGT GGGCGCAAGC ATCCGTTTGT      900
    GTCTAACTAC CGTCCTCAGG CGTTTATACG TACTGGAGAC GTTTGCTGCT      950
    CAGTTCATTT GGATRAGGGT GTTGAGATGG CAGCTCCTGG TGACAACGTG     1000
    CGTTGCAAGA TCAAGTTACT TTATCCCATG CCTGTCCATG AAGGTTTACG     1050
30  ATTTGCG                                     1057

```

2) INFORMATION FOR SEQ ID NO: 844

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 943 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania aethiopica*

(B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844

```

50  CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
    GCGAGCACCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
    TTCATCAACA AAGTGGATAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
    CATGGAGGTG CGCGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAGGAGA      200
    CACCAATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG      250
55  TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AGTGATCCC      300
    CGACCCGCCG CGCAACACAG ACAAGCCTTT CCTTATGGCC ATCGAGCACG      350
    TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
    GATCAGGGCG TGCTGAAGCT CAACACAGAC GCCGAGCTGG CCGGCTTCAG      450
    CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATCGAGATG TACCACAAGA      500
60  CGCTGAGCGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTCGGC      550

```



```

ACCGGCGACA CAACCAGTCT GTCCAAGGAC AACGTGGAAC GCGGCATGGT 600
AATGGCGGCG ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG 650
TGTACGTGCT GACGAAGGAT GAGGGCGGCC GCCACACCGG CTTCAGCCCC 700
CACTACCGCC CGCAGCTCTT CTTCCATTGC GCTGACGTGA CAGCGGACAT 750
5 GAGCTTCCCG GAGGCGGAGA AGCACC GGGA GGAGCTGAAC AAGAAATTCG 800
GCCGCGGCCC CGAGGAGGAC AAGAAGAAAG AGGCGGAGAT GAAGGAGTTC 850
GAGAGCAAGC TCGTCTGCAT GCCGGGCGAT AACCGCGAGC TGATCCTGAC 900
GCTCGCGTAC CCGATGCCCA TTGAAAAGGG CCTGAAGTTC ACC 943

```

10

2) INFORMATION FOR SEQ ID NO: 845

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 939 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania amazonensis*
(B) STRAIN: ATCC 50131
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845

```

CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC 50
GCGAGCATCT CTTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG 100
30 TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA 150
CATGGAGGTG CGTGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAAGAGA 200
CGCCCATCGT GCGCGGCTCG GCCCTCAAAG CCGTCGAGGG CGACGCGAAG 250
TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AATGGATCCC 300
CGACCCGCCG CGCAACACAG ACAAGCCTTT CCTTATGGCC ATTGAGCAGC 350
35 TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC 400
GATCAGGGCG TGCTGAAGCT CAACACAGAG GCCGAGCTGG CCGGCTTCAG 450
CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATCGAGATG TACCACAAGA 500
CGCTGAGTGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTCGGC 550
ACCGGCGACA CGATCAGTCT CTCCAAGGAC AACGTTGAAC GCGGCATGGT 600
40 AATGGCGGCA ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG 650
TGTACGTGCT GACGAAGGAT GAGGGCGGCC GCCACACTGG CTTCAGCCCC 700
CACTACCGCC CGCAGCTCTT CTTCCATTGT GCTGACGTGA CGGCGGACAT 750
GAGCTTCCCG GAGGCGGAGA AGCACC GGGA GGAGCTCAAC AAGAAATTCG 800
GCCGCGGCCC CGAGGAGGAC AAGCAGAAGG AGGCGGAGAT GAAAGAGTTC 850
45 GAGAGCAAGC TCGTCTGCAT GCCGGGCGAC AACCGCGAGC TGATCCTGAC 900
GCTGGCGTAC CCGATGCCCA TTGACAAGGG TCTGAAGTT 939

```

50 2) INFORMATION FOR SEQ ID NO: 846

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 945 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846

```

5  CATTGTGGTG GCGGCCACCG ACGGCGTCAT GCCGCAGACA CGCGAGCACC 50
   TCCTGATCTG CTCGCAGATC GGGCTTCCGG CGCTCGTAGG GTTCATCAAC 100
   AAGGTGGACA TGACGGACGA GGACACGTGC GACCTGGTGG ACATGGAGCT 150
   GCGCGAGCAG CTGGAGAAAT ACAAGTTTCC GGCGGAGGAG ACGCCAATCG 200
10  TGC GCGGCTC AGCCCTCAAA GCCGTCGAGG GCGATGCGAA GTACGAGGAG 250
   AACATTCTCG AACTGGTGCG GAAGTGTGAC GAGTGGATCC CTGACCCGCC 300
   GCGCAACACA GACAAGCCTT TCCTTATGGC CATCGAGCAC GTTTACGAGA 350
   TCGGCAAGGA CAAGAAGAGC GTTGTCTGTA CCGGCCGCGT CGATCAGGGC 400
   ATTCTGAAGC TCAACACAGA CGCCGAGCTG GCCGGCTTCA GCTCCAAGAA 450
15  GTCGACGGTG AGGGTGACGG GCATCGAGAT GTACCACAAG ACGCTGAGCG 500
   AGTGCATGCC TGGTGACTCC GTCGGCGTCA GCATTGTCGG GACCGGCGAC 550
   ACGACCAGTC TATCCAAGGG CAACGTGGAA CGCGGCATGG TGATGGCGGC 600
   GACGGGTAGC ACGAACCTGT ACAACAAGGT GAAGGCGCAG GTGTACGTGC 650
   TGACGAAGGA TGAGGGCGGC CGCCACACTG GCTTTAGTCC TCACTACCGC 700
20  CCGCAGCTCT TCTTCCATTG TGCTGACGTG ACGGCGGACA TGAGCTTCCC 750
   GGAGGCGGAG AAGCACCGCG AAGAGCTCAA CAAGAAATTC GGCCGCGGCC 800
   CCGAGGAGGA CAAGAAGAAA GAGGCAGCGA TGAAGGAGTT CGAGAGCAAG 850
   CTCGTCTGCA TGCCGGGCGA TAACCGCGAG CTGATCCTGA CGCTGGCGTA 900
   CCCGATGCCC ATTGAAAAGG GTCTGAAGTT CACCATCCGT GAGGG 945
25

```

2) INFORMATION FOR SEQ ID NO: 847

```

30  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 939 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
35
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Leishmania infantum
          (B) STRAIN: MOU
40

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847

```

45  GGCATCATTG TGGTGGCGGC CACCGACGGC GTCATGCCGC AGACACGCGA 50
   GCACCTCCTG ATCTGCTCGC AGATCGGGCT TCCGGCGCTC GTAGGGTTCA 100
   TCAACAAGGT GGACATGACG GACGAGGACA CGTGCGACCT GGTGGACATG 150
   GAGCTGCGCG AGCAGCTGGA GAAATACAAG TTTCCGGCGG AGGAGACGCC 200
   AATCGTGCGC GGCTCAGCCC TCAAAGCCGT CGAGGGCGAT GCGAAGTACG 250
   AGGAGAACAT TCTCGAACTG GTGCGGAAGT GTGACGAGTG GATCCCTGAC 300
50  CCGCCGCGCA ACACAGACAA GCCTTTCCTT ATGGCCATCG AGCACGTTTA 350
   CGAGATCGGC AAGGACAAGA AGAGCGTTGT CGTGACCGGC CGCGTCGATC 400
   AGGGCGTTCT GAAGCTCAAC ACAGACGCCG AGCTGGCCGG CTTCAGCTCC 450
   AAGAAGTCGA CGGTGAGGGT GACGGGCATC GAGATGTACC ACAAGACGCT 500
   GAGCGAGTGC ATGCCTGGTG ACTCCGTCGG CGTCAGCATT GTCGGCACCG 550
55  GCGACACGAC CAGTCTATCC AAGGGCAACG TGAACGCGG CATGGTGATG 600
   GCGGCGACGG GTAGCACGAA CCTGTACAAC AAGGTGAAGG CGCAGGTGTA 650
   CGTGCTGACG AAGGATGAGG GCGGCCGCCA CACTGGCTTT AGTCCTCACT 700
   ACCGCCCGCA GCTCTTCTTC CATTGTGCTG ACGTGACGGC GGACATGAGC 750
   TTCCCGGAGG CCGAGAAGCA CCGCGAAGAG CTCAACAAGA AATTCGGCCG 800
60  CGGCCCCGAG GAGGACAAGA AGAAAGAGGC AGCGATGAAG GAGTTCGAGA 850

```

GCAAGCTCGT CTGCATGCCG GGCGATAACC GCGAGCTGAT CCTGACGCTG 900
 GCGTACCCGA TGCCCATGGA AAAGGGTCTG AAGTTCACC 939

5

2) INFORMATION FOR SEQ ID NO: 848

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*
 (B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848

25 CACCGACGGC GTCATGCCGC AGACACGGGA GCACCTGCTC ATCTGCTCGC 50
 AGATCGGGCT GCCGGCGCTT GTAGGGTTCA TCAATAAAGT TGACATGACG 100
 GACGAGGATA CGTGCGACCT CGTGGACATG GAGGTGCGGG AACAGCTGGA 150
 GAAGTACAAG TTTCCGGCCG AGGAGACGCC CATCGTACGT GGCTCGGCCC 200
 TCAAGGCCCT CGAGGGGGAT GCGCAATACG AGGGGAGTAT TCTCGAGCTG 250
 GTGCGAAAGT GCGACGAGTG GATCCCCGAC CCGCCGCGCA ACACCGAAAA 300
 GCCTTTTCCTC ATGGCTATCG AGCACGTTTA CGAGCTCGGC AAAGACAAGA 350
 AGAGCGTCAT CGTTACCGGC CGCGTCGATC AAGGTGTGCT GAAGCTCAAC 400
 30 ACAGACGCCG AGCTGGCCGG CTTACGCGCC AAGAAGGCGA CAGTCAAAGT 450
 GACGGGCATC GAGATGTATC ACAAGACACT EAATGAGTGC ATGCCCCGCG 500
 ACTCTGTGCG TGTCAGCATC GTCGGTACCG GTGACACGAC CAGCTTATCC 550
 AAGGATAATG TTGAGCGCGG TATGGTAATG GCGGCAACGG GTAGCACGAA 600
 CCTGTACAAC AAGCTGAAGG CGCAGGTTTA CGTGCTGACA AAGGAGGAGG 650
 35 GTGGCCGCCA CACCGGGTTC AGCCCCCACT ACCGCCCGCA GCTCTTCTTC 700
 CACTGCGCTG ACGTGACCGC AGACATGAGC TTCCCGGAGG CGGAGAAGTA 750
 CCGCGAGGAG CTCAACAAGA AGTTCGGCCG TGGCCCTGAG GAGGACAAGA 800
 AGAAAGAGGC GGAGATGAAG GAGTTCGAAA GCAAACCTGT CTGCATGCCA 850
 GGCGATAACC GCGAGCTGAT CCTAACTCTG GCGTACCCGA TGCCCATCGA 900
 40 CAAGGGCCTG AAGTTCACCA TCCGTGAGGG CGG 933

2) INFORMATION FOR SEQ ID NO: 849

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849

60 CCGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC 50

```

5  GCGAGCACCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG 100
   TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA 150
   CATGGAGGTG CGCGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAGGAGA 200
   CACCAATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG 250
10 TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AGTGGATCCC 300
   CGACCCGCCG CGCAACACAG ACAAGCCTTT CCTTATGGCC ATCGAGCACG 350
   TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC 400
   GATCAGGGCG TGCTGAAGCT CAACACGGAC GCCGAGCTGG CCGGCTTCAG 450
   CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATTGAGATG TACCACAAGA 500
15 CGCTGAGCGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATGTGTCGGC 550
   ACCGGCGACA CGACCACTCT GTCCAAGGAC AACGTGGAAC GCGGCATGGT 600
   AATGGCGGCG ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG 650
   TGTACGTGCT GACGAAGGAT GAGGGCGGCC GCCACACTGG CTTAGCCCC 700
   CACTACCGCC CGCAGCTCTT CTTCCATTGC GCTGACGTGA CAGCGGACAT 750
15 GAGCTTCCCG GAGGCGGAGA AGCACC GCGA GGAGCTCAAC AAGAAATTCG 800
   GCCGCGGCCG CGAGGAGGAC AAGAAGAAAG AGGCGGAGAT GAAGGAGTTC 850
   GAGAGCAAGC TCGTCTGCAT GCCGGGCGAT AACC GCGAGC TGATCCTGAC 900
   GCTGGCGTAC CCGATGCCCC TTGAAAAGGG TCTGAAGTTC ACC 943

```

20

2) INFORMATION FOR SEQ ID NO: 850

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 918 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania major*
- (B) STRAIN: ATCC 50122
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850

```

40 GGCATCATTG TGGTGGCGGC CACCGACGGC GTCATGCCGC AGACACGCGA 50
   ACACCTCCTG ATCTGCTCGC AAATTGGCCT TCCGGCGCTC GTAGGGTTCA 100
   TCAACAAAGT GGACATGACG GACGAGGACA CGTGTGACCT GGTGGACATG 150
   GAGGTGCGCG AGCAGCTGGA GAAATACAAG TTTCCGGCGG AGGAGACACC 200
   AATCGTGCGC GGCTCGGCCG TCAAGGCCGT CGAGGGCGAC GCGAAGTACG 250
   AGGAGAACAT CCTCGAACTG GTGCGGAAGT GCGACGAGTG GATCCCCGAC 300
   CCGCCGCGCA ACACAGACAA GCCTTTCCTT ATGGCCATCG AGCACGTTTA 350
45 CGAGATCGGC AAGGACAAGA AGAGCGTCAT CGTGACCGGC CGCGTCGATC 400
   AGGGCGTGCT GAAGCTCAAC ACAGACGCCG AGCTGGCCGG CTTAGCGGCC 450
   AAGAAGTCGA CGGTGAGGGT GACGGGCATT GAAATGTACC ACAAGACGCT 500
   GAGCGAGTGC ATGCCCAGGT ACTCCGTCGG CGTCAGCATT GTCGGCACCG 550
   GCGACACGAC CAGTCTGTCC AAGGACAACG TGGAGCGCGG CATGGTAATG 600
50 GCGGCGACGG GTAGCACGAA CCTGTACAAC AAGGTGAAGG CGCAGGTGTA 650
   CGTGCTGACG AAGGATGAGG GCGGCCGCCA CACTGGCTTC AGCCCCCACT 700
   ACCGCCCGCA GCTCTTCTTC CATTGCGCTG ACGTGACAGC GGACATGAGC 750
   TTCCCGGAGG CGGAGAAGCA CCGCGAGGAG CTCAACAAGA AATTCGGCCG 800
   CGGCCCCGAG GAGGACAAGA AGAAAGAGGC GGAGATGAAG GAGTTCGAGA 850
55 GCAAGCTCGT CTGCATGCCG GGCATAACC GCGAGCTGAT CCTGACGCTG 900
   GCGTACCCGA TGCCCATT 918

```

60 2) INFORMATION FOR SEQ ID NO: 851

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851

```

15  CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
    GCGAGCATCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
    TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
    CATGGAGGTG CGTGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAAGAGA      200
20  CGCCCATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG      250
    TACGAGGAGA ACATCCTCGA ACTGGTGCGG AAGTGCGACG AATGGATCCC      300
    CGACCCGCCG CGCAACACAG ACAAGCCTTT CCTTATGGCC ATTGAGCACG      350
    TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
    GATCAGGGCG TGCTGAAGCT CAACACAGAC GCCGAGCTGG CCGGCTTCAG      450
25  CGTCAAGAAG TCGACGGTGA GGGTGACGGG CATCGAGATG TACCACAAGA      500
    CGCTGAGTGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTGCGC      550
    ACCGGCGACA CGATCAGTCT CTCCAAGGAC AACGTTGAAC GCGGCATGGT      600
    AATGGCGGCA ACGGGTAGCA CGAACCCTGTA CAACAAGGTG AAGGCGCAGG      650
    TGTACGTGCT GACGAAGGAT GAGGGCGGCC GCCACACTGG CTTCAGCCCC      700
30  CACTACCGCC CGCAGCTCTT CTTCCATTGT GCTGACGTGA CGGCGGACAT      750
    GAGCTTCCCG GAGGCGGAGA AGCACCGCGA GGAGCTCAAC AAGAAATTCG      800
    GCCGCGGCCG CGAGGAGGAC AAGCAGAAGG AGGCGGAGAT GAAAGAGTTC      850
    GAGAGCAAGC TCGTCTGCAT GCCGGGCGAC AACC GCGAGC TGATCCTGAC      900
    GCTGGCGTAC CCGATGCCCA TTGAGAAGGG TCTGAAGTT      939
35

```

2) INFORMATION FOR SEQ ID NO: 852

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: MOU-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

```

55  TCATTGTGGT GGCCGCCACC GACGGCGTCA TGCCGCAAAC ACGGGAGCAC      50
    CTTTGTGATCT GCTCGCAGAT CGGGCTGCCG GCGCTCGTAG GGTTCATCAA      100
    CAAAGTGGAC ATGACAGACG AAGACACGTG CGACCTGGTA GACCTGGAGG      150
    TGCGTGAGCA GCTGGAGAAG TACAAGTTTC CGGCAGAGGA AACACCAATC      200
    GTGCGTGGCT CGGCCCTCAA GGCCGTTGAG GGCGATGCAA AGTACGAGGA      250
    GAACATCCTC GAACTGGTGC GGAAGTGCGA CGAGTGGATC CCAGACCCGC      300
60  CACGCAATAC GGACAAGCCT TTCCTTATGG CCATTGAACA CGTGTACGAG      350

```

	ATCGGCAAGG	ATAGGAAAAG	CGTCATCGTA	ACCGGCCGCG	TCGATCAAGG	400
	TGTGCTGAAG	CTGAACACAG	ACGCCGAGCT	GGCCGGCTTC	AGCGCCAAGA	450
	AGTCGACGGT	GAAAGTGACG	GGCATTGAGA	TGTACCACAA	GACACTGACA	500
	GAGTGCATGC	CCGGCGACTC	TGTCGGCGTC	AGCATTGTGG	GCACTGGYGA	550
5	CACGACCAGC	CTCTCTAAGG	ACAATGTTGA	GCGTGGCATG	GTA CTGGCCG	600
	CTACGGGTAG	CACGAACCTG	TACAACAAAG	TAAAGGCGCA	GGTGTATGTA	650
	CTCACGAAGG	ATGAGGGCGG	CCGCCACACC	GGCTTCAGCC	CCCACTACCG	700
	TCCGCAGCTC	TTCTTCCACT	GCGCTGACGT	AACGGCGGAC	ATGAGCTTCC	750
	CGGAGGCGGA	GAAGCACCGC	GAGGAACTCA	ATAAGAAATT	CGGCCGCGGC	800
10	CCCGAGGAGG	ACAAGAAAAA	GGAGGCGGAG	ATGAAGGAGT	TCGAGAGCAA	850
	GCTGGTCTGC	ATGCCAGGCG	ATAACCGCGA	GCTGATCCTG	ACATTGGCGT	900
	ACCCGATGCC	TA				912

15

2) INFORMATION FOR SEQ ID NO: 853

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 936 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trypanosoma cruzi*
 - (B) STRAIN: MM3

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853

	ATTCTTGTGG	TGGCAGCTAA	CGACGGATGC	ATGCCGCAGA	CGCGTGAGCA	50
	CCTGCTTATT	TGTTTCGAGA	TTGGCCTTCC	TGCTCTTGTA	TGCTTTATCA	100
	ATAAGTGTGA	CATGATGCAA	GGGCAGGAGG	AAATGATTGA	ACTTGTTGAA	150
35	ATGGAGGTAC	GTGAACTTTT	GGAGAAGTAC	AAGTTCCCTG	CGGAGGAGAC	200
	GCCATTTGTG	CGGGGGTCTG	CGGTGAAGGC	ATTGGAGGGT	GATGCTGAAA	250
	ATGAAGGAAA	GATTTTGGAG	CTTGTA AAAA	AATGTGATGA	ATGGATTCCC	300
	GACCCACCGC	GTGCCATTGA	AAAACCGTTC	CTTATGGCCA	TTGAGCACGT	350
	TTTTGAGGTT	GGAAAGGATA	AGAAGGCCGT	TGTTGTGAGC	GGGCGTGTGG	400
40	ACCAGGGGCA	GTTGAAGGTC	GGCGCAGATG	CAGAACTTTC	CGGGTTTAGC	450
	GCAAAGAAGC	TGACGGTGAA	GGTTGCTAGC	ATCGAAATGT	ACCATAAAAAT	500
	TCTGGAGGAT	TGCATGCCTG	GTGACTCTGT	TGGCGCGAAG	ATCGTTGGCA	550
	GCGGTGAAAC	AGTGAACCTG	TCGAAGGAAA	ATGTGGAACG	CGGCATGGTA	600
	CTCTCCGCAC	CAGGTGCAAC	GACACTGTTC	AACAAGGTCC	GCGCGCAGGT	650
45	GTACGTGTTG	ACAAAGGAAG	AAGGCGGTCT	TCACACAGCC	TTTAGTCCTC	700
	ACTATCGTCC	GCAGCTTTTC	TTCCACTGTG	CTGATGTCAC	GGCAGATATT	750
	AACTTCCCGG	AAAGCGAGAA	GCTTGCAGGG	GAGCTGAACA	AAAAGTATGG	800
	CCGTGATGCG	GCGGAACAGA	AGAAGAAGGA	GGCAGA ACTG	AAAGAGTTTG	850
	AAAAGACGCT	TGTCTGCATG	CCTGGTGATA	ACCGCGAACT	CCTGCTCACC	900
50	CTTGCCTATC	CAATGCCAAT	GGAAAAGGGA	CTCAAG		936

55 2) INFORMATION FOR SEQ ID NO: 854

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 934 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
(B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854

10	CGGCATTCTT	GTGGTGGCAG	CTAACGACGG	ATGCATGCCG	CAGACGCGTG	50
	AGCACCTGCT	TATTTGTTTCG	CAGATTGGCC	TTCCTGCTCT	TGTATGCTTT	100
	ATCAATAAGT	GTGACATGAT	GCAAGGGCAG	GAGGAAATGA	TTGAGCTTGT	150
	TGAAATGGAG	GTACGTGAAC	TTTTGGAGAA	GTACAAGTTC	CCTGCGGAGG	200
	AGACGCCATT	TGTGCGGGGG	TCTGCGGTGA	AGGCATTGGA	GGGTGATGCT	250
15	GAAAATGAAG	GAAAGATTTT	GGAGCTTGTA	AAAAAATGTG	ATGAATGGAT	300
	TCCCGACCCA	CCGCGTGCCA	TTGAAAAACC	GTTCCCTTATG	GCCATTGAGC	350
	ACGTTTTTTG	GGTTGGAAAG	GATAAGAAGG	CCGTTGTTGT	GAGCGGGCGT	400
	GTGGACCAGG	GGCAGTTGAA	GGTCGGCGCA	GATGCAGAAC	TTTCCGGGTT	450
	TAGTGCAAAG	AAGCTGACGG	TGAAGGTTGC	TAGCATCGAA	ATGTACCATA	500
20	AAATTCTGGA	GGATTGCATG	CCTGGTGAAT	CTATTGGCGC	GAAGATCGTT	550
	GGCAGCGGTG	AAACAGTGAA	CCTGTGCAAG	GAAAATGTGG	AACGCGGCAT	600
	GGTACTCTCC	GCACCAGGTG	CAACGACACT	GTTCAACAGG	GTCCGCGCGC	650
	AGGTGTACGT	GTTGACAAAG	GAAGAAGGCG	GTCGTCACAC	AGCCTTTAGT	700
	CCTCACTATC	GTCCGCAGCT	TTTCTTCCAC	TGTGCTGATG	TCACGGCGGA	750
25	TATTAACCTC	CCGGAAAGCG	AGAAGCTTGC	AGGGGAGCTG	AACAAAAAGT	800
	ATGGCCGTGA	CGCGGCGGAA	CAGAAGAAGA	AGGAGGCAGA	ACTGAAAGAG	850
	TTTGAAAAGA	CGCTTGCTCTG	CATGCCTGGT	GATAACCGCG	AACCTCTGCT	900
	CACCCTTGCC	TATCCAATGC	CAATGGAAAA	GGGA		934

30

2) INFORMATION FOR SEQ ID NO: 855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
(B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855

50	TGGCGGCATT	CTTGTGGTGG	CAGCTAACGA	CGGATGCATG	CCGCAGACGC	50
	GTGAGCACCT	GCTTATTTGT	TCGCAGATTG	GCCTTCCTGC	TCTTGTATGC	100
	TTTATCAATA	AGTGTGACAT	GATGCAAGGG	CAGGAGGAAA	TGATTGAACT	150
	TGTTGAAATG	GAGGTACGTG	AACTTTTGGA	GAAGTACAAG	TTCCCTGCGG	200
	AGGAGACGCC	ATTTGTGCGG	GGGTCTGCGG	TGAAGGCATT	GGAGGGTGAT	250
	GCTGAAAATG	AAGGAAAGAT	TTTGGAGCTT	GTAAAAAAT	GTGATGAATG	300
	GATTCCTCGAC	CCACCGCGTG	CCATTGAAAA	ACCGTTCCTT	ATGGCCATTG	350
55	AGCACGTTTT	TGAGGTTGGA	AAGGATAAGA	AGGCCGTTGT	TGTGAGCGGG	400
	CGTGTGGACC	AGGGGCAGTT	GAAGGTCGGC	GCAGATGCAG	AACCTTCCGG	450
	GTTTAGCGCA	AAGAAGCTGA	CGGTGAAGGT	TGCTAGCATC	GAAATGTACC	500
	ATAAAATTCT	GGAGGATTGC	ATGCCTGGTG	ACTCTGTTGG	CGCGAAGATC	550
	GTTGGCAGCG	GTGAAACAGT	GAACCTGTCTG	AAGGAAAATG	TGGAACGCGG	600
60	CATGGTACTC	TCCGCACCAG	GTGCAACGAC	ACTGTTCAAC	AAGGTCCGGC	650

	CGCAGGTGTA	CGTGTGACA	AAGGAAGAAG	GCGGTCGTCA	CACAGCCTTT	700
	AGTCCTCACT	ATCGTCCGCA	GCTTTTCTTC	CACTGTGCTG	ATGTCACGGC	750
	AGATATTAAC	TTCCCGGAAA	GCGAGAAGCT	TGCAGGGGAG	CTGAACAAAA	800
	AGTATGGCCG	TGATGCGGCG	GAACAGAAGA	AGAAGGAGGC	AGAACTGAAA	850
5	GAGTTTGAAA	AGACGCTTGT	CTGCATGCCT	GGTGATAACC	GCGAACTCCT	900
	GCTCACCTT	GCCTATCCAA	TGCCAATGGA	AAAGGGA		937

10 2) INFORMATION FOR SEQ ID NO: 856

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856

25	CTTATTATGG	AGCTGATCAA	CAACGTCGCG	AAGAAGCACG	GTGGTTTCTC	50
	CGTGTTCGCC	GGCGTCGGCG	AGCGCACCAG	GGAGGGCAAC	GAGCTGTACC	100
	ACGAGATGAT	GGAGACCGGC	GTCATCAAGC	GCCGCCAGCT	GGATGACGGC	150
	ACGTTTCGACT	TCTCCGGCTC	CAAGGCCGCG	CTGGTGTACG	GCCAGATGAA	200
30	CGAGCCGCCA	GGTGCCAGGG	CGCGTGTGTC	CCTCACTGGC	CTGACGGTGG	250
	CCGAGTACTT	CCGTGATGAG	GACGGCCAGG	ACGTGCTGCT	CTTCATCGAC	300
	AACATCTACC	GTTTCACCCA	GGCTGGTTCT	GAGGTGAGTG	CCCTTTTGGG	350
	GCGCATCCCG	TCCGCCGTCG	GTTACCAGCC	GACCCTCGCC	ACCGACCTTG	400
	GCGCGCTGCA	GGAGCGTATC	ACGACGACCA	ACAAGGGCTC	CATCACCTCC	450
35	GTGCAGGCCG	TCTACGTGCC	GGCCGACGAT	ATCACCGACC	CGGCGCCTGC	500
	GACCACCTTC	ACCCATCTGG	ACGCGACCAC	TGTGCTCTCC	CGTTCCATCG	550
	CCGAGCTGGG	TATCTACCCC	GCCGTCGACC	CGCTCGACTC	CACCTCGCGT	600
	ATGCTGTCCG	CGAACATCGT	CGGCGAGGAG	CAGTACAACG	TGGCGCGTGG	650
	CGTGCAGAAA	ATACTGCAGG	ACTACAAATC	GCTGCAGGAT	ATCATCGCCA	700
40	TCCTGGGTAT	GGACGAGCTG	TCTGAGCAGG	ACAAGTTTCG	CGTCGCGCGT	750
	GCGCGCAAGG	TTCAGCGTTT	CCTATCCCAG	CCCTTCCAGG	TGGCTGAGGT	800
	ATTACCGGC	AAGCCCGGAC	GTTTCGTCTG	GCTGCAGGAC	ACCATCAGCG	850
	GCGTCAAGGA	GATTTTGGAC	GGCGAGTGCG	ACGACATG		888

45

2) INFORMATION FOR SEQ ID NO: 857

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857

	TGATTATGGA	ATTGATCAAC	AATGTCGCCA	AGAAACACGG	TGGGTCTCTCC	50
	GTGTTTCGCTG	GTGTTGGTGA	ACGTACGAGG	GAAGGTAACG	AACTGTACCA	100
5	TGAAATGATG	GAAACGGGTG	TCATCAAGCG	CCGTCAACTG	GAAGACGGAA	150
	CATTTGACTT	CTCGGGCTCT	AAAGCTGCTT	TGGTGTACGG	ACAAATGAAC	200
	GAACCACCAG	GTGCTAGAGC	CCGTGTTGCA	CTCACGGGAT	TGACCGTTGC	250
	CGAGTATTTT	CGTGATGAAG	AGGGGCAGGA	TGTGCTACTC	TTCATCGATA	300
	ACATCTACCG	TTTCACCCAG	GCCGGTTCCG	AAGTGAGTGC	GCTGTTAGGA	350
10	AGAATTCCAT	CCGCCGTGGG	TTATCAACCT	ACATTGGCCA	CTGATCTCGG	400
	AGCACTCCAG	GAACGCATTA	CTACAACCAA	CAAGGGTTTCG	ATTACATCAG	450
	TCCAGGCAGT	ATACGTCCCA	GCCGATGATA	TCACTGATCC	CGCTCCAGCT	500
	ACCACTTTCT	CGCACTTGGA	TGCCACTACA	GTGCTTTCTC	GTTCAATTGC	550
	GGAGTTGGGT	ATTTACCCTG	CGGTTCGACCC	GCTTGACTCA	ACGTCACGTA	600
15	TGCTGTCCGC	CAACATTGTA	GGACAGGAAC	AGTACGATGC	CGCACGTGGT	650
	GTACAGAAAA	TTTTACAGGA	CTACAAATCA	CTGCAGGATA	TCATTGCCAT	700
	TCTGGGTATG	GACGAGCTGT	CTGAGCAGGA	CAAGTTCGTT	GTAGCACGCG	750
	CCCGTAAGGT	ACAGCGTTTC	CTGTCTCAGC	CGTTCCAAGT	GGCTGAGGTG	800
	TTCACCGGCA	AGCCTGGGAG	GTTCGTTGAA	CTACAGGATA	CCATCAGCGG	850
20	TGTCAAGGAA	ATCTGGAAGG	TGAGTGTGAC	GATA		884

2) INFORMATION FOR SEQ ID NO: 858

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858

40	TGGAAC TGAT	TAATAATGTG	GCCAAAAAGC	ATGGCGGTTA	CTCTGTTTTT	50
	GCAGGTGTAG	GTGAAAGGAC	GAGGGAGGGT	AATGAATTGT	ACCATGAAAT	100
	GATGGAGACA	GGTGTTATAA	AGAAAAAGGC	ACTAGGTGGT	GGGAAGTTTG	150
	ATTTCA GTGG	ATCTAAAGCA	GCGCTGGTCT	ATGGACAAAT	GAACGAGCCA	200
	CCTGGGGCCC	GTGCTAGAGT	GGCACTAACT	GGATTAACAG	TCGCAGAATA	250
45	TTTCCGTGAC	GAACAAGGAC	AAGACGTGTT	GTTGTTTATT	GATAATATTT	300
	ACCGATTTAC	TCAGGCAGGG	TCTGAGGTTT	CAGCCTTGCT	AGGCCGTATA	350
	CCTTCAGCTG	TGGGATACCA	GCCTACATTG	GCAACAGATC	TTGGCTGTTT	400
	ACAAGAACGA	ATTACTACGA	CCAAATCTGG	TTCAATCACC	AGTGTAACAAG	450
	CTGTGTATGT	GCCAGCAGAT	GATATTACTG	ATCCAGCGCC	TGCCACAAC T	500
50	TTTACTCACT	TGGACGCTAC	TACTGTACTT	AGCAGGCCAA	TTGCTGAACT	550
	CGGTATTTAT	CCAGCGGTAG	ACCCGTTGGA	TTCAACAAGC	CGTATGCTAA	600
	GCGCGAACAT	TGTGGGAAAT	GAACACTATA	GTGTAGCCCG	TTCCGTGCAG	650
	AAGATACTGC	AAGATTACAA	ATCGCTTCAG	GACATTATTG	CCATTTTGGG	700
	TATGGATGAA	CTGTCCGAAC	AAGACAAAAA	TATAGTAGCC	CGAGCAAGGA	750
55	AGATGCAAAG	GTTCTTATCA	CAGCCATTCC	AAGTGCGCGA	AGTTTTTACT	800
	GGTAAACCGG	GAAGATTTGT	GGAATTGGAA	GATACAATTG	CCGGGGCACG	850
	AGATATAATT	GCGGGTAATT	G			871

2) INFORMATION FOR SEQ ID NO: 859

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1286 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania guyanensis*
 (B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859

TCTCGGAGGG	CGTCCCGCCC	GTGCTGACGG	CGCTGGATGT	GACGGAGGAC	50
CTTGCCGCG	ATGAGCCGCT	GACGCTGGAG	ATCGTGCAGC	ACCTGGACGC	100
GAACACCGGC	CGCTGCATTG	CGATGCAGAC	GACGGACCTG	CTGAAGCTGA	150
AGTCGAAGGT	TGTGTCGACC	GGCGGCAACA	TCTCTGTGCC	GGTGGGCCGT	200
GAGACGCTGG	GCCGCATCTT	CAACGTGCTG	GGCGACGCGA	TCGACCAGCG	250
CGGCCCCGTG	GGTGAGAAGA	TGCGCATGGC	GATCCACGCC	GAGGCCCCGA	300
AGCTGGCGGA	TCAGGCCGCG	GAGGACACGA	TCCTGACGAC	CGGCATCAAG	350
GTGATCGACC	TGATTCTGCC	CTACTGCAAG	GGTGGCAAGA	TCGGCCTGTT	400
TGGCGGCGCC	GGTGTGGGCA	AGACCGTGAT	CATCATGGAG	CTGATTAACA	450
ACGTCGCGAA	GGGCCACGGT	GGTTTCTCGG	TGTTTGCCGG	CGTTGGCGAG	500
CGCACGCGCG	AGGGCACGGA	CCTGTACCTG	GAGATGATGC	AGTCGAAGGT	550
GATTGACCTG	AAGGGCGAGT	CGAAGTGCGT	GCTTGTGTAC	GGGCAGATGA	600
ACGAGCCCCC	GGGTGCGCGC	GCGCGCGTTG	CGCAGTCTGC	GCTGACGATG	650
CGCGAGTACT	TCCGAGACGT	GGAGGGCCAG	AATGTGCTGC	TGTTTCATCGA	700
CAACATCTTC	CGCTTCACGC	AGGCGAACTC	CGAGGTCTCT	GCGCTGCTGG	750
GCCGCATTCC	GGCCGCCGTG	GGCTACCAGC	CGACGCTTGC	GGAGGATCTT	800
GGTATGCTGC	AGGAGCGCAT	CACGTCGACG	ACGAAGGGGT	CGATCACGTC	850
CGTGACAGCC	GTGTACGTGC	CTGCGGATGA	TATCACGGAT	CCGCGCGCCG	900
CGACGACGTT	CTCGCACCTG	GACGCGACGA	CTGTGCTGGA	CCGCGCGGTG	950
GCGGAGTCGG	GGATCTACCC	TGCCGTGAAC	CCGCTGGAGT	GCGCGTCGCG	1000
TATCATGGAG	CCCGATGTGA	TCGACGTGGA	CCACTACAAC	GTTGCGCAGG	1050
ATATCGTGCA	GATGCTGACC	AAGTACAAGG	AGCTGCAGGA	TATCATTGCG	1100
GTGCTTGTA	TCGACGAGCT	GAGCGAGGAG	GACAAGGTCG	TGGTGGACCG	1150
CGCGCGCAAG	GTGACCCGGT	TCCTGTGCGA	GCCGTTCAG	GTTGCGGAGG	1200
TGTTACGCGG	CATGACGGGC	CACTACGTGC	AGCTGGCCGA	CACGGTGGAG	1250
TCGTTCTCTG	GGCTGCTGAT	GGGGTCGTAC	GACCAG		1286

2) INFORMATION FOR SEQ ID NO: 860

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1222 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860

```

CTCGGAGGGC GTCCCGCCCC TGCTGACGGC GCTGGATGTG ACGGAGGACC 50
TTGGCCGCGA TGAGCCGCTG ACGCTGGAGA TCGTGACGCA CCTGGACGCG 100
AACACCGGCC GCTGCATTGC GATGCAGACG ACGGACCTGC TGAAGCTGAA 150
5  GTCGAAGGTT GTGTGACCCG GCGGCAACAT CTCTGTGCCG GTGGGCCGTG 200
AGACGCTGGG CCGCATCTTC AACGTGCTGG GCGACGCGAT CGACCAGCGC 250
GGCCCCGTGG GTGAGAAGAT GCGCATGGCG ATCCACGCCG AGGCCCCGAA 300
GCTGGCGGAT CAGGCCGCGG AGGACACGAT CCTGACGACC GGCATCAAGG 350
TGATCGACCT GATTCTGCCC TACTGCAAGG GTGGCAAGAT CGGCCTGTTT 400
10 GGCGGCGCCG GTGTGGGCAA GACCGTGATC ATCATGGAGC TGATTAACAA 450
CGTCGCGAAG GGCCACGGTG GTTTCTCGGT GTTTGCCGGC GTTGCGGAGC 500
GCACGCGCGA GGGCACGGAC CTGTACCTGG AGATGATGCA GTCGAAGGTG 550
ATTGACCTGA AGGGCGAGTC GAAGTGCGTG CTTGTGTACG GGCAGATGAA 600
CGAGCCCCCG GGTGCGCGCG CGCGCGTTGC GCAGTCTGCG CTGACGATGG 650
15 CGGAGTACTT CCGAGACGTG GAGGGCCAGA ATGTGCTGCT GTTCATCGAC 700
AACATCTTCC GCTTCACGCA GCGCAACTCC GAGGTCTCTG CGCTGCTGGG 750
CCGCATTCCG CCGCGCCGTG GCTACCAGCC GACGCTTGCG GAGGATCTTG 800
GTATGCTGCA GGAGCGCATC ACGTCGACGA CGAAGGGGTC GATCACGTCC 850
GTGCAGGCCG TGTACGTGCC TGC GGATGAT ATCACGGATC CGGCGCCCCG 900
20 GACGACGTTT TCGCACCTGG ACGCGACGAC TGTGCTGGAC CGCGCGGTGG 950
CGGAGTCGGG GATCTACCC T GCGTGAACC CGCTGGAGTG CGCGTCGCGT 1000
ATCATGGACC CCGATGTGAT CGACGTGGAC CACTACAACG TTGCGCAGGA 1050
TATCGTGCAG ATGCTGACCA AGTACAAGGA GCTGCAGGAT ATCATTGCGG 1100
TGCTTGGTAT CGACGAGCTG AGCGAGGAGG ACAAGGTCGT GGTGGACCGC 1150
25 GCGCGCAAGG TGACCCGGTT CCTGTCGCAG CCGTTCAGG TTGCGGAGGT 1200
GTTCACGGGC ATGACGGGCC AC 1222

```

30 2) INFORMATION FOR SEQ ID NO: 861

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861

```

45 CCGTGCTGAC GCGCTGGAT GTGACGGAGG ACCTTGGCCG CGATGAGCCG 50
CTGACGCTGG AGATCGTGCA GCACTTGGAC GCGAACACCG GCCGCTGCAT 100
TGCGATGCAG ACGACGGACC TGCTGAAGCT GAAGTCGAAG GTTGTGTCGA 150
CCGGCGGCAA CATCTCTGTG CCGGTGGGCC GTGAGACGCT GGGCCGCATC 200
50 TTCAACGTTT TGGGCGACGC GATCGACCAG CGCGGCCCGG TGGGCGAGAA 250
GATGCGCATG GCGATCCACG CCGAGGCCCC GAAGCTGGCG GATCAGGCCG 300
CGGAGGACAC GATCCTGACG ACCGGCATCA AGGTGATCGA CCTGATTCTG 350
CCCTACTGCA AGGGTGGCAA GATCGGCCTG TTCGGCGGTG CCGGTGTGGG 400
CAAGACTGTG ATCATCATGG AGCTGATCAA CAACGTCGCG AAGGGCCACG 450
55 GTGGTTTCTC CGTGTTTGCC GGC GTTGGCG AGCGCACGCG CGAGGGCACG 500
GACCTGTACC TGGAGATGAT GCAGTCGAAG GTGATTGACC TGAAGGGCGA 550
GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT GAACGAGCCC CCGGTGCGC 600
GCGCGCGCGT TCGCAGTCT GCGCTGACGA TGGCGGAGTA CTTCCGCGAC 650
GTGGAGGGCC AGAACGTGCT GCTGTTCATC GACAACATCT TCCGCTTCAC 700
60 GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT GGGCCGCATT CCGGCCGCCG 750

```

	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	GCAGGAGCGC	800
	ATCACGTCGA	CAACGAAGGG	GTTCGATCACG	TCCGTGCAGG	CCGTGTACGT	850
	GCCAGCGGAT	GATATCACGG	ATCCC GCGCC	CGCGACGACG	TTCTCGCACC	900
	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	GGGCATCTAC	950
5	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	ACCCCGATGT	1000
	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	CAGATGCTGA	1050
	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	CATCGACGAG	1100
	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	AGGTGACCCG	1150
	GTTCTGTGTCG	CAGCCGTTCC	AGGTTGCGGA	GGTGTTCACG	GGCATGACGG	1200
10	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	TGGCCT	1246

2) INFORMATION FOR SEQ ID NO: 862

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862

30	GGCGTGCCGC	CCGTGCTGAC	GCGGCTGGAT	GTGACGGAGG	ACCTTGGCCG	50
	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACGG	100
	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	150
	GTCGTGTGCA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	200
	GGGCCGCAATC	TTCAAYGTTC	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	250
35	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	300
	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	350
	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	400
	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	450
	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	500
40	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	550
	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	GAACGAGCCC	600
	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	650
	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	GACAACATCT	700
	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	750
45	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	800
	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTTCGATCACG	TCCGTGCAGG	850
	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCC GCGCC	CGCGACGACG	900
	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	950
	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	1000
50	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	1050
	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	1100
	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	1150
	AGGTGACCCG	GTTCTGTGTCG	CAGCCGTTCC	AGGTTGCGGA	GGTGTTCACG	1200
	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	1250
55	TGGCCTGCTG	ATGGG				1265

2) INFORMATION FOR SEQ ID NO: 863

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863

```

15 ATGGCAAAAG GCAAGTTTGA ACGTACCAAG CCGCACGTGA ACGTGGGTAC      50
   GATTGGTCAC GTTGACCACG GCAAAACGAC GTTGACGGCG GCGATCACGA      100
   CCGGTGCTGTC GAACAAGTTC GGCGGCGAGG CTCGCGGCTA CGACCAGATT      150
   GACGCGGCGC CGGAAGAGAA GGCGCGTGGG ATCACGATCA ACACCTCGCA      200
   CGTTGAGTAC GAGACGGAGA CGCGTCACTA CGCGCACGTT GATTGCCCGG      250
   GTCACGCTGA CTACGTGAAG AACATGATCA CGGGTGCTGC GCAGATGGAC      300
20 GGCGCGATCC TGGTGGTGTG GGCCGCAGAC GGCCCGATGC CGCAGACGCG      350
   CGAGCACATT TTGCTGTCTG GCCAGGTTGG CGTGCCGTAC ATCATCGTGT      400
   TCCTGAACAA GGCGGACATG GTTGATGACG CGGAGCTGCT CGAGCTGGTG      450
   GAGATGGAAG TCCGCGAACT GCTGAGCAAG TACGATTTCC CGGGCGATGA      500
   CACGCCGATC GTGAATGGTG CGGCCAAGCT GGCGCTGGAA AGCGACAACG      550
25 GCGACCTGGG CGAGCAGGCG ATTCTGTCTG TGGCGCAAGC GCTGGACACG      600
   TACATTCCGA CGCCGGAGCG CGCGGTCGAC GGTGCGTTCC TGATGCCGGT      650
   GGAAGACGTG TTCTCGATCT CGGGCCGTGG CACGGTGGTG ACTGGCCGTA      700
   TCGAGCGCGG CGTGGTGAAG GTTGCGCAGG AAAATCGAAAT CGTGGGCATC      750
   AAGCCGACGG TGAAGACGAC CTGCACGGGC GTGGAGATGT TCCGCAAGCT      800
30 GCTGGACCAg GGCCAGGCGG GCGACAACGT GGGTATCTTG CTGCGCGGCA      850
   CCAAGCTGTA AGACGTCGAG CGTGGCCAGG TGCTGGCCAA GCCGGGTTCTG      900
   ATCAACCTGC ACACGGACTT CACGGCCGAG GTGTACATTC TGTCCAAGGA      950
   AGAGGGTGGC CGTCACACGC CGTTCCTTAA CGGCTATCGT CCGCAGTTCT      1000
   ACTTCCGCAC GACGGACGTG ACCGGCACGA TCGACCTGCC GGCGGACAAG      1050
35 GAAATGGTGC TGCCGGGCGA CAACGTGTCT ATGACCGTCA AGCTGCTGGC      1100
   CCCGATCGCC ATGGAAGAAG GTCTGCGTTT CGCCATCCGT GAAGGCGGTC      1150
   GTACCGTCGG TGCCGGCGTC GTCGCCAAGA TCATCAAGTA A              1191

```

2) INFORMATION FOR SEQ ID NO: 864

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*
 (B) STRAIN: LVH/75/USAMRU-K/18
 (C) ACCESSION NUMBER: extracted from U10562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864

```

60 ATGGGAAAGG AAAAGGTGCA CATGAATCTT GTGGTGGTGG GCCACGTGCA      50
   TGCCGGTAAA TCCACTGCAA CGGGTCACTT GATCTACAAG TGCGGTGGTA      100
   TTGACAAACG TACGATCGAG AAGTTCGAGA AAGAAGCTGC CGACATTGGT      150

```

	AAGGCCTCAT	TCAAGTACGC	ATGGGTGCTG	GACAAGCTGA	AGGCTGAGCG	200
	CGAACGTGGT	ATCACGATCG	ACATTGCACT	GTGGAAATTC	GAGTCACCCA	250
	AGTCTGTCTT	CACTATTATT	GATGCTCCTG	GGCACCGTGA	CTTCATCAAG	300
	AACATGATCA	CCGGCACATC	GCAAGCCGAC	GCAGCCATCC	TCATCATTGC	350
5	CTCTGCGCAG	GGTGAGTTTC	AGGCTGGTAT	CTCCAAGGAT	GGACAGACCC	400
	GCGAGCACGC	GTTGCTGGCC	TTCACTTTGG	GTGTGAAGCA	GATGGTTGTG	450
	TGCTGCAACA	AAATGGACGA	CAAGACTGTG	AACTACGGAC	AGGAGCGGTA	500
	TGACGAGATT	GTGAAGGAGG	TGTCTGCTTA	CATCAAGAAG	GTTGGGTACA	550
	ACGTGGAGAA	GGTGCGCTTC	GTCCCCATCT	CCGGATGGCA	GGGCGACAAC	600
10	ATGATTGAGA	AATCCGAGAA	GATGCCATGG	TACAAGGGTC	CAACGCTCCT	650
	GGAGGCACTA	GACATGCTGG	AGCCACCAGT	GCGTCCGAGC	GACAAGCCCC	700
	TGCGTCTGCC	ACTGCAGACG	TGTACAAAGA	TCGGTGGTAT	TGGCACCCTG	750
	CCCGTTGGTC	GTGTGGAGAC	CGGCGTGATG	AAGCCTGGTG	ATGTGGTGAC	800
	GTTTGCCCCC	GCCAACGTGA	CGACCGAGGT	GAAATCGATC	GAGATGCACC	850
15	ACGAGCAGCT	CGCTGAGGCG	ACCCCCGGTG	ACAACGTCGG	CTTTAACGTG	900
	AAGAACGTTT	CTGTAAAGGA	CATCCGCCGT	GGCAACGTCT	GCGGTAACAC	950
	CAAGAACGAC	CCCCCAAAGG	AGGCCGCCGA	CTTCACGGCA	CAGGTGATCA	1000
	TCCTGAACCA	CCCCGGACAG	ATTGGAAACG	GTTATGCGCC	CGTGCTGGAC	1050
	TGCCACACAT	CGCACATTGC	CTGCAAGTTC	GCGGAGATCG	AGTCGAAGAT	1100
20	CGACCGTCGC	TCTGGCAAGG	AGCTGGAGAA	GGCTCCCAAG	TCGATCAAGT	1150
	CTGGCGACGC	CGCGATCGTG	CGCATGGTGC	GCGAGAAGCC	TATGTGCGTG	1200
	GAGGTC'TTCA	ACGACTACGC	GCCACTCGGC	CGCTTTGCCG	TGCGTGACAT	1250
	GCGCCAGACC	GTCGCTGTCT	GTATCATCAA	GGCCGTGACC	AAGAAGGACG	1300
25	GTTCTGGTGG	TAAGGTGACG	AAGGCTGCGG	TGAAGGCTTC	GAAGAAATAA	1350

2) INFORMATION FOR SEQ ID NO: 865

30 (i) SEQUENCE CHARACTERISTICS:

- (A) —LENGTH: 1052-bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865

	AAGCTCAAGG	CTGAGAGAGA	AAGAGGTATT	ACCATCGATA	TTGCTTTATG	50
	GCAATTCGAA	ACCCCAAAT	ACCACTACAC	TGTCATTGAT	GCCCCAGGTC	100
45	ACAGAGATTT	CATCAAGAAT	ATGATTACTG	GTACCTCTCA	AGCTGATGTT	150
	GCTTTATTTG	TTGTCCCAGC	CGATCGTTTC	GAAGGTGCCT	TCTCCAAGGA	200
	AGGTCAAACC	AGAGAACATG	CTTTATTGGC	CTTCACTTTG	GGTGTCAGAC	250
	AAATGATTGT	CGGTATTAAC	AAGATGGATA	CCTGTGAATA	CAAGCAATCT	300
	CGTTTTGATG	AAATCTTCAA	CGAAGTTGAT	GGTTACCTCA	AGAAGGTTGG	350
50	TTACAACACC	GAGAAGATCC	CATTCTGTTG	CATTCTGGT	TTCTGTTGGTG	400
	ATAATATGGT	TGAGAGATCT	GACAAGATGC	CATGGTATAA	GGGTAAGACC	450
	TTAGTCGAAG	CCCTCGACAC	TATGGAACCA	CCAAAGAGAC	CAACTGACAA	500
	GCCACTCCGT	CTCCCATTAC	AAGATGTTTA	CAAGATAGGT	GGTGTAAGTA	550
	CTGTCCCAGT	CGGTCGTGTT	GAGACTGGTA	TCATCAGACC	AGGTATGAAT	600
55	GTTACCTTCG	CTCCAGCTGG	TGTTACCACT	GAAGTTAAGT	CAGTAGAAAT	650
	GCACCATGAG	CAGATGCCAG	AGGCCGTCCC	AGGTGACAAC	GTTGGTTTCA	700
	ATGTTAAGAA	CGTCTCCATC	AAGGATATCA	AGAGAGGTTT	CGTTGCTTCT	750
	GATGCCAAGA	ATGACCCAGC	TAAGGGCTGT	GAAGACTTCA	CTGCTCAAGT	800
	TATCGTCCCT	AACCACCCAG	GTGAAATCAA	GAACGGTTAC	TCTCCAGTCG	850
60	TTGACTGTCA	CACCGCTCAC	ATTCCTTGCA	AATTCCAGAC	TATCACTGCT	900

AAGATGGACA	AGAGATCTGG	TAAGGTTTTG	GAAGAAAACC	CAAAGCTTAT	950
CAAGTCTGGT	GATGCTGCTT	TGGTTGTTAT	GCAACCTTTG	AAGCCACTTT	1000
GTGTTGAGGC	CTTCACTGAC	TACCCACCTC	TAGGTCGTTT	CGCTGTCCGT	1050
GA					1052

5

2) INFORMATION FOR SEQ ID NO: 866

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866

25	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
	TACAGAAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCT	GTTGGTGTATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
30	TGCATTGCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
	TTCCGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
35	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
40	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

2) INFORMATION FOR SEQ ID NO: 867

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

60	AAGGTATTCG	ATGCCTTGAA	AATGGAAGGC	TCCGAGCTGA	CCCTGGAAGT	50
----	------------	------------	------------	------------	------------	----

690

```

5   ACAACAGCAG CTGGGCGACG GCATTGTCCG TACCATTGCA CTGGGTACCT 100
    CCGACGGCCT GCGTCGCGGC ATGATGATCC AGAACACCGG CAAACCTATC 150
    ATGGTGCCAG TCGGTAAAGC AACCTGGGGT CGCATCATGG ACGTGCTGGG 200
    TAACCCGATC GACGAATGCG GCGCGGTCGC TCACGACCAG ATCGCTTCGA 250
    TCCACCGCGC TCCTCCTGCG TACGACGAAC TGTCGCCATC GCAAGATCTG 300
    CTGGAAACCG GCATTAAAGT TATTGACCTG GTGTGCCCGT TCGCCAAGGG 350
    CGGTAAAGTC GGTCTGTTCG GCGGTGCAGG TGTGGGCAAG ACCGTGAACA 400
    TGATGGAAC TATCAACAAC ATCGCCAAAG CACACTCGGG TCTGTCCGTG 450
    TTTGCCGGTG TGGGTGAGCG TACCCGTGAA GGTAACGACT TCTACCACGA 500
10  GATGGCTGAC GCCAAAGTGG TCGATCTGGA AAATCCAGAG AACTCCAAGG 550
    TTGCGATGGT CTACGGTCAG ATGAATGAAC CACCAGGCAA CCGTCTGCGC 600
    GTGGCGCTGA CCGGTCTGAC CATGGCTGAA GCATTCCGTG ACGAAGGCAA 650
    AGACGTTCTG TTCTTCGTGG ACAACATCTA CCGCTTCACC CTGGCCGGTA 700
    CCGAAGTATC GGCACGTGCT GGCCGTATGC CATCGGCTGT GGGTTACCAG 750
15  CCTACGCTGG CCGAAGAAAT GGGTCGCCTG CAAGAGCGCA TCACTTCGAC 800
    CAAGACCGGT TCGATCAC 818

```

20 2) INFORMATION FOR SEQ ID NO: 868

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868

```

35  CTATCTTAGT AGTATCTGCT GCTGATGGCC CAATGCCACA AACTCGTGAA 50
    CACATTCTTT TATCACGTAA CGTTGGTGTT CCAGCATTAG TTGTATTCTT 100
    AAACAAAGTT GACATGGTTG ACGATGAAGA ATTATTAGAA TTAGTAGAAA 150
    TGGAAGTTCG TGACTTATTA AGCGAATATG ACTTCCCAGG TGACGATGTA 200
40  CCTGTAATCT CTGGTTCTGC ATTAAAAGCT TTAGAAGGCG ACGCTGACTA 250
    TGAGCAAAAA ATCTTAGACT TAATGCAAGC TGTGATGAC TTCATTCCAA 300
    CACCAGAACG TGATTCTGAC AAACCATTCA TGATGCCAGT TGAGGACGTA 350
    TTCTCAATCA CTGGTCGTGG TACTGTTGCT ACAGGCCGTG TTGAACGTGG 400
    TCAAATCAAA GTCGGTGAAG AAATCGAAAT CATCGGTATG CAAGAAGAAT 450
45  CAAGCAAAAC AACTGTTACT GGTGTAGAAA TGTTCGGTAA ATTATTAGAC 500
    TACGCTGAAG CTGGTGACAA CATTGGTGCA TTATTACGTG GTGTTTCACG 550
    TGATGACGTA CAACGTGGTC AAGTTTTAGC TGCTCCTGGT ACTATTACAC 600
    CACATACAAA ATTCAAAGCG GATGTTTACG TTTTATCTAA AGATGAAGGT 650
    GGTCGTCATA CACCATTCTT CACTAACTAC CGCCACAAT TCTATTTCGG 700
50  TACTACTGAC GTAACGTGGT TTGTTAACTT ACCAGAAGGT ACTGAAATGG 750
    TTATGCCTGG CGATAACGTT GAAATGGA 778

```

55 2) INFORMATION FOR SEQ ID NO: 869

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869

```

10 TGGTCCTATG CCTCAAACAC GTGAACACAT CTTGTTATCA CGTAACGTTG      50
   GTGTACCATA CATCGTTGTT TTCTTAAACA AAATGGATAT GGTTGATGAC      100
   GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTGTCAGA      150
   ATATGACTTC CCAGGCGACG ATGTTCCCTGT AATCGCTGGT TCTGCTTTGA      200
15 AAGCTCTTGA AGGCGATGCT TCATACGAAG AAAAAATCAT GGAATTAATG      250
   GCTGCAGTTG ACGAATACGT TCCAACCTCA GAACGTGACA CTGACAAACC      300
   ATTCATGATG CCAGTCGAAG ACGTATTCTC AATCACTGGA CGTGGTACTG      350
   TTGCTACAGG CCGTGTTGAA CGTGGACAAG TTCGCGTTGG TGACGAAGTT      400
   GAAATCGTTG GTATTGCTGA AGAACTGCT AAAACAACCTG TAACTGGTGT      450
20 TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG      500
   GTGCATTGCT ACGTGGTGTG GTCGTGAAG ACATCCAACG TGGACAAGTA      550
   TTGGCTAAAG CTGGTACAAT CACACCTCAT ACAAATTTTA AAGCTGAAGT      600
   TTACGTTTTA ACAAAGAAG AAGGTGGACG TCACACTCCA      640

```

25

2) INFORMATION FOR SEQ ID NO: 870

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 644 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: R754

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870

```

   GTCCTATGCC TCAAACACGT GAACACATCT TGTTATCACG TAACGTTGGT      50
   GTACCATACT TCGTTGTTTT CTAAACAAA ATGGATATGG TTGATGACGA      100
45 AGAATTACTA GAATTAGTTG AAATGGAAGT TCGTGAAGTA TTGTCAGAAT      150
   ATGACTTCCC AGGCGACGAT GTTCCTGTAA TCGCTGGTTC TGCTTTGAAA      200
   GCTCTTGAAG GCGATGCTTC ATACGAAGAA AAAATCATGG AATTAATGGC      250
   TGCAGTTGAC GAATACGTTT CAACTCCAGA ACGTGACACT GACAAACCAT      300
   TCATGATGCC AGTCGAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT      350
50 GCTACAGGCC GTGTTGAACG TGGACAAGTT CGCGTTGGTG ACGAAGTTGA      400
   AATCGTTGGT ATTGCTGAAG AACTGCTAA AACAACGTA ACTGGTGTG      450
   AAATGTTCCG TAAATTGTTA GACTATGCTG AAGCAGGGGA TAACATTGGT      500
   GCATTGCTAC GTGGTGTGTC TCGTGAAGAC ATCCAACGTG GACAAGTATT      550
   GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTTAAA GCTGAAGTTT      600
55 ACGTTTTAAC AAAAGAAGAA GGTGGACGTC ACACACCATT CTTC      644

```

60

2) INFORMATION FOR SEQ ID NO: 871

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871

```

15 TCCTATGCCT CAAACACGTG AACACATCTT GTTATCACGT AACGTTGGTG      50
   TACCATACAT CGTTGTTTTC TTAAACAAAA TGGATATGGT TGATGACGAA      100
   GAATTACTAG AATTAGTTGA AATGGAAGTT CGTGACTTAT TGTCAGAATA      150
   TGAATTCCCA GGCGACGATG TTCCTGTAAT CGCTGGTTCT GCTTTGAAAG      200
   CTCTTGAAGG CGATGCTTCA TACGAAGAAA AAATCATGGA ATTAATGGCT      250
20 GCAGTTGACG AATACGTTCC AACTCCAGAA CGTGACACTG ACAAACCATT      300
   CATGATGCCA GTCGAAGACG TATTCTCAAT CACTGGACGT GGTACTGTTG      350
   CTACAGGCCG TGTGGAACGT GGACAAGTTC GCGTTGGTGA CGAAGTTGAA      400
   ATCGTTGGTA TTGCTGAAGA AACTGCTAAA ACAACTGTAA CTGGTGTTGA      450
   AATGTTCCGT AAATTGTTAG ACTATGCTGA AGCAGGGGAT AACATTGGTG      500
25 CATTGCTACG TGGGGTTGCT CGTGAAGACA TCCAACGTGG ACAAGTATTA      550
   GCTAAAGCTG GTACAATCAC ACCTCATACA AAATTTAAAG CTGAAGTTTA      600
   CGTTTAAACA AAAGAAGAAG GTGGACGTCA CACTCCA                    637

```

2) INFORMATION FOR SEQ ID NO: 872

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872

```

GTCCTATGCC TCAAACCTCGT GAACACATCT TGTTATCACG TAACGTTGGC      50
GTACCATACA TCGTTGTTTT CTTGAACAAA ATGGATATGG TTGATGACGA      100
AGAATTGCTA GAATTAGTTG AAATGGAAGT TCGTGACCTA TTGTCTGAAT      150
50 ATGACTTCCC AGGCGACGAT GTTCCTGTAA TCGCCGGTTC TGCTTTGAAA      200
   GCTCTTGAAG GAGATCCTTC ATACGAAGAA AAAATCATGG AATTGATGGC      250
   TGCAGTTGAC GAATACGTTT CAACTCCAGA ACGTGATACT GACAAACCAT      300
   TCATGATGCC AGTCGAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT      350
   GCTACAGGCC GTGTTGAACG TGGACAAGTT CGCGTTGGTG ATGAAGTAGA      400
55 AATCGTTGGT ATTGCTGACG AACTGCTTAA ACAAACGTGA ACAGGTGTTG      450
   AAATGTTCCG TAAATTGTGA GACTATGCTG AAGCAGGGGA TAACATTGGT      500
   GCATTGCTAC GTGGGGTTGC TCGTGAAGAC ATCCAACGTG GACAAGTATT      550
   GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTCAAA GCTGAAGTTT      600
   ATGTTTTGAC AAAAGAAGAA GGTGGACGTC ACACTCCATT CTT                    643

```

2) INFORMATION FOR SEQ ID NO: 873

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus gallinarum*
 15 (B) STRAIN: R691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873

	GTCCTATGCC	TCAAACCTCGT	GAACACATCT	TGTTATCACG	TAACGTTGGC	50
20	GTACCATACA	TCGTTGTTTT	CTTGAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTGCTA	GAATTAGTTG	AAATGGAAGT	TCGTGACCTA	TTGTCTGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCCGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GAGATCCTTC	ATACGAAGAA	AAAATCATGG	AATTGATGGC	250
	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGATACT	GACAAACCAT	300
25	TCATGATGCC	AGTCGAAGAC	GTATCTCTCA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ATGAAGTAGA	400
	AATCGTTGGT	ATTGCTGACG	AAACTGCTAA	AACAACGTGA	ACAGGTGTTG	450
	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGGGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
30	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTCAAA	GCTGAAGTTT	600
	ATGTTTTGAC	AAAAGAAGAA	GGTGGACGTC	ACACTCCATT	C	641

35 2) INFORMATION FOR SEQ ID NO: 874

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 681 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: LSPQ 2514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874

50	ACCAGCATT	A	GTAGTATTCT	TAAATAAAGT	TGACATGGTT	GACGATGAAG	50
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTAC	GTGACTTATT	ATCTGAATAC		100
	GACTTCCCAG	GTGACGATGT	ACCTGTAATC	GCTGGTTCAG	CATTAAAAGC		150
	TTTAGAAGGC	GATGCTCAAT	ACGAAGAAAA	AATCTTAGAA	TTAATGCAAG		200
55	CAGTTGATGA	CTACATTCCA	ACTCCAGAAC	GTGATTCTGA	CAAACCATTC		250
	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	GTACTGTTGC		300
	TACAGGCCGT	GTTGAACGTG	GGCAAATCAA	AGTTGGTGAA	GAAGTTGAAA		350
	TCATTGGTAT	CCATGACACT	TCTAAAACAA	CTGTTACTGG	TGTAGAAATG		400
	TTCCGTAAAT	TATTAGACTA	CGCTGAAGCT	GGTGACAACA	TCGGTGCATT		450
60	ATTACGTGGT	GTTGCTCGTG	AAGACGTACA	ACGTGGTCAA	GTATTAGCTG		500

CTCCAGGTTC	AATCACACCT	CACACAAAAT	TTAAAGCAGA	CGTATACGTT	550
TTATCTAAAG	ACGAAGGTGG	ACGTCACACT	CCATTCTTCA	CAAACATATCG	600
TCCACAATTC	TATTTCCGTA	CTACTGACGT	AACTGGTGTG	GTTAACCTAC	650
CAGAAGGTAC	TGAAATGGTT	ATGCCTGGCG	A		681

5

2) INFORMATION FOR SEQ ID NO: 875

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 675 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: R591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875

ATTATCACGT	AACGTTGGTG	TACCAGCATT	AGTTGTATTC	TTAAACAAAG	50
TTGACATGGT	AGACGACGAA	GAATTATTAG	AATTAGTTGA	AATGGAAGTT	100
CGTGACTTAT	TAAGCGAATA	TGACTTCCCA	GGTGACGATG	TACCTGTAAT	150
CGCTGGTTCT	GCATTAAAAG	CATTAGAAGG	CGATGCTGAA	TACGAACAAA	200
AAATCTTAGA	CTTAATGCAA	GCAGTTGATG	ATTACATTCC	AACTCCAGAA	250
CGTGATTCTG	ACAAACCATT	CATGATGCCA	GTTGAGGACG	TATTCTCAAT	300
30 CACTGGTCGT	GGTACTGTTG	CTACAGGCCG	TGTTGAACGT	GGTCAAATCA	350
AAGTTGGTGA	AGAAGTTGAA	ATCATCGGTA	TGCACGAAAC	TTCTAAAACA	400
ACTGTTACTG	GTGTAGAAAT	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	450
TGGTGACAAC	ATCGGTGCTT	TATTACGTGG	TGTTGCACGT	GAAGACGTAC	500
AACGTGGTCA	AGTATTAGCT	GCTCCTGGTT	CTATTACACC	ACACACAAAA	550
35 TTCAAAGCTG	AAGTATACGT	ATTATCTAAA	GATGAAGGTG	GACGTCACAC	600
TCCATTCTTC	ACTAACTATC	GCCCACAATT	CTATTTCCGT	ACTACTGACG	650
TAAGTGGTGT	TGTAAACTTA	CCAGA			675

40

2) INFORMATION FOR SEQ ID NO: 876

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 704 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: CSG 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876

TCTTATTATC	ACGTAACGTT	GGTGTACCAG	CATTAGTTGT	ATTCTTAAAC	50
AAAGTTGACA	TGGTAGACGA	CGAAGAATTA	TTAGAATTAG	TTGAAATGGA	100
AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
60 TAATCGCTGG	TTCTGCATTA	AAAGCATTAG	AAGGCGATGC	TGAATACGAA	200

	CAAAAAATCT	TAGACTTAAT	GCAAGCAGTT	GATGATTACA	TTCCAACTCC	250
	AGAACGTGAT	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTATGCACG	AAACTTCTAA	400
5	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATCGGT	GCTTTATTAC	GTGGTGTTCG	ACGTGAAGAC	500
	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCTATTA	CACCACACAC	550
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	TAAAGATGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCACTAAC	TATCGCCCAC	AATTCTATTT	CCGTACTACT	650
10	GACGTAAGT	GTGTTGTAAA	CTTACCAGAA	GGTACAGAAA	TGGTTATGCC	700
	TGGC					704

15 2) INFORMATION FOR SEQ ID NO: 877

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 35984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877

30	TCTTAGTTGT	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	50
	ATCTTATTAT	CACGTAACGT	TGGTGTACCA	GCATTAGTTG	TATTCTTAAA	100
	CAAAGTTGAC	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTTCGTGA	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	200
35	GTAATCGCTG	GTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	250
	ACAAAAAATC	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAACCTC	300
	CAGAACGTGA	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	400
	AATCAAAGTT	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	450
40	AAACAACGTG	TACTGGTGTG	GAAATGTTCC	GTAAATTATT	AGACTACGCT	500
	GAAGCTGGTG	ACAACATCGG	TGCTTTATTA	CGTGGTGTTC	CACGTGAAGA	550
	CGTACAACGT	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	600
	CAAAATTCAA	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	700
45	TGACGTAAGT	GGTGTGTGTA	ACTTACCAGA	AGGTACAGAA	ATGGTTATGC	750
	CTGGCGACAA	CGTTGAAATG				770

50 2) INFORMATION FOR SEQ ID NO: 878

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 35983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

```

5      TTGTATTCTT AAACAAAGTT GACATGGTAG ACGACGAAGA ATTATTAGAA      50
      TTAGTTGAAA TGGAAGTTCG TGAATTATTA AGCGAATATG ACTTCCCAGG      100
      TGACGATGTA CCTGTAATCG CTGGTTCTGC ATTAAAAGCA TTAGAAGGCG      150
      ATGCTGAATA CGAACAAAAA ATCTTAGACT TAATGCAAGC AGTTGATGAT      200
10     TACATTCCAA CTCCAGAACG TGATTCTGAC AAACCATTCA TGATGCCAGT      250
      TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT ACAGGCCGTG      300
      TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT CATCGGTATG      350
      CACGAAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT TCCGTAAATT      400
      ATTAGACTAC GCTGAAGCTG GTGACAACAT CGGTGCTTTA TTACGTGGTG      450
15     TTGCACGTGA AGACGTACAA CGTGGTCAAG TATTAGCTGC TCCTGGTTCT      500
      TTATACCCAC ACACAAAAAT CAAAGCTGAA GTATACGTAT TATCTAAAGA      550
      TGAAGGTGGA CGTCACACTC CATTCTTCAC TAACTATCGC CCACAATTCT      600
      ATTTCCGTAC TACTGACGTA ACTGGTGTTG TAAACTTACC AGAAGGTACA      650
      GAAATGGTTA TGCCTGGCGA CAACGTTGAA ATGACAGTTG AATTAATCGC      700
20     TCCAATCGCT ATCGAA      716
  
```

2) INFORMATION FOR SEQ ID NO: 879

```

25     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 640 bases
          (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
30     (D) TOPOLOGY: Linear

          (ii) MOLECULE TYPE: Genomic DNA

          (vi) ORIGINAL SOURCE:
35     (A) ORGANISM: Enterococcus gallinarum
          (B) STRAIN: R764
  
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879

```

40     CGGTCCTATG CCTCAAACCTC GTGAACACAT CTTGTTATCA CGTAACGTTG      50
      GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT GGTTGATGAC      100
      GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA      150
      ATATGACTTC CCAGGCGACG ATGTTCTCTG AATCGCCGGT TCTGCTTTGA      200
      AAGCTCTTGA AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG      250
45     GCTGCAGTTG ACGAATACGT TCCAACCTCCA GAACGTGATA CTGACAAACC      300
      ATTCATGATG CCAGTCGAAG ACGTATTCTC AATCACTGGA CGTGGTACTG      350
      TTGCTACAGG CCGTGTTGAA CGTGGACAAG TTCGCGTTGG TGATGAAGTA      400
      GAAATCGTTG GTATTGCTGA CGAAACTGCT AAAACAACCTG TAACAGGTGT      450
      TGAATGTTTC CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG      500
50     GTGCATTGCT ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA      550
      TTGGCTAAAG CTGGTACAAT CACACCTCAT ACAAATTCA AAGCTGAAGT      600
      TTATGTTTTG ACAAAGAAG AAGGTGGACG TCACACTCCA      640
  
```

55 2) INFORMATION FOR SEQ ID NO: 880

```

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 831 bases
60     (B) TYPE: Nucleic acid
  
```

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: PAO-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880

CGGCGCGATC	CTGGTTTGCT	CGGCTGCCGA	CGGCCCCATG	CCGCAGACCC	50
GCGAGCACAT	CCTGCTGTCC	CGCCAGGTAG	GCGTTCCTTA	CATCGTCGTG	100
TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TGGAACCTGGT	150
CGAGATGGAA	GTTCGCGATC	TGCTGAACAC	CTACGACTTC	CCGGGCGACG	200
ACACTCCGAT	CATCATCGGT	TCCGCGCTGA	TGGCGCTGGA	AGGCAAGGAT	250
GACAACGGCA	TCCGCGTAAG	CGCCGTGCAG	AAGCTGGTAG	AGACCCTGGA	300
CTCCTACATT	CCGGAGCCGG	TTCGTGCCAT	CGACCAGCCG	TTCCTGATGC	350
CGATCGAAGA	CGTGTTCTCG	ATCTCCGGCC	GCGGTACCGT	GGTAACCGGT	400
CGTGTAGAGC	GCGGCATCAT	CAAGGTCCAG	GAAGAAGTGG	AAATCGTCGG	450
CATCAAGGCG	ACCACCAAGA	CTACCTGCAC	CGGCGTTGAA	ATGTTCCGCA	500
AGCTGCTCGA	CGAAGGTCGT	GCTGGTGAGA	ACGTTGGTAT	CCTGCTGCGT	550
GGCACCAAGC	GTGAAGACGT	AGAGCGTGGC	CAGGTTCTGG	CCAAGCCGGG	600
CACCATCAAG	CCGCACACCA	AGTTCGAGTG	CGAAGTGTAC	GTGCTGTCCA	650
AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TCAAGGGCTA	CCGTCCGCAG	700
TTCTACTTCC	GTACCACCGA	YGTGACCGGT	AACTGCGAAC	TGCCGGAAGG	750
CGTAGAGATG	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTCACCCTGA	800
TCGCTCCGAT	CGCCATGGAA	GATGGCCTGC	G		831

2) INFORMATION FOR SEQ ID NO: 881

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 642 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: R421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881

CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCCTG	CTTTGAAAGC	200
TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
TACAGGCCGT	GTTGAACGTG	GACAAGTTTCG	CGTTGGTGAC	GAAGTTGAAA	400
TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
GTTTTAACAA	AAGAAGAAGG	TGGACGTCAC	ACACCATTCT	TC	642

2) INFORMATION FOR SEQ ID NO: 882

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882

```

20 CCTATGCCTC AAACACGTGA ACACATCTTG TTATCACGTA ACGTTGGTGT      50
   ACCATACATC GTTGTTTTCT TAAACAAAAT GGATATGGTT GATGACGAAG      100
   AATTACTAGA ATTAGTTGAA ATGGAAGTTC GTGACTTATT GTCAGAATAT      150
   GACTTCCCAG GCGACGATGT TCCTGTAATC GCTGGTTCTG CTTTGAAAGC      200
   TCTTGAAGGC GATGCTTCAT ACGAAGAAAA AATCATGGAA TTAATGGCTG      250
25 CAGTTGACGA ATACGTTCCA ACTCCAGAAC GTGACACTGA CAAACCATTC      300
   ATGATGCCAG TCGAAGACGT ATTCTCAATC ACTGGACGTG GTACTGTTGC      350
   TACAGGCCGT GTTGAACGTG GACAAGTTCG CGTTGGTGAC GAAGTTGAAA      400
   TCGTTGGTAT TGCTGAAGAA ACTGCTAAAA CAACTGTAAC TGGTGTGTA      450
   ATGTTCCGTA AATTGTTAGA CTATGCTGAA GCAGGGGATA ACATTGGTGC      500
30 ATTGCTACGT GGTGTTGCTC GTGAAGACAT CCAACGTGGA CAAGTATTGG      550
   CTAAAGCTGG TACAATCACA CCTCATACAA AATTTAAGC TGAAGTTTAC      600
   GTTTTAACAA AAGAAGAAGG TGGACGTCAT ACACCA                      636

```

2) INFORMATION FOR SEQ ID NO: 883

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883

```

GGTCCTATGC CTCAAACACG TGAACATATC TTATTATCAC GTAACGTTGG      50
TGTACCATAC ATCGTTGTAT TCTTAAACAA AATGGATATG GTTGATGACG      100
AAGAATTATT AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCAGAA      150
55 TACGATTTCC CAGGCGATGA TGTTCCAGTT ATCGCAGGTT CTGCTTTGAA      200
   AGCTTTAGAA GGCGACGAGT CTTATGAAGA AAAAACTCTT GAATTAATGG      250
   CTGCAGTTGA CGAATATATC CCAACTCCAG AACGTGATAC TGACAAACCA      300
   TTCATGATGC CAGTCGAAGA CGTATTCTCA ATCACTGGAC GTGGTACTGT      350
   TGCTACAGGC CGTGTTGAAC GTGGTGAAGT TCGCGTTGGT GACGAAGTTG      400
60 AAATCGTTGG TATTAAAGAC GAAACATCTA AAACAACGTG TACAGGTGTT      450

```


GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCAGGCG	ACAACATCGG	500
TGCTTTATTA	CGTGGTGTAG	CACGTGAAGA	TATCGAACGT	GGACAAGTAT	550
TAGCTAAACC	AGCTACAATC	ACTCCACACA	CAAATTCAA	AGCTGAAGTA	600
TACGTATTAT	CAAAAGAAGA	AGGCGGACGT	CACACTCCAT	T	641

5

2) INFORMATION FOR SEQ ID NO: 884

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 640 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

15

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: R575

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884

TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
TTTCCCAGGC	GATGATGTTT	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
TAGAAGGCCA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
30 GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
TATTACGTGG	TGTTGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
35 AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCATTCTTC		640

40 2) INFORMATION FOR SEQ ID NO: 885

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 632 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

45

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R492

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885

55 TGCCTCAAAC	TCGTGAACAC	ATCCTATTGT	CTCGTCAAGT	TGGTGTTCCT	50
TACATCGTTG	TATTCTTGAA	CAAAGTAGAC	ATGGTTGATG	ACGAAGAATT	100
ACTAGAATTA	GTTGAAATGG	AAGTTCGTGA	CCTATTAACA	GAATACGAAT	150
TCCCTGGTGA	CGATGTTTCT	GTAAGTGTCT	GATCAGCTTT	GAAAGCTCTA	200
60 GAAGGCGACG	CTTCATACGA	AGAAAAAATT	CTTGAATTAA	TGGCTGCAGT	250

700

	TGACGAATAC	ATCCCAACTC	CAGAACGTGA	CAACGACAAA	CCATTCATGA	300
	TGCCAGTTGA	AGACGTGTTT	TCAATTACTG	GACGTGGTAC	TGTTGCTACA	350
	GGTCGTGTTG	AACGTGGACA	AGTTCGCGTT	GGTGACGAAG	TTGAAGTTGT	400
	TGGTATTGCT	GAAGAACTT	CAAAAACAAC	AGTTACTGGT	GTTGAAATGT	450
5	TCCGTAAATT	GTTAGACTAC	GCTGAAGCTG	GAGACAACAT	TGGTGCTTTA	500
	CTACGTGGTG	TTGCACGTGA	AGACATCCAA	CGTGGACAAG	TTTTAGCTAA	550
	ACCAGGTACA	ATCACACCTC	ATACAAAATT	CTCTGCAGAA	GTATACGTGT	600
	TGACAAAAGA	AGAAGGTGGA	CGTCATACTC	CA		632

10

2) INFORMATION FOR SEQ ID NO: 886

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R576

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886

	CGGCCCAATG	CCTCAAACCTC	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	50
	GTGTTCTCTTA	CATCGTTGTA	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	100
30	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	150
	ATACGAATTC	CCTGGTGACG	ATGTTCTCTGT	AGTTGCTGGA	TCAGCTTTGA	200
	AAGCTCTAGA	AGGCGACGCT	TCATACGAAG	AAAAAATTCT	TGAATTAATG	250
	GCTGCAGTTG	ACGAATACAT	CCCAACTCCA	GAACGTGACA	ACGACAAACC	300
	ATTCATGATG	CCAGTTGAAG	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	350
35	TTGCTACAGG	TCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAGTTGTTG	GTATTGCTGA	AGAACTTCA	AAAACAACAG	TTACTGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTACGC	TGAAGCTGGA	GACAACATTG	500
	GTGCTTTACT	ACGTGGTGTG	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	550
	TTAGCTAAAC	CAGGTACAAT	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	600
40	ATACGTGTTG	ACAAAAGAAG	AAGGTGGACG	TCATACTCCA		640

2) INFORMATION FOR SEQ ID NO: 887

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887

60	ATCCTGGTTT	GCTCCGCAGC	TGACGGCCCA	ATGCCACAGA	CCCGCGAGCA	50
----	------------	------------	------------	------------	------------	----

```

CATCCTGCTG GCCCGCCAAG TTGGCGTTCC ATACATCATC GTGTTCTCTGA 100
ACAAGTGCGA CCTGGTTGAC GACGCAGAAC TGCTGGAAC TGTGCGAAATG 150
GAAGTGCGTG AATTGCTGTC GAAATACGAG TTCCCAGGCG ACGACGTACC 200
AATCATCAAG GGTTCGGCAC GTATGGCGCT GGAAGGCAAA GAAGGCGAGA 250
5 TGGGCGTTGA CGCCATCATG CGTCTGGCCG ATGCACTGGA CAGCTACATC 300
CCTACGCCAG AGCGCGCAGT CGATGGCGCC TTCCTGATGC CAGTGGAAGA 350
CGTGTTCCTCG ATCTCGGGTC GCGGTACCGT TGTGACCGGT CGTATCGAGC 400
GCGGCGTGAT CAAGGTCGGC GAAGAGATCG AAATCGTCGG CATTATCGAC 450
ACCGTCAAAA CCACTTGCAC CGGCGTGGA ATGTTCCGCA AGCTGCTGGA 500
10 CCAGGGTCAA GCCGGCGACA ACGTTGGTCT GCTGCTGCGC GGCACCAAGC 550
GTGAAGACGT ACAGCGTGGT CAGGTTCTGG CCAAGCCAGC GTCGATCAAG 600
CCGCACAACC ACTTACCGG CGAGATCTAC GTTCTGTCGA AAGATGAAGG 650
CGGCCGTCAC ACCCCGTTCT TCAACAATA TCGTCCACAG TTCTACTTCC 700
GTACGACTGA CGTGACCGGT TCGATCGAAC TGCCAGCAGA CAAAGAAATG 750
15 GTCATGCCAG GCGACAACGT GTCGATCACC GTCAAGCTGA TCAACCCGAT 800
CGCGAT 806

```

20 2) INFORMATION FOR SEQ ID NO: 888

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888

```

35 TATGCCTCAA ACACGTGAAC ATATCTTATT ATCACGTAAC GTTGGTGTAC 50
CATAATCGT TGTATTCTTA AACAAAATGG ATATGGTTGA TGACGAAGAA 100
TTATTAGAA TAGTAGAAAT GGAAGTTTCG TACTTATTAT CAGAATACGA 150
TTTCCCAGGC GATGATGTTT CAGTTATCGC AGGTTCTGCT TTGAAAGCTT 200
40 TAGAAGGCGA CGAGTCTTAT GAAGAAAAAA TCTTAGAATT AATGGCTGCA 250
GTTGACGAAT ATATCCCAAC TCCAGAACGT GATACTGACA AACCATTTCAT 300
GATGCCAGTC GAAGACGTAT TCTCAATCAC TGGACGTGGT ACTGTTGCTA 350
CAGGCCGTGT TGAACGTGGT GAAGTTCGCG TTGGTGACGA AGTTGAAATC 400
GTTGGTATTA AAGACGAAAC ATCTAAAAAC ACTGTTACAG GTGTTGAAAT 450
45 GTTCCGTAAA TTATTAGACT ACGTGAAGC AGGCGACAAC ATCGGTGCTT 500
TATTACGTGG TGTAGCACGT GAAGATATCG AACGTGGACA AGTATTAGCT 550
AAACCAGCTA CAATCACTCC ACACACAAAA TTCAAAGCTG AAGTATACGT 600
ATTATCAAAA GAAGAAGGCG GACGTCACAC TCCA 634

```

50

2) INFORMATION FOR SEQ ID NO: 889

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889

	TGTCTTCATC	CAGGAATTGA	TTGTGAGTCG	TTCCACATGC	TCACCTAGTT	50
	TTCGCTCGAT	CTTTTCACTA	ACGCAAACCA	TGTAGAACAA	CATTGCCAAG	100
10	GCCCACGGTG	GTTACTCCGT	CTTCACTGGT	GTTGGTGAGC	GTA CTCTGTA	150
	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	GACTGGTGTC	ATTCAGCTCG	200
	AGGGTGAATC	CAAGGTCGCA	CTGGTGTTTCG	GACAGATGAA	CGAGCCCCCC	250
	GGTGCCCCGTG	CCCGTGTCTGC	CCTTACCGGT	CTGACCATTG	CCGAGTACTT	300
	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	CTTCATTGAC	AACATTTTCC	350
15	GTTTCACCCA	GGCCGGTTCT	GAGGTGTCTG	CCCTTCTCGG	TCGTATCCCC	400
	TCTGCCGTCG	GTTACCAGCC	CACCCTGGCC	GTCGACATGG	GTGGTATGCA	450
	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	TATTACCTCC	GTC	493

(i) SEQUENCE CHARACTERISTICS: 890

- (A) LENGTH: 466 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890

35	TTGATTGTAC	GTCTTTACCT	TTCTGCCTGA	CTGTTTACGA	CAACTAACGA	50
	AAGCGTAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	TGTCTTCACT	100
	GGTGTGCGTG	AACGTACTCG	TGAGGGTAAC	GATTTGTACC	ACGAAATGCA	150
	GGAAACTGGT	GTCATTTCAGC	TCGAGGGTGA	ATCCAAGGTC	GCCCTCGTGT	200
	TCGGTCAGAT	GAACGAGCCC	CCCGGTGCCC	GTGCCCCTGT	CGCTCTTACT	250
40	GGTTTGACCA	TTGCCGAGTA	CTTCCGTGAC	GAGGAAGGTC	AGGACGTGCT	300
	TCTCTTCATT	GACAACATT	TCCGTTTCAC	TCAGGCCGGT	TCTGAGGTGT	350
	CTGCCCTTCT	GGGTCTGATC	CCCTCTGCCG	TCGGTTACCA	GCCCACCCTT	400
	GCCGTGACCA	TGGGTATCAT	GCAGGAGCGT	ATTACCACCA	CCACCAAGGG	450
45	TTCCATCACC	TCCGTC				466

2) INFORMATION FOR SEQ ID NO: 891

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891

```

5  AGGAGCTGAT CAACAACATC GCCAAGGCTC ACGGTGGTTA CTCCGTCTTC      50
   ACTGGTGTCTG GTGAGCGTAC CCGTGAGGGT AACGATCTGT ACCACGAAAT      100
   GCAGGAGACC TCGGTCATTC AGCTCGAGGG CGAGTCTAAG GTGGCCCTGG      150
   TCTTTGGTCA GATGAACGAG CCCCCGGGTG CTCGTGCCCC TGTCGCTCTT      200
   ACTGGTCTTA CCGTCGCCGA GTACTTCCGT GACCAGGAGG GTCAGGATGG      250
   TTAGTTCTCG TCCACTCATG CCGAAACATG TGC GTGTTCC GAGGCTAATC      300
10 AACGTGCCAG TGCTGCTTTT CATCGACAAC ATTTTCCGAT TCACACAGGC      350
   CGGTTCCGAG GTGTCTGCCC TGCTGGGTCG TATCCCCCTCT GCCGTCGGTT      400
   ACCAGCCAC CCTCGCCGTC GACATGGGTG GCATGCAGGA GCGTATCACC      450
   ACCACCAAGA AGGGCTCTAT CACCTCCG      478

```

15

2) INFORMATION FOR SEQ ID NO: 892

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 481 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

```

25 (ii) MOLECULE TYPE: Genomic DNA

```

```

    (vi) ORIGINAL SOURCE:

```

```

    (A) ORGANISM: Penicillium marneffei
    (B) STRAIN: ATCC 58950

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892

```

35 GTCTTTATCC AGGAGTTGAT TGTACGTCTT TACCTTTCTG CCTGACTGTT      50
   TACGACAAC TACGAAAGCG TAGAACAACA TTGCCAAGGC TCACGGTGGT      100
   TACTCTGTCT TCACTGGTGT CCGTGAACGT ACTCGTGAGG GTAACGATTT      150
   GTACCAGGAA ATGCAGGAAA CTGGTGTCTAT TCAGCTCGAG GGTGAATCCA      200
   AGGTCGCCCT CGTGTTCGGT CAGATGAACG AGCCCCCGG TGCCCGTGCC      250
   CGTGTCTGCTC TTA CTGGTTT GACCATTGCC GAGTACTTCC GTGACGAGGA      300
   AGGTCAGGAC GTGCTTCTCT TCATTGACAA CATTTTCCGT TTCACTCAGG      350
40 CCGGTTCTGA GGTGTCTGCC CTTCTGGGTC GTATCCCCCTC TGCCGTCGGT      400
   TACCAGCCCA CCCTTGCCGT CGACATGGGT ATCATGCAGG AGCGTATTAC      450
   CACCACCACC AAGGGTTCCA TCACCTCCGT C      481

```

45

2) INFORMATION FOR SEQ ID NO: 893

```

50 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1208 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

```

55 (ii) MOLECULE TYPE: Genomic DNA

```

```

    (vi) ORIGINAL SOURCE:

```

```

    (A) ORGANISM: Sporothrix schenckii
    (B) STRAIN: ATCC 14285

```

```

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893

```

	CTCGTCCGTG	GTGCTAAGGC	CACTGACACT	GGTTSCCCCA	TTACCATCCS	50
	CGTCGGCCCC	GGTACCCTCG	GTGCGATCAT	GAACGTCACC	GGTGACCCGA	100
	TCGACGAGCG	CGGTCCCATC	AAGACCGACA	AGTTCGGTCC	CATCCACGCT	150
5	GAGGCTCCCG	AGTTCGTTGA	CCAGTCGACC	ACCGCTGAGG	TTCTCGTGAC	200
	TGGTATCAAG	GTCGTCGATC	TGCTTGCTCC	CTACGCCCGT	GGTGGTAAGA	250
	TTGGTCTGTT	TGGCGGTGCC	GGTGTGGCA	AGACCGTGTT	CATCCAGGAG	300
	CTCATCAACA	ACATCGCCAA	GGCCACGCGT	GGTTACTCCG	TCTTCACCGG	350
	TGTCGGCGAG	CGTACCCGTG	AGGGTAACGA	TCTGTACCAC	GAAATGCAGG	400
10	AGACCTCTGT	CATTACAGCTT	GACGGTGACT	CCAAGGTCGC	CCTGGTGTTT	450
	GGTCAGATGA	ACGAGCCCCC	TGGTGCTCGT	GCCCGTGTCG	CCTTGACCGG	500
	TTTGACTGTC	GCTGAGTACT	TCCGTGACGA	GGAGGGCCAG	GATGGTATGT	550
	TTTGAATTAT	TTCTTGTGTC	TACAGTTCCA	AATCGAAGAA	TACTAACTT	600
	GTCAGTGCTT	CTCTTCATCG	ACAACATTTT	CCGCTTCACC	CAGGCCGGTT	650
15	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATT	CCTCCGCTGT	CGGTTACCAG	700
	CCCACGCTCG	CCGTGGACAT	GGGTCTGATG	CAGGAGCGTA	TTACCACCAC	750
	CCGCAAGGGC	TCAATTACCT	CCGTCCAGGC	CGTCTACGTG	CCCGCTGACG	800
	ATCTGACGGA	TCCCGCCCCC	GCCACCACCT	TCGCCCATCT	GGACGCCACC	850
	ACTGTGCTGT	CCCGAGGTAT	CTCTGAGCTG	GGTATCTACC	CCGCTGTCTGA	900
20	CCCCCTCGAC	TCCAAGTCGC	GTATGCTGGA	CCCCCGTATT	GTCGGTGACG	950
	ACCACTACGA	GACCGCCACT	CGCGTCCAGT	AGATCCTCCA	AGAGTACAAG	1000
	TCGCTGCAGG	ACATCATCGC	CATTCTGGGT	ATGGACGAGC	TGTCTGAGGC	1050
	CGACAAGCTT	ACAGTCGAGC	GTGCTCGTAA	GATCCAGCGT	TTCCTGAGCC	1100
	AGCCGTTTAC	GGTCGCGCAG	GTCTTCACTG	GTATCGAAGG	CCAGCTGGTC	1150
25	GATCTGAAGG	ACACTATCGC	TTCGTTCAAG	GCTATCCTGA	GCGGTGAGGG	1200
	TGACAGCC					1208

30 2) INFORMATION FOR SEQ ID NO: 894

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894

45	TTCAGGA	ACT	TATTGTA	AAGC	CGCCCTCTTT	ATGCATTGAG	GGTGAATAAG	50
	AAGGCTG	ACA	GGTAATA	GAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	100
	CGTGTTCA	CT	GGTGTCG	GGTG	AGCGTACCCG	TGAAGGAAAC	GATCTGTACC	150
	ATGAAATG	CA	GGAAACCC	CGC	GTCATCCAGC	TTGATGGCGA	GTCTAAGGTC	200
50	GCCCTTGT	TGT	TCGGTCAG	AT	GAACGAGCCC	CCTGGAGCCC	GTGCCCCTGT	250
	CGCTCTTA	CT	GGTCTTACC	G	TTGCCGAATA	CTTCCGTGAC	GAGGAGGGCC	300
	AAGATGGT	AC	GCCTTTTT	TAC	TCTTCTTATT	CTTCGGGTCTG	GACTACAGAA	350
	CTAACCTG	CT	CCAGTGCTT	C	TCTTCATTGA	TAACATTTTC	CGTTTCACAC	400
	AAGCCGGT	TC	TGAGGTGT	CT	GCCTTGCTTG	GACGTATTCC	CTCTGCCGTC	450
55	GGTTACCAG	C	CCACTCTCG	C	CGTCGACATG	GGTGGTATGC	AGGAACGTAT	500
	CACAACCAC	C	AACAAGGGT	T	CCATTACTTC	CGTG		534

60 2) INFORMATION FOR SEQ ID NO: 895

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895

15	CAAGGCTCAC	GGTGGTTACT	CCGTCTTCAC	TGGTGTCGGT	GAGCGTACCC	50
	GTGAGGGTAA	CGATCTGTAC	CACGAAATGC	AGGAGACCTC	GGTCATTACG	100
	CTCGAGGGCG	AGTCTAAGGT	GGCCCTGGTC	TTTGGTCAGA	TGAACGAGCC	150
	CCCGGGTGCT	CGTGCCCGTG	TCGCTCTTAC	TGGTCTTACC	GTCGCCGAGT	200
20	ACTTCCGTGA	CCAGGAGGGT	CAGGATGGTT	AGTTCTCGTC	CACTCATGCC	250
	GAAACATGTG	CGTGTTCCGA	GGCTAATCAA	CGTGCCAGTG	CTGCTTTTCA	300
	TCGACAACAT	TTTCCGATTC	ACCCAGGCCG	GTTCCGAGGT	GTCTGCCCTG	350
	CTGGGTCGTA	TCCCCTCTGC	CGTCGGTTAC	CAGCCCACCC	TCGCCGTCGA	400
25	CATGGGTGGC	ATGCAGGAGC	GTATCACCAC	CACCAAGAAG	GGCTCTAT	448

2) INFORMATION FOR SEQ ID NO: 896

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896

45	ATTCAGGAGC	TGATTGTAAG	TTGCCAATCC	ATGAACTGGA	GATTTGGTGT	50
	GACCCATAGA	ACTAACAAAT	TATTTAGAAC	AACATCGCCA	AGGCTCACGG	100
	TGGTTACTCC	GTCTTCTGTG	GTGTCGGTGA	GCGTACTCGT	GAGGGTAACG	150
	ATCTGTACCA	CGAAATGCAG	GAGACTGGTG	TCATCCAGCT	CGAGGGTGAC	200
	TCCAAGGTCG	CTCTGGTCTT	CGGTCAGATG	AACGAGCCCC	CGGGTGCCCC	250
	TGCCCCGTGTC	GCCCTTACCG	GTCTGACCAT	TGCCGAGTAC	TTCCGTGACG	300
50	AGGAGGGTCA	GGACGTGCTG	CTCTTCATTG	ACAACATTTT	CCGTTTCACC	350
	CAGGCCGGTT	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATCC	CCTCTGCCGT	400
	CGGTTACCAG	CCCACTCTGG	CCGTCGACAT	GGGTGGTATG	CAGGAGCGTA	450
55	TTACCACCAC	CACCAAGGGT	TCCATTACCT	CCG		483

2) INFORMATION FOR SEQ ID NO: 897

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
15	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
20	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAACCTGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTY	CAACAAGCCC	600
25	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCGGC	CGTGTGAGAG	CCGGTATCAT	CAAGCCCGGC	ATGGTTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCGAAG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
30	CCAAGAACAG	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
35	CGAGTCCTTC	ACTGACTACC	CCCC			1124

2) INFORMATION FOR SEQ ID NO: 898

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1363 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*
 (D) STRAIN: WSA-214

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898

55	CTCAAGGCTG	AGCGTGAGCG	TGGTATCACC	ATCGATATTG	CTCTCTGGAA	50
	GTTCCAGACT	GCCAAGTACG	AGGTTACCGT	CATTGACGCC	CCCGGTCACC	100
	GTGATTTTCA	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	CGATTGCGCT	150
	ATTCTCATCA	TTGCCCTCTG	TACTGGTGAA	TTCGAGGCTG	GTATCTCCAA	200
	GGATGGCCAG	ACTCGTGAGC	ACGCTCTTTT	GGCTTTTACC	CTCGGTGTCC	250
60	GTCAGCTCAT	TGTTGCCCTC	AACAAGATGG	ACACTTGCAA	GTGGTCTCAG	300


```

GGTGAGTACT CGTACCTGCG TTTGGCCTTG AATATCTTAC TAATGCACCA 350
TAGATCGTTA CAACGAAATT GTCAAGGAGA CTTCCAACCTT CATCAAGAAG 400
GTCGGATACA ACCCTAAGAA CGTTCCCTTTT GTTCCTATCT CCGGTTTCAA 450
CGGTGACAAC ATGCTTGAGC CCTCCCCCAA CTGCCCTTGG TACAAGGGTT 500
5 GGGAGAAGGA GACCAAGGCC GGTAAGGTCA CTGGTAAGAC CCTCCTCGAG 550
GCCATCGACG CCATTGAGCC CCCTACCCGT CCCGCCAACA AGGTTAGTCC 600
CTCCTCGACT ACTCAAACCC TCCTCATAAG TTCATGATTA CGACTCGTTC 650
ACAGCCCCTC CGTCTTCCCC TCCAGGATGT CTACAAGATC GGTGGTATTG 700
GAACGGTTCC CGTCGGTCGT GTTGAGACTG GTACCATCGT TCCTGGTATG 750
10 GTTGTACACT TGTAAGTCAC TCTCCTCGCT TATCCTACCT GAAATCATCA 800
TGTGCTAACT TGACACTCAG CGCTCCCGCC AACGTCACCA CTGAAGTCAA 850
GAGTGTTGAA ATGCACCACC AGCAGCTCAC TGCCGGTCAG CCCGGTGACA 900
ACGTTGGTTT CAACGTGAAG AACGTCTCCG TCAAGGAAAT CCGTCGTGGT 950
AACGTTGCTG GTGACAGCAA GAACGACCCC CCTGCCGGTG CTGCCCTCCTT 1000
15 CAACGCCCAG GTCATCGTCC TCAACCACCC CGGTCAGGTC GGTGCTGGTT 1050
ACGCCCCAGT CCTCGATTGC CACACTGCCC ACATTGCTTG CAAGTTCGCT 1100
GAGCTCCTCG AGAAGATTGA CCGTCGTACC GGAAAGTCTG TTGAGGACCA 1150
CCCCAAGTTC ATCAAGTCCG GTGACGCTGC CATCGTCAAG ATGATTCCTT 1200
CCAAGCCCAT GTGTGTTGAG GCTTTCACCG AGTACCCTCC TCTCGGTCGT 1250
20 TTCGCCGTTT GCGAGTAAGT TTTATCTCCG TTGTCTATTT TCCATCCTTC 1300
CCTTCTCCTC CGTCTTCCAT ATATATTTTT TCAGTTATAT GTGACTAACC 1350
ACAAATCACG GGA 1363

```

25

2) INFORMATION FOR SEQ ID NO: 899

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 1147 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Piedraia hortai
    (B) STRAIN: ATCC 24292

```

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899

```

CAAGCTGAAA GCCGAGCGTG AGCGTGGTAT CACTATCGAC ATTGCCCTCT 50
GGAAGTTCGA GACTCCCAAG TACTATGTCA CCGTCATTGG TACGTCGCAT 100
TATCTCACTC CTCACAGAAG CACGCTCCTA ACATCACACA GACGCTCCCG 150
45 GTCACCGTGA TTTCATCAAG AACATGATCA CTGGTACCTC CCAGGCCGAC 200
TGCGCTATCC TCATTATCGC TGCCGGTACT GGTGAGTTCG AGGCTGGTAT 250
CTCCAAGGAT GGCCAGACTC GTGAGCACGC CCTGCTCGCC TACACCCTCG 300
GTGTGCGTCA GCTCATCGTC GCCATCAACA AGATGGACAC CACCAAGTGG 350
TCTGAGGCCG GTTACCAGGA GATCATCAAG GAGACCTCCA ACTTCATCAA 400
50 GAAGGTCGGC TACAACCCCA AGACCGTCGC TTTCGTCCCC ATCTCTGGCT 450
TCAACGGCGA CAACATGCTT GCCCCCTCCA CCAACTGCCC CTGGTACAAG 500
GGATGGGAGC GTGAGGTCAA GGGCAACAAG CAGACCGGCA AGACCCTCCT 550
CGAGGCCATT GACGGCATTG AGCCCCCAA GCGTCCCTTC GACAAGCCCC 600
TCCGTCTTCC TCTCCAGGAT GTTTACAAGA TCGGTGGTAT CGGAAGTGT 650
55 CCTGTCGGCC GTATCGAGAC TGGTGTCTTC AAGCCCGGTA TGGTCGTTAC 700
CTTCGCTCCC GCCAACGTCA CCACTGAAGT CAAGTCCGTC GAGATGCACC 750
ACGAGCAGCT CACTGAGGGT CTTCCCGGTG ACAACGTCGG TTTCAACGTG 800
AAGAAGCTTT CCGTCAAGGA CATCCGCGGT GGTAACGTTG CCAGTGACTC 850
CAAGAACGAC CCCGCTCTGG GTGCCGCTTC TTTCGACGCC CAGGTCATCG 900
60 TCCTCAACCA CCCCGGTCAG GTCGGTGCTG GTTACGCCCC GGTCCCTCGAT 950

```

TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGATCA	AGGAGAAGAT	1000
CGACCGCCGT	ACCGGCAAGT	CTGTTGAGGA	CGCCCCCAAG	TTCATCAAGT	1050
CTGGTGACTC	TGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTT	1100
GAGGCTTTCA	CCGACTACCC	TCCTCTGGGC	CGTTTCGCCG	TCCGTGA	1147

5

2) INFORMATION FOR SEQ ID NO: 900

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900

CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
GTTCGAGACT	CCCAAGTACT	ATGTCACCGT	CATTGGTACG	TCGACTCGCG	100
CGAGACTGGT	CGCAATTTCC	ACGTCGCTAA	CGTGCTTGAA	CAGACGCTCC	150
CGGCCACCGT	GACTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCTG	200
ACTGCGCTAT	CCTCATTATC	GCTGCCGGCA	CTGGTGAGTT	CGAGGCTGGT	250
ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	300
CGGTGTTAAG	CAGCTCATCG	TCGCTATCAA	CAAGATGGAC	ACCACCAAGT	350
GGTGTGAGGC	CCGTTTCCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	400
AAGAAGGTCG	GCTACAACCC	CAAGACCGTC	GCTTTCGTCC	CCATCTCTGG	450
TTTCCACGGC	GACAACATGC	TTTCCCCCTC	CACCAACTGC	CCCTGGTACA	500
AGGGCTGGGA	GAAGGAGACC	AAGGCTGGCA	AGTCCACCGG	CAAGACCCTC	550
CTTGAGGCCA	TCGACTCCAT	CGAGCCCCCC	AAGCGCCCCA	GCGACAAGCC	600
CCTCCGCTTT	CCCCTTTCAGG	ATGTGTACAA	GATCGGCGGT	ATCGGCACAG	650
TCCCTGTTCG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCGG	CATGGTCGTG	700
ACCTTCGCTC	CTTCCAACGT	CACCACCGAA	GTCAAGTCCG	TTGAGATGCA	750
CCACGAGCAG	CTCTCCGAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
TCAAGAACGT	CTCCGTCAAG	GAGATCCGTC	GTGGCAACGT	CGCCGGTGAC	850
TCCAAGAACG	ACCCCCCTCT	GGGTGCCGCT	TCTTTCGATG	CCCAGGTCAT	900
CGTCCTCAAC	CACCCCGGCC	AGGTCGGTGC	TGGCTACGCC	CCCGTCCTCG	950
ACTGCCACAC	CGCCCACATT	GCCTGCAAGT	TCGCCGAGAT	CAAGGAGAAG	1000
ATCGACCGCC	GTACCGGCAA	GTCTGTGCGAG	TCCGCCCCCA	AGTTCATCAA	1050
GTCTGGCGAC	TCTGCCATCG	TCAAGATGAT	TCCCTCCAAG	CCCATGTGCG	1100
TTGAGGCTTT	CACCGACTAC	CCTCCTCTGG	GCCGCTTCGC	CGTCCGTGAC	1150

50 2) INFORMATION FOR SEQ ID NO: 901

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 55
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 60

(A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901

5	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTTTCTG	GTTTTCGAGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
10	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250
	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
	TATTGGCACT	GTTCTGTGCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
15	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAA	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
	GCCCAGGTCA	TCGTCTCTCA	CCACCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCCT	CTGTCCCTCA	CTGCCACAT	TGCCTGCAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACCGGAA	AGTCTGTTGA	GAACAACCCC	700
20	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
	G					751

25 2) INFORMATION FOR SEQ ID NO: 902

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1056 bases
	(B) TYPE: Nucleic acid
30	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: ATCC 7968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902

40	CGTGAGCGCG	GTATCACCAT	CGATATTGCT	CTGTGGAAGT	TCGAGACCCC	50
	CAAGTACTAC	GTCACCGTCA	TTGACGCCCC	CGGTCATCGC	GATTTTCATCA	100
	AGAACATGAT	CACTGGTACC	TCGCAGGCCG	ACTGCGCCAT	TCTCATCATT	150
	GCCGCTGGTA	CTGGTGAGTT	CGAGGCTGGT	ATCTCCAAGG	ATGGCCAGAC	200
45	TCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	GGGTGTGCGG	CAGCTGATCG	250
	TCGCCATCAA	CAAGATGGAC	ACGGCCAAGT	GGGCTGAGGC	TCGTTACCAG	300
	GAGATCATCA	AGGAGACCTC	CAACTTCATC	AAGAAGGTCG	GCTACAACCC	350
	CAAGACTGTT	GCCTTCGTCC	CCATCTCGGG	CTTCCACGGC	GACAACATGC	400
	TTACTCCCTC	GACCAACTGC	CCCTGGTACA	AGGGCTGGGA	GAAGGAGGGC	450
50	AAGAGCGGCA	AGGTTACCGG	TAAGACTCTG	CTGGACGCCA	TTGACGCCGT	500
	CGAGCCCCCC	AAGCGCCCCA	CGGACAAGCC	CCTGCGTCTG	CCCCTCCAGG	550
	ATGTCTACAA	GATCGGCGGT	ATCGGCACTG	TCCCTGTCTG	CCGTATCGAG	600
	ACTGGTGTCC	TGAAGCCCGG	CATGGTCTGC	ACCTTTGCC	CGTCCAACGT	650
	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	CCACGAGCAG	CTTGTTGAGG	700
55	GTGTTCCCGG	CGACAACGTC	GGCTTCAACG	TCAAGAACGT	CTCCGTCAAG	750
	GAGATCCGTC	GTGGCAACGT	TGCCGGTGAC	TCCAAGAACG	ACCCCCCCTC	800
	GGGCGCCGCC	ACCTTCAACG	CCCAGGTCAT	TGTCCTGAAC	CACCCCGGCC	850
	AGGTCGGCAA	CGGCTACGCC	CGGTTCTGG	ACTGCCACAC	CGCCACATT	900
	GCCTGCAAGT	TCACCGAGAT	CCTTGAGAAG	ATCGACCGCC	GTACCGGCAA	950
60	GTCGGTTGAG	AACAACCCCA	AGTTCATCAA	GTCGGGTGAC	GCCGCCATTG	1000

TCAAGCTGAC GCCCTCGAAG CCCATGTGCG TTGAGGCCTT CACTGACTAC 1050
 CCCCCT 1056

5

2) INFORMATION FOR SEQ ID NO: 903

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1366 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903

CAAGGCTGAG	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	50
TCCAGACTGC	CAAGTACGAG	GTTACCGTCA	TTGACGCCCC	CGGTCACCGT	100
GATTTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCCG	ATTGCGCTAT	150
TCTCATCATT	GCCTCTGGTA	CTGGTGAATT	CGAGGCTGGT	ATCTCCAAGG	200
ATGGCCAGAC	TCGTGAGCAC	GCTCTTTTGG	CTTTCACCCT	CGGTGTCCGT	250
CAGCTCATTG	TTGCCCTCAA	CAAGATGGAC	ACTTGCAAGT	GGTCTCAGGG	300
TGAGTACTCG	TACCTGCGTT	TGGCCTTGAA	TATCTTACTA	ATGCACCATA	350
GATCGTTACA	ACGAAATTGT	CAAGGAGACT	TCCAACCTCA	TCAAGAAGGT	400
CGGATACAAC	CCTAAGAACG	TTCTTTTCGT	TCCTATCTCC	GGTTTCAACG	450
GTGACAACAT	GCTTGAGCCC	TCCCCCAACT	GCCCCCTGGT	CAAGGGTTGG	500
GAGAAGGAGA	CCAAGGCCGG	TAAGGTCACT	GGTAAGACCC	TCCTCGAGGC	550
CATCGACGCC	ATTGAGCCCC	CTACCCGTCC	CGCCAACAAG	GTTAGTCCCT	600
CCTCGACTAC	TCAAACCCTC	CTCATAAGTT	CAGATTACTG	ACTCGTTTAC	650
AGCCCCCTCCG	TCTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATTGGA	700
ACGGTTCCCCG	TCGGTCGTGT	TGAGACTGGT	ACCATCGTTC	CTGGTATGGT	750
TGTCACCTTG	TAAGTCACTC	TCCTCGCTTA	TCCTACCTGA	AATCATCATG	800
TGCTAACCTTG	ACACTCAGCG	CTCCCCGCCAA	CGTCACCACT	GAAGTCAAGA	850
GTGTTGAAAT	GCACCACCAG	CAGCTCACTG	CCGGTCAGCC	CGGTGACAAC	900
GTTGGTTTCA	ACGTGAAGAA	CGTCTCCGTC	AAGGAAATCC	GTCGTGGTAA	950
CGTTGCTGGT	GACAGCAAGA	ACGACCCCCC	TGCCGGTGCT	GCCTCCTTCA	1000
ACGCCCAGGT	CATCGTCCTC	AACCACCCCCG	GTCAGGTCGG	TGCTGGTTAC	1050
GCCCCAGTCC	TCGATTGCCA	CACTGCCCCAC	ATTGCTTGCA	AGTTCGCTGA	1100
GCTCCTCGAG	AAGATTGACC	GTCGTACCGG	AAAGTCTGTT	GAGGACCACC	1150
CCAAGTTCAT	CAAGTCCGGT	GACGCTGCCA	TCGTCAAGAT	GATTCTTCC	1200
AAGCCCATGT	GTGTTGAGGC	TTTCACCGAG	TACCCTCCTC	TCGGTCGTTT	1250
CGCCGTTCGC	GAGTAAGTTT	TATCTCCGTT	GTCTATTTTC	CATCCTTCCC	1300
TTCTCCTCCG	TCTTCCATAT	ATATTTTTC	AGTTATATGT	GACTAACCAC	1350
AAATCACGGG	AATAGC				1366

50

2) INFORMATION FOR SEQ ID NO: 904

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904

	CTATTATCGT	TGTTGCCGCT	TCCGACGGTC	AAATGCCCCA	GA	50
10	CATCTGCTGC	TCGCCCCGCA	GGTCGGTGTC	CAGAAGATCG	TTGTCTTCGT	100
	CAACAAGGTC	GATGCTGTTG	AGGACAAGGA	GATGTTGGAG	CTCGTCGAGA	150
	TGGAGATGCG	CGAATTGCTC	AGCAGCTACG	GCTTCGAGGG	CGACGAGACT	200
	CCCATCATCA	TGGGATCTGC	CCTCTGCGCC	ATTGAGGGCC	GCGAACCTGA	250
	GATTGGTGTC	AACCGAATTG	ATGAGCTGCT	CGAGGCCGTT	GATACTTGGA	300
15	TCCCCACCCC	TCAGCGTGAG	ACCGACAAGC	CTTTCCTCAT	GGCCGTCGAG	350
	GATGTCTTCT	CCATTGCTGG	TCGTGGCACT	GTCGTCTCTG	GCCGTGTCGA	400
	GCGAGGTATC	CTGAAGCGCG	ATGCTGAAGT	TGAGCTCGTC	GGCAAGGGCA	450
	CCGCCCCCAT	CAAGACCAAG	GTTACCGATA	TCGAGACCTT	CAAGAAGTCC	500
	TGCGAGGAGT	CTCGCGCTGG	TGACAACTCC	GGTCTCCTTC	TTCGTGGTGT	550
20	CAAGCGTGAT	GAAGTCCGCC	GTGGTATGGT	CGTTTCCGTC	CCTGGACAGG	600
	TCAAGGCGCA	CAAGAAGTTC	CTTGTCTCCA	TGTACGTGTT	GAGCAAGGAG	650
	GAAGGTGGTC	GTCACACTGG	CTTCGGTGAG	AACTACAGGC	CGCAAATGTT	700
	CATCCGCACT	GCCGACGAGT	CGTGTGCCCT	GTA	CTGGGCA	750
	AGGACGCCCC	TGACAAGCTT	GTTATGCCCC	GTGACAACGT	CGAGATGGTT	800
25	TGCGAGCTCC	ATGCACCACA	CGTCTTGAG	CCTGGTCAAC	G	841

2) INFORMATION FOR SEQ ID NO: 905

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 967 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus niger*

(B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905

45	CGGTGCTATC	ATTGTCGTCG	CCGCCTCCGA	CGGTCAGATG	TACGTTAACC	50
	TTAAAAGAAT	AACTCTCCTT	CAGTATATAT	GCTTACACTG	GCGATCAACA	100
	GGCCCCAGAC	TCGTGAGCAC	TTGCTGCTTG	CTCGTCAGGT	CGGTGTCCAG	150
	AAGATCGTTG	TCTTCGTCAA	CAAGGTCGAT	GCTATCGATG	ACCCCGAGAT	200
	GCTGGAGCTC	GTTGAGCTGG	AAATGCGCGA	GCTTCTCAGC	ACCTACGGAT	250
50	TCGAGGGTGA	GGAGACCCCC	ATCGTCTTCG	GCTCTGCTCT	CTGCGCCATT	300
	GAGGACCGCC	GCCCCGACAT	CGGTACCGAG	CGTATCGACG	CTCTCCTCGA	350
	GGCCGTTGAC	ACCTGGATCC	CCACTCCCCA	GCGTGACCTT	GACAAGCCTT	400
	TCTTGATGTC	CATTGAGGAA	GTTTTCTCCA	TCCCCGGTCG	TGGTACCGTC	450
	GCCTCCGGCC	GTGTCGAGCG	TGGTCTCCTG	AAGCGTGATA	GCGAGGTTGA	500
55	GATCATCGGT	ACCACCAACG	AGGTCATCAA	GACCAAGGTT	ACCGACATTG	550
	AGACCTTCAA	GAAGTCCTGC	TCCGAGTCCC	GCGCCGGTGA	CAACTCCGGT	600
	CTCCTGCTCC	GTGGTGTCGG	CCGTGAGGAT	CTCCGCCCGTG	GTATGGTCAT	650
	TGCCGCTCCT	GGCAGCGCCA	AGGCCAACAC	CAAGTTCATG	GTCTCCATGT	700
	ACGTCCTGAC	CGAGGCTGAR	GGTGGTCGCC	GTACCGGTTT	CGGTGTCCAG	750
60	TACCGTCCCC	AGCTGTTTCAT	CCGCACTGCC	GGTAAGTAAA	ATTGCATTCT	800

ATTCCGCTAC	TAGGGAACCA	TCTCTAATTC	TATTTGCTAC	AGATGAGGCT	850
GCTGAGTTCA	GCTTCCCCGA	CGGAGACCAG	TCCCGCCGTA	TCATGCCCCG	900
TGACAAACGTC	GAGATGATCG	TCAAGACCCA	CCGCCCCGTC	GCCGCCGAGG	950
CCGGTCAGCG	CTTCAAC				967

5

2) INFORMATION FOR SEQ ID NO: 906

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bipolaris hawaiiensis*
 - (B) STRAIN: ATCC 26067
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906

TGGTGCTATT	ATTGTTGTTG	CCGCTTCCGA	CGGTCAAATG	CCCCAGACTC	50
GTGAGCATCT	GCTGCTCGCC	CGTCAGGTCG	GTGTTTCAGAA	GATCGTTGTC	100
TTCGTTAACA	AGGTCGACGC	TGTCGAGGAC	AAGGAGATGT	TGGAGCTTGT	150
CGAGATGGAG	ATGCGCGAAC	TGCTCAGCAG	CTATGGCTTC	GAGGGCGACG	200
AGACCCCTAT	CATCATGGGT	TCTGCTCTCT	GCGCCATTGA	AGGCCGTCAA	250
CCCGACATTG	GTGTCGAACG	AATTGACGAG	CTGCTCGAGG	CTGTTGATAC	300
30 TTGGATTCCC	ACCCCTCAGC	GTGAGACCGA	AAAGCCTTTC	CTCATGGCCG	350
TCGAGGATGT	CTTCTCCATT	GCTGGTCGTG	GTACCGTCGT	CTCTGGCCGT	400
GTGGAACGAG	GTATCCTGAA	GCGCGATGCT	GAAGTTGAGC	TTGTGGGCAA	450
GGGCAGCGCA	CCCATCAAGA	CCAAGGTTAC	CGATATCGAG	ACCTTCAAGA	500
AGTCTTGCGA	GGAGTCCCGC	GCTGGTGACA	ACTCCGGTCT	CCTTCTTCGT	550
35 GGTGTTAAGC	GTGATGAAGT	CCGCCGTGGT	ATGGTCGTTT	CCGTCCCTGG	600
ACAGGTTAAG	GCGCACAAGA	AGTTCCTTGT	CTCCATGTAT	GTGCTGAGCA	650
AGGAGGAAGG	TGGCCGACAC	ACTGGCTTCG	GTGAGAATA	CAGGCCGCAA	700
ATGTTCATCC	GCACTGCCGA	CGAGTCGTGT	GCCCTGTACT	GGCCAGAAGG	750
CACCGAGGAT	GCCCACGACA	AGCTTGTCAT	GCCCGGTGAC	AACGTCGAGA	800
40 TGGTTTGCGA	GCTCCATGCA	CCACACGTCT	TGGAGACTGG	TCAGCGCTTC	850
AA					852

45 2) INFORMATION FOR SEQ ID NO: 907

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 966 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Aspergillus flavus*
 - (B) STRAIN: ATCC 26947
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907
- 60

```

GGTGCTATTG TTGTCGTTGC TGCTTCGGAT GGTTCATGATG TATGGACAGG      50
CCCTTTGCTA CTGAATGGTT TCAAGATCTC GCGCTTACAC GTATTATAAT      100
AGGCCCCAGA CCCGGGAGCA CTTGCTGCTT GCCCGTCAGG TCGGTGTCCA      150
GAAGATCGTC GTTTTTGTCA ACAAGATTGA TGCCGTTGAG GACCCTGAGA      200
5  TGTGAGGCT TGTCGAGTTG GAAATGCGCG AGCTCCTTAG CAGCTACGGC      250
TTCGAGGGCG AAGAGACTCC CATCATCTTC GGTCTGCTC TGTGTGCTTT      300
GGAGGACCGT CGCCCCGACA TTGGTGCCGA GCGTATCGAC GAGCTCATGA      350
AGGCCGTTGA CACCTGGATC CCTACCCCTC AGCGTGATCT TGACAAGCCT      400
10 TTCTCATGT CTGTCGAGGA AGTCTTCTCC ATCGCCGGTC GTGGTACCGT      450
TGCTCCGGC CGTGTCAAC GTGGTATCCT GAAGAAGGAC AGCGAAGTCG      500
AGATCATCGG AGGTAGCTTC GATGCTACCA AGACCAAGGT CACCGACATT      550
GAGACCTTCA AGAAGTCTTG TGACGAGTCC CGCGCTGGTG ACAACTCTGG      600
CTTGCTTCTC CGTGGTATCC GTCGTGAAGA CGTCCGCCGC GGAATGATCA      650
TTGCTGCTCC TGGCAGCACC AAGGCCACG ACCAGTTCTT GGTGTCCATG      700
15 TACGTTCTCA CTGAGGCTGA GGGTGGTCGT CGTACTGGCT TCGGCTCCAA      750
CTACCGCCCC CAGGTGTTCTG TTCGCACTGC TGGTAAGTCA AGCCTTTTGC      800
TCACTTAACG GTATTGATTA AGTTCTAACT GTTGATCCT AGATGAGGCT      850
GCTGACCTCA GCTTCCCCGA CGGTGATGAG TCCCGGAGGG TGATGCCTGG      900
TGACAACGTC GAGATGGTCC TCAAGACTCA CCGCCCATTT GCTGCTGAGG      950
20 CTGGCCAGCG CTTCAA      966

```

2) INFORMATION FOR SEQ ID NO: 908

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 845 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
35 (A) ORGANISM: Alternaria alternata
    (B) STRAIN: ATCC 62099

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908

```

40 GGTGCTATCA TCGTCGTTGC TGCTTCCGAT GGTTCAGATGC CCCAGACCCG      50
TGAGCACTTG CTGCTCGCCC GTCAGGTCGG TGTTTCAAG ATCGTTGTCT      100
TCGTCAACAA GGTGATGCT GTCGAAGACC CGGAGATGTT GGAACCTCGTC      150
GAGATGGAGA TGCGTGAGTT ACTCACCAGC TACGGCTTCG AGGGCGACGA      200
GACACCCATC ATCATGGGTT CCGCTCTATG CGCCATCGAG GGCCGCCAGC      250
45 CCGAGATCGG TGTTACCAAG GTCGACGAG TAATGGACGC TGTCGACTCA      300
TGATATCCCA CCCCTCAGCG TGAGACCGAG AAGCCTTTCC TCATGGCTGT      350
TGAGGATGTC TTCTCGATTG CTGGACGTGG TACCGTCGTT TCGGGCCGTG      400
TCGAGCGCGG TATCTTGAAG CGTGACGCTG AAGTCGAGCT TGTCGCAAG      450
GGCACCAGCG CAATCAAGAC CAAGGTCACT GATATTGAGA CCTTCAAGAA      500
50 GTCGTGCGAG GAGTCGCGCG CGGGTGATAA CTCCGGTCTT CTCCTCCGTG      550
GTGTCAAGCG TGATGACGTT CGCCGCGGTA TGTTGTTTC CGTTCCCGGA      600
CAAGTCAAGG CTCACAAGAA GTTCCTTGTC TCCATGTACG TTCTAAGCAA      650
AGAGGAGGGT GGTGCTCACA CCGGCTTCGG CGAGAACTAC AGGCCGCAA      700
TGTTTCATCCG AACTGCCGAT GAATCCTGCG CACTTCACTT CCCAGAGGGT      750
55 ACCGAGGATG CGCACGACAA GCTAGTTATG CCCGGTGACA ACGTCGAGAT      800
GGTCTGCGAA CTCCACCAGC CCCACGTTCT AGAGACCGGT CAGCG      845

```

60 2) INFORMATION FOR SEQ ID NO: 909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909

```

15  CGCTGTTGTT  GTCGTCGCTG  CTTCTGATGG  TCAAATGTAA  CATATCCACG      50
    AGCTGCCAAT  TATGGACACT  GCTGATAAGA  ATAGGCCCCA  AACCCGTGAG      100
    CACTTGCTCC  TCGCCCGTCA  GGTCGGTGTT  CAAAAGATCG  TCGTCTTCGT      150
    CAACAAGGTT  GATGCCGTCG  AGGACCCCGA  GATGTTGGAA  CTTGTCTGAAT      200
20  TGGAAATGCG  TGAAGTCTTG  ACCACCTACG  GTTTCGAGGG  TGAAGAGACC      250
    CCTATCATTT  TCGGATCCGC  TCTTTGCGCC  TTGGAAGGCC  GCAAGCCCGA      300
    GATTGGCGAA  CAGAAGATTG  ACGAGCTCAT  GAACGCCGTT  GATACCTGGA      350
    TCCCCACCCC  CCAGCGTGAC  CTTGACAAGC  CCTTCTTGAT  GTCCGTTGAG      400
    GAAGTTTTCT  CCATCTCTGG  TCGTGGTACC  GTTGCATCTG  GTCGTGTTGA      450
25  GCGTGGTATT  TTGCGCAAGG  ATTCTGAGGT  TGAGATTATC  GGATACCAGA      500
    AGAACCCCTAT  CAAGACCAAG  GTTACCGACA  TTGAGACCTT  CAAGAAGTCT      550
    TGCGATGAAT  CTCGTGCTGG  TGACAACTCT  GGCTTGCTTC  TCCGTGGTAT      600
    CAAGCGTGAG  GACATTTCGT  GTGGTATGGT  TATCGCTGCT  CCTGGAACCA      650
    CCAAGGCTCA  TGACAACTTC  TTGGTCTCCA  TGTATGTCTT  GACTGAGGCT      700
30  GAAGGTGGTC  GTCGTACTGG  ATTCGGCGCC  AACTACCGTC  CTCAAGCTTT      750
    CATCCGTACT  GCCGTATGT  TCCCTTTCAA  AGTCAATTAA  TGAGCGATTT      800
    GCTAACGAGT  TATAGATGAG  GCTGCTACTC  TCAGCTTCCC  CGGTGACGAT      850
    CAGTCCAAGC  AGGTCATGCC  CGGTGACAAC  GTTGAGATGA  TCTTGAAGAC      900
    ACACCGTCCC  GTTGCCGCCG  AAGCTGGTCA  G              931
35

```

2) INFORMATION FOR SEQ ID NO: 910

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910

```

55  CGCTGTTGTT  GTCGTCGCTG  CTTCTGATGG  TCAAATGTAA  CATATCCACG      50
    AGCTGCCAAT  TATGGACACT  GCTGATAAGA  ATAGGCCCCA  AACCCGTGAG      100
    CACTTGCTCC  TCGCCCGTCA  GGTCGGTGTT  CAAAAGATCG  TCGTCTTCGT      150
    CAACAAGGTT  GATGCCGTCG  AGGACCCCGA  GATGTTGGAA  CTTGTCTGAAT      200
    TGGAAATGCG  TGAAGTCTTG  ACCACCTACG  GTTTCGAGGG  TGAAGAGACC      250
    CCTATCATTT  TCGGATCCGC  TCTTTGCGCC  TTGGAAGGCC  GCAAGCCCGA      300
60  GATTGGCGAA  CAGAAGATTG  ACGAGCTCAT  GAACGCCGTT  GATACCTGGA      350

```


	TCCCCACCCC	CCAGCGTGAC	CTTGACAAGC	CCTTCTTGAT	GTCCGTTGAG	400
	GAAGTTTTCT	CCATCTCTGG	TCGTGGTACC	GTTGCATCTG	GTCCGTGTTGA	450
	GCGTGGTATT	TTGCGCAAGG	ATTCTGAGGT	TGAGATTATC	GGATACCAGA	500
	AGAACCCTAT	CAAGACCAAG	GTTACCGACA	TTGAGACCTT	CAAGAAGTCT	550
5	TGCGATGAAT	CTCGTGCTGG	TGACAACTCT	GGCTTGCTTC	TCCGTGGTAT	600
	CAAGCGTGAG	GACATTTCGT	GTGGTATGGT	TATCGCTGCT	CCTGGAACCA	650
	CCAAGGCTCA	TGACAACTTC	TTGGTCTCCA	TGTATGTCTT	GACTGAGGCT	700
	GAAGGTGGTC	GTCGTACTGG	ATTCGGCGCC	AACTACCGTC	CTCAAGCTTT	750
	CATCCGTAAT	GCCGGTATGT	TCCCTTTCAA	AGTCAATTAA	TGAGCGATTT	800
10	GCTAACGAGT	TATAGATGAG	GCTGCTACTC	TCAGCTTCCC	CGGTGACGAT	850
	CAGTCCAAGC	AGGTCATGCC	CGGTGACAAC	GTTGAGATGA	TCTTGAAGAC	900
	ACACCGTCCC	GTTGCCGCCG	AAGCTGGTCA	G		931

15

2) INFORMATION FOR SEQ ID NO: 911

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911

GACGGMKKCA TGCCGCARAC

20

30

2) INFORMATION FOR SEQ ID NO: 912

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912

GACGGCGKCA TGCCGCARAC

20

45

2) INFORMATION FOR SEQ ID NO: 913

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913

GACGGYSYCA TGCKCAGAC

20

60

2) INFORMATION FOR SEQ ID NO: 914

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914

GAARAGCTGC GGRCGRTAGT G

21

2) INFORMATION FOR SEQ ID NO: 915

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915

AAACGCCTGA GGRCGGTAGT T

21

2) INFORMATION FOR SEQ ID NO: 916

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916

GCCGAGCTGG CCGGCTTCAG

20

2) INFORMATION FOR SEQ ID NO: 917

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917

TCGTGCTACC CGTYGCCGCC AT

22

5

2) INFORMATION FOR SEQ ID NO: 918

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1391 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Escherichia coli*
 (E) ACCESSION NUMBER: J01672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918

25	AGAGAAGCCT	GTCGGCACCG	TCTGGTTTGC	TTTTGCCACT	GCCCGCGGTG	50
	AAGGCATTAC	CCGGCGGGAT	GCTTCAGCGG	CGACCGTGAT	GCGGTGCGTC	100
	GTCAGGCTAC	TGCGTATGCA	TTGCAGACCT	TGTGGCAACA	ATTTCTACAA	150
	AACACTTGAT	ACTGTATGAG	CATACAGTAT	AATTGCTTCA	ACAGAACATA	200
	TTGACTATCC	GGTATTACCC	GGCATGACAG	GAGTAAAAAT	GGCTATCGAC	250
	GAAAACAAAC	AGAAAGCGTT	GGCGGCAGCA	CTGGGCCAGA	TTGAGAAACA	300
30	ATTTGGTAAA	GGCTCCATCA	TGCGCCTGGG	TGAAGACCGT	TCCATGGATG	350
	TGGAAACCAT	CTCTACCGGT	TGCGCTTTCAC	TGGATATCGC	GCTTGGGGCA	400
	GGTGGTCTGC	CGATGGGCCG	TATCGTCGAA	ATCTACGGAC	CGGAATCTTC	450
	CGGTAAAACC	ACGCTGACGC	TGCAGGTGAT	CGCCGCAGCG	CAGCGTGAAG	500
	GTAAAACCTG	TGCGTTTATC	GATGCTGAAC	ACGCGCTGGA	CCCAATCTAC	550
35	GCACGTAAAC	TGGGCGTCTGA	TATCGACAAC	CTGCTGTGCT	CCCAGCCGGA	600
	CACCGGCGAG	CAGGCACTGG	AAATCTGTGA	CGCCCTGGCG	CGTTCTGGCG	650
	CAGTAGACGT	TATCGTCGTT	GACTCCGTGG	CGGCACTGAC	GCCGAAAGCG	700
	GAAATCGAAG	GCGAAATCGG	CGACTCTCAC	ATGGGCCTTG	CGGCACGTAT	750
	GATGAGCCAG	GCGATGCGTA	AGCTGGCGGG	TAACCTGAAG	CAGTCCAACA	800
40	CGCTGCTGAT	CTTCATCAAC	CAGATCCGTA	TGAAAATTGG	TGTGATGTTC	850
	GGTAACCCGG	AAACCACTAC	CGGTGGTAAC	GCGCTGAAAT	TCTACGCCTC	900
	TGTTTCGTCTC	GACATCCGTC	GTATCGGCGC	GGTGAAAGAG	GGCGAAAACG	950
	TGGTGGGTAG	CGAAACCCGC	GTGAAAGTGG	TGAAGAACAA	AATCGCTGCG	1000
	CCGTTTAAAC	AGGCTGAATT	CCAGATCCTC	TACGGCGAAG	GTATCAACTT	1050
45	CTACGGCGAA	CTGGTTGACC	TGGGCGTAAA	AGAGAAGCTG	ATCGAGAAAG	1100
	CAGGCGCGTG	GTACAGCTAC	AAAGGTGAGA	AGATCGGTCA	GGGTAAAGCG	1150
	AATGCGACTG	CCTGGCTGAA	AGATAACCCG	GAAACCGCGA	AAGAGATCGA	1200
	GAAGAAAGTA	CGTGAGTTGC	TGCTGAGCAA	CCCGAACTCA	ACGCCGGATT	1250
	TCTCTGTAGA	TGATAGCGAA	GGCGTAGCAG	AAACTAACGA	AGATTTTAA	1300
50	TCGTCTTGTT	TGATACACAA	GGGTCGCATC	TGCGGCCCTT	TTGCTTTTTT	1350
	AAGTTGTAAG	GATATGCCAT	GACAGAATCA	ACATCCCGTC	G	1391

55 2) INFORMATION FOR SEQ ID NO: 919

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

60

718

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919

GGICCGART CITMIGGIAA RAC

23

10

2) INFORMATION FOR SEQ ID NO: 920

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

15

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920

TCICCVATIT CICCITCIAI YTC

23

25

2) INFORMATION FOR SEQ ID NO: 921

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921

TIYRTIGAYG CIGARCAIGC

20

40

2) INFORMATION FOR SEQ ID NO: 922

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922

TARAAATTIA RIGCIYKICC ICC

23

55

2) INFORMATION FOR SEQ ID NO: 923

60

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923

GACGCIGCCA TCCTGATGAT C

21

2) INFORMATION FOR SEQ ID NO: 924

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924

ACCTCAGTCG TCACGTTGGC G

21

2) INFORMATION FOR SEQ ID NO: 925

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925

AAGCAGATGG TTGTGTGCTG

20

2) INFORMATION FOR SEQ ID NO: 926

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926

CAGCTGCTCG TGGTGCATCT CGAT

24

2) INFORMATION FOR SEQ ID NO: 927

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927

15 ACGCGGAGAA GGTGCGCTT 19

2) INFORMATION FOR SEQ ID NO: 928

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928

30 GGTCGTTCTT CGAGTCACCG CA 22

2) INFORMATION FOR SEQ ID NO: 929

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacteroides fragilis*
 (B) STRAIN: ATCC 25285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929

50 TTCAGCATGC CATTTCAAAA CAGGCCGAAG CCGATATCGT GATTATCGCT 50
 GCTTGTGGGG AGCGTGCAAA TGAAGTTGTG GAAATCTTTA CCGAATTTCC 100
 GGAATTGGTG GACCCGCACA CGGGACGTAA GCTGATGGAG CGTACCATTA 150
 TTATCGCAAA TACATCGAAC ATGCCGGTAG CAGCGCGTGA AGCTTCTGTG 200
 55 TATACGGCCA TGACGATTGC CGAATACTAT CGTGCCATGG GATTGAAAGT 250
 CCTGCTGATG GCAGACTCCA CTTCCCGTTG GGCGCAGGCA TTGCGTGAGA 300
 TGTCGAACCG TATGGAGGAG TTGCCCGGAC CGGATGCATT CCCGATGGAC 350
 CTGTCCTCAA TCATTCTTAA CTTCTATGGC CGTGCAGGCT ACGTGAAACT 400
 60 GAATAACGGC GAGAGCGGTT CTATTACCTT TATCGGTACA GTATCACC 448

2) INFORMATION FOR SEQ ID NO: 930

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 438 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacteroides distasonis*
 15 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930

	GCTATCTCTA	AACAAGCGGA	AGCGGATATC	GTGATTATCG	CCGCCTGCGG	50
20	TGAGCGTGCG	AATGAGGTCG	TAGAGGTATT	TACGGAGTTC	CCGGAATTGG	100
	TAGACCCGCA	TACGGGACGT	AAATTGATGG	AACGTACGAT	CATTATCGCC	150
	AATACATCCA	ACATGCCGGT	AGCCGCTCGT	GAGGCATCCG	TATATACGGC	200
	GATGACCATC	GCCGAGTATT	ATCGCAGCAT	GGGTTTGAAG	GTTCTGTTGA	250
	TGGCCGACTC	TACTTCCCGC	TGGGCACAGG	CTTTGCGTGA	GATGTCCAAC	300
25	CGTTTGGAGG	AGTTGCCGGG	ACCGGATGCT	TTCCCGATGG	ACTTGTCCGC	350
	TATCGTGGCG	AACTTCTACG	CTCGTGCGGG	ATTTCGTTTCAT	TTGAATAACA	400
	ACGCTACAGG	CTCCGTCACT	TTCATCGGTA	CGGTATCG		438

30 2) INFORMATION FOR SEQ ID NO: 931

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931

	CCTCCAGCAC	GCTATCTCTA	AGCAGGCGGA	GGCTGATATC	GTCATTATGG	50
	CAGCCTGCGG	TGAGCGTGCT	AATGAGGTGG	TGGAGATCTT	TGCCGAGTTC	100
	CCTGAGCTCG	AAGACCCACA	CACGGGACGC	AAGCTGATGG	AGCGTACGAT	150
50	CATCATCGCT	AACACGAGTA	ACATGCCAGT	GGCTGCTCGT	GAGGCTTCGG	200
	TCTACACCGC	TATGACCATC	GCTGAGTACT	ACCGCTCGAT	GGGTCTCAAA	250
	GTA CTCTAA	TGGCTGACTC	GACCTCTCGC	TGGGCACAGG	CACTGCGTGA	300
	GATGTCTAAC	CGTCTAGAGG	AGCTGCCTGG	ACCAGATGCA	TTCCCGATGG	350
	ACTTGTCCGC	TATCGTGGCA	AACTTCTACG	CTCGTGCCGG	CTTCGTCTAT	400
55	CTCAACAACG	GTGAGACAGG	TTCTGTAACC	TTCATCGGTA	CGGTCTCTCC	450
	AGC					453

60 2) INFORMATION FOR SEQ ID NO: 932

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932

```

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC      50
GTGAACATAT CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA      100
TTCATGAACA AATGTGACAT GGTGACGAT  GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA ATTCGTGATC TATTAAGTGA ATATGAATTC CCTGGCGATG      200
ACATTCCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA AGGTGAAGCT      250
GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT      300
TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG      350
ATGTATTCTC AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGGTTGAA      400
CGTGGACAAG TTAAAGTTGG TGACGAAGTA GAAGTTATCG GTATCGAAGA      450
AGAAAGCAAA AAAGTAGTAG TAACTGGAGT AGAAATGTTT CGTAAATTAC      500
TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT ACGTGGTGTT      550
GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT      600
TACTCCACAC ACTAAGTTCA AAGCTGAAAC TTATGTTTTA ACTAAGAAG      650
AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACGCCC ACAATTCTAT      700
TTCCGTACTA CTGACGTAAC TGGTATTGTT ACACCTCCAG AAGGTACTGA      750
AATGGTAAYG CCTGGTGATA ACATTGAGCT TGCAGTTGAA CTAATTGCAC      800
CAATCGCTAT CGAAGACGGT ACTAAATTCT CTATC                      835

```

2) INFORMATION FOR SEQ ID NO: 933

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933

CATCATCGTI TTCMTGAACA ARTG

24

2) INFORMATION FOR SEQ ID NO: 934

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934

TCACGYTTRR TACCACGCAG IAGA

24

5

2) INFORMATION FOR SEQ ID NO: 935

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935

20 GGIAARWSIC ARYTITGYCA YAC

23

2) INFORMATION FOR SEQ ID NO: 936

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936

35

TCISIIYTCIG GIARRCAIGG

20

40 2) INFORMATION FOR SEQ ID NO: 937

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937

ATACIGARG YITTYGGIGA RTT

23

55 2) INFORMATION FOR SEQ ID NO: 938

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938

CYIGTIGYIS WIGCRTGIGC

20

10

2) INFORMATION FOR SEQ ID NO: 939

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1203 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(C) ACCESSION NUMBER: D10023

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939

ATGTCTCAAG	TTCAAGAACA	ACATATATCA	GAGTCACAGC	TTCAGTACGG	50
GAACGGTTCG	TTGATGTCCA	CTGTACCAGC	AGACCTTTCA	CAGTCAGTCG	100
TTGATGGAAA	CGGCAACGGT	AGCAGCGAAG	ATATTGAGGC	CACCAACGGC	150
30 TCCGGCGATG	GTGGCGGATT	GCAGGAGCAA	GCGGAAGCGC	AAGGTGAAAT	200
GGAGGATGAA	GCATACGATG	AAGCTGCCTT	AGGTTTCGTTT	GTGCCAATAG	250
AAAAACTGCA	AGTGAACGGG	ATTACTATGG	CGGATGTGAA	AAAACATAAGG	300
GAGAGTGGGC	TTCACACTGC	TGAAGCGGTA	GCATATGCTC	CCAGAAAGGA	350
TTTATTGGAA	ATCAAAGGTA	TATCGGAAGC	TAAGGCAGAT	AAGTTGCTAA	400
35 ACGAAGCGGC	AAGGCTAGTG	CCTATGGGAT	TTGTCACGGC	TGCTGATTTT	450
CATATGAGAA	GATCGGAGCT	GATTTGTTTG	ACAACGGGTT	CTAAGAATTT	500
GGACACTCTT	TTGGGTGGTG	GTGTGGAAAC	TGGTTCTATT	ACTGAGCTTT	550
TCGGTGAATT	CAGGACAGGT	AAGTCCCAGC	TATGTCACAC	TTTGGCCGTG	600
ACATGCCAAA	TTCCATTGGA	TATTGGTGGC	GGTGAAGGTA	AGTGTGTTGTA	650
40 TATCGATACC	GAAGGTACTT	TCAGGCCGGT	AAGATTGGTA	TCCATAGCTC	700
AGCGGTTCGG	ATTAGACCCG	GATGATGCTT	TGAACAACGT	TGCGTATGCA	750
AGAGCCTATA	ACGCCGATCA	TCAGTTAAGA	CTTCTGGATG	CTGCTGCCCA	800
AATGATGAGC	GAGTCTCGGT	TTTCCTTGAT	TGTGGTCGAT	TCTGTTATGG	850
CTCTATACCG	TACGGATTTT	TCTGGTCGTG	GTGAACTAAG	CGCAAGGCAA	900
45 ATGCATTTAG	CCAAATTTAT	GCGTGCTTTG	CAAAGGCTGG	CCGACCAATT	950
TGGTGTGTC	GTCGTCGTTA	CTAACCAAGT	GGTCGCCCAA	GTTGATGGTG	1000
GTATGGCTTT	TAATCCAGAT	CCAAAGAAGC	CTATCGGTGG	TAATATTATG	1050
GCACATTCTT	CCACCACGCG	ATTAGGTTTC	AAAAAGGGTA	AGGGATGTCA	1100
AAGATTATGC	AAAGTTGTTG	ACTCACCTTG	CTTACCAGAG	GCTGAATGTG	1150
50 TGTTCGCGAT	CTATGAAGAT	GGTGTTGGTG	ACCCCAGAGA	AGAAGACGAG	1200
TAG					1203

55 2) INFORMATION FOR SEQ ID NO: 940

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1800 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(B) STRAIN: GRF88

(C) ACCESSION NUMBER: M87549

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940

	CGATCCAATT	GCTGGTCTTA	AGATGCATTT	GATTGATCTA	GGTATTGCCA	50
	CTGAAGCTGA	AGTCAAAGCT	TACGACAAGT	CCGCTAGAAA	ATACGTTGAC	100
	GAACAAGTTG	AATTAGCTGA	TGCTGCTCCT	CCTCCAGAAG	CCAAATTATC	150
15	CATCTTGTTT	GAAGACGTCT	ACGTGAAAGG	TACAGAAACT	CCAACCCCTAA	200
	GAGGTAGGAT	CCCTGAAGAT	ACTTGGGACT	TCAAAAAGCA	AGGTTTTGCC	250
	TCTAGGGATT	AATTAAATCG	TAAGGAAAAA	TAAAATAATA	GTGCTGTGAT	300
	CGCATGATAT	TCTTCCCTGG	AAGCGCCATT	TTATAGCAAG	AAATGTAAGT	350
	CAAGTATATT	TTAACTGTAT	ATACAACAAT	ATGACTCTTT	TTTATGCCCTT	400
20	GTTGTTTTTC	TTCGGGTTTT	CCCACACATT	GTGTGGAGAG	ATAGTTATTA	450
	ACAGACCGAA	AATAGCCGCC	CAAGGATAAA	CTTTTATATA	AAGGGAAGGG	500
	TAGTTGACCC	AAAAATTTGG	ATTCTACTTT	CCAGATTTAC	TTTCACCCCTT	550
	TTATATTTGC	TGTAGTCTGT	TGTCCCAATG	AGGAAAGCAT	TTGAACAAAT	600
	ATGTCTGTTA	CAGGAAGTGA	GATCGATAGT	GATACAGCAA	AAAATATTCT	650
25	TAGTGTAGAT	GAATTACAGA	ACTATGGTAT	TAATGCCTCA	GATCTTCAAA	700
	AATTGAAGTC	TGGTGGGATA	TACACAGTCA	ATGTATGTTA	TAATAACATT	750
	TTTAAACCTT	CTGCTGTAGA	GGTTCTTTCC	CCCTTTCTTT	TACTAACTAA	800
	TAATTTGGAA	AGGAACTTTT	ATAGACCGTT	TTGTCAACAA	CAAGAAGACA	850
	TCTATGTAAA	ATTAAAGGGT	TAAGTGAGGT	GAAAGTGGAA	AAAATTAAAG	900
30	AAGCTGCTGG	AAAAATCATA	CAGGTGGGAT	TTATCCCCGC	TACTGTACAA	950
	TTAGATATAA	GACAGCGTGT	GTACTCCTTA	TCAACTGGAT	CTAAGCAACT	1000
	AGATTCAATC	CTAGGTGGTG	GAATAATGAC	AATGAGTATC	ACTGAAGTAT	1050
	TTGGTGAATT	TAGGTGTGGT	AAGACACAGA	TGTCTCATA	TTTGTGTGTT	1100
	ACCACGCAGC	TTCCGAGGGA	AATGGGTGGT	GGTGAAGGGA	AAGTAGCATA	1150
35	TATTGATACA	GAAGGCACTT	TCAGGCCCGA	GAGGATTAAG	CAAATTGCAG	1200
	AAGGTTATGA	ATTGGATCCC	GAGTCATGTT	TGGCAAACGT	TTCATATGCT	1250
	AGAGCCTTGA	ATAGTGAACA	TCAAATGGAA	CTTGTTGAAC	AATTGGGTGA	1300
	AGAACTTAGT	TCTGGAGATT	ATCGCCTTAT	CGTGGTAGAT	TCTATAATGG	1350
	CAAACCTCAG	AGTAGACTAC	TGCGGTAGAG	GTGAACTAAG	CGAAAGACAG	1400
40	CAAAAGCTAA	ATCAACATCT	TTTCAAATTG	AATAGATTGG	CAGAGGAATT	1450
	TAATGTTGCA	GTATTTCTGA	CAAACCAAGT	TCAATCAGAC	CCAGGTGCTT	1500
	CTGCATTATT	TGCCTCGGCA	GATGGTAGGA	AACCAATTGG	AGGGCACGTT	1550
	CTGGCACATG	CGTCAGCAAC	AAGGATTTTG	TTGAGAAAAG	GGCGTGGTGA	1600
	CGAAAGAGTT	GCCAAGTTAC	AAGATTCCCC	AGATATGCCT	GAAAAAGAAT	1650
45	GTGTCTACGT	AATTGGTGAA	AAAGGTATTA	CCGATTCAAG	TGACTAGTTT	1700
	TTGTATACTT	TTTTAATGAA	GATGACATTG	CTCCTTTATT	AAACTTTTCT	1750
	TTTACTTTGT	GTTACTAATA	TTATTAATAT	CTTGTTATGA	TTCTTTGTTT	1800

50

2) INFORMATION FOR SEQ ID NO: 941

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus humicola*
 (B) STRAIN: ATCC 38294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941

```

CGTCCTTATC CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT      50
TCTCCGTCTT CACCGGTGTC GGTGAGCGTA CCCGTGAGGG TAACGACCTG      100
TACCACGAGA TCGGTGAGAC TGGTGTCAAT AACCTCGAGG GCGACTCCAA      150
GGTCGCTCTC GTCTTCGGCC AGATGAACGA GCGGCGGCGA GCGGCTGCCC      200
GTGTGCGCCT TACCGGCCTC ACCATCGCCG AGTACTTCCG TGACGAGGAG      250
GGTCAGGACG TGCCTTCTCT CATCGACAAC ATTTTCCGTT TCACCCAGGC      300
CGGTTCCGAG GTGTCTGCCC TTCTCGGTCG TATCCCTCGG GCGGTCGGTT      350
ACCAGCCAC  CCTCGCTACC GACATGGGTT CCATGCAGGA GCGTATCACC      400
ACCACCAAGA AGGGTTCGAT TACCTCCGTC      430

```

2) INFORMATION FOR SEQ ID NO: 942

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942

```

CGTGACGAT  GCTCTTGAGG TGCAAAATGG TAATGAGCGT CTGGTGCTGG      50
AAGTTCAGCA GCAGCTCGGC GCGGCTATCG TGCGTACCAT CGCAATGGGT      100
TCCTCCGACG GTCTGCGTCG CCGTCTGGAT GTAAAAGACC TCGAACACCC      150
GATCGAAGTC CCGGTAGGTA AAGCGACTCT GGGCCGTATC ATGAACGTAC      200
TGGGTGAACC GGTGACATG AAAGGCGAGA TCGGTGAAGA AGAGCGTTGG      250
GCGATTACAC GCGCAGCACC TTCCTACGAA GAGCTGTCAA ACTCTCAGGA      300
ACTGCTGGAA ACCGGTATCA AAGTTATCGA CCTGATGTGT CCGTTCGCTA      350
AGGGCGGTAA AGTTGGTCTG TTCGGTGGTG CGGGTGTAGG TAAAACCGTA      400
AACATGATGG AGCTCATTCG TAACATCGCG ATCGAGCACT CCGGTTACTC      450
TGTGTTTTCG GCGGTAGGTG AACGTACTCG TGAGGGGAAC GACTTCTACC      500
ACGAAATGAC CGACTCCAAC GTTATCGATA AAGTATCCCT GGTGTATGGC      550
CAGATGAACG AGCCGCCGGG AAACCGTCTG CGCGTAGCTC TGACCGGTCT      600
GACCATGGCT GAGAAATTCG GTGACGAAGG TCGTGACGTT CTGCTGTTCT      650
TTGACAACAT CTATCGTTAC ACCCTGGCCG GTACGGAAGT ATCCGCACTG      700
CTGGGCCGTA TGCCTTCAGC GGTAGGTTAT CAGCCGACCC TGGCGGAAGA      750
GATGGGCGTT CTGCAGGAAC GTATCACCTC CACCAAAACC GGTT          794

```

2) INFORMATION FOR SEQ ID NO: 943

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943

20	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GCGGCGGGTA	TCGTACGTAC	100
	CATCGCAATG	GGTTCTCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATTGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
25	AGAAGAGCGT	TGGGCGATTTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAACGTCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
30	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
35	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAA	800
	ACTGGTTCTA	TCAC				814

2) INFORMATION FOR SEQ ID NO: 944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 11775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944

55	GTGTACGATG	CTCTTGAGGT	GCAAAATGGT	AATGAGCGTC	TGGTGCTGGA	50
	AGTTCAGCAG	CAGCTCGGCG	GCGGTATCGT	GCGTACCATC	GCAATGGGTT	100
	CCTCCGACGG	TCTGCGTCGC	GGTCTGGATG	TAAAAGACCT	CGAACACCCG	150
	ATCGAAGTCC	CGGTAGGTAA	AGCGACTCTG	GGCCGTATCA	TGAACGTACT	200
60	GGGTGAACCG	GTCGACATGA	AAGGCGAGAT	CGGTGAAGAA	GAGCGTTGGG	250

	CGATTCACCG	CGCAGCACCT	TCCTACGAAG	AGCTGTCAAA	CTCTCAGGAA	300
	CTGCTGGAAA	CCGGTATCAA	AGTTATCGAC	CTGATGTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTTGGTCTGT	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTAA	400
	ACATGATGGA	GCTTATTCGT	AACATCGCGA	TCGAGCACTC	CGGTTACTCT	450
5	GTGTTTGCGG	GCGTAGGTGA	ACGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
	CGAAATGACC	GACTCCAACG	TTATCGACAA	AGTATCCCTG	GTGTATGGCC	550
	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	CGTGACGTTT	TGCTGTTCGT	650
	TGACAACATC	TATCGTTACA	CCCTGGCCGG	TACGGAAGTA	TCCGCACTGC	700
10	TGGGCCGTAT	GCCTTCAGCG	GTAGGTTATC	AGCCGACCCT	GGCGGAAGAG	750
	ATGGGCGTTC	TGCAGGAACG	TATCACCTCC	ACCAAACCG	GTTCTATC	798

15 2) INFORMATION FOR SEQ ID NO: 945

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945

30	ATGCCGTACC	GCGCGTGATC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATCGAA	GTCCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
35	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTA	GGAACGTCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	GCGATCGAGC	450
40	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CTTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTATTGCTGT	TCGTGATATA	CATCTATCGT	TACACCCTGG	CCGGTACCGA	700
45	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

50 2) INFORMATION FOR SEQ ID NO: 946

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946

```

GCGACGCTAT CCCGCATGTT TACGATGCCC TGAAATTGGA CGAGAACGGT      50
CTGACTCTGG AAGTTCAACA ACTTCTGGGT GACGGCGTTG TCCGTACTAT      100
TGCAATGGGT AGTTCAGACG GCCTGAAACG CGGCATGTCT GTAAGCAATA      150
10 CTGGTGCGCC AATCACTGTG CCGGTAGGTA AAGGTACTTT GGGTCGTATT      200
GTCGACGTAT TGGGTACGCC TGTGTATGAA GCAGGTCCGA TCGATAACCGA      250
CAAGAGCCGT GCCATTACCC AAACCTGCTCC GAAATTCGAC GAGTTGTCTG      300
CAACTACCGA ATTGTTGGAA ACCGGTATTA AAGTGATCGA CTTGCTGTGT      350
CCGTTTGCTA AAGGCGGTAA AGTAGGTCTG TTCGGTGGTG CCGGTGTAGG      400
15 CAAAACCGTG AACATGATGG AATTGATCAA CAACATCGCC AAAGCGCACA      450
GCGGTCTGTC CGTGTTCGCA GGTGTGGGCG AGCGTACCCG TGAAGGTAAC      500
GACTTCTACC ACGAGATGAA AGATTCCAAC GTATTGGATA AAGTGGCAAT      550
GGTTTACGGT CAGATGAACG AACCTCCGGG CAACCGTTTG CGCGTCGCAT      600
TGACCGGTTT GACCATGGCG GAATACTTCC GTGACGAAAA AGACGAAAAAC      650
20 GGTAAGGTTT GCGACGTATT GTTCTTCGTT GACAACATCT ACCGTTACAC      700
TCTGGCCGGT ACCGAAGTAT CTGCACTGTT GGGCCGTATG CCTTCTGCAG      750
TGGGTTACCA ACCGACATTG GCTGAAGAAA TGGGTCGTTT GCAAGAGCGT      800
ATTACCTCTA CCCAAACCGG TTCCATTACT TC                          832

```

25

2) INFORMATION FOR SEQ ID NO: 947

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947

```

TCCGCGCGAT GCCATTCCGC ATGTTTACGA CGCCCTGAAA TTGGATGCAA      50
ACGGCCTGAC TTTGGAAGTA CAACAGCTTC TGGGCGACGG CGTGGTTCGT      100
45 ACTATTGCAA TGGGTAGTTC GGACGGTCTG AAACGCGGCA TGA CTGTAAAG      150
CAATACAGAT GCGCCGATTA CTGTGCCGGT AGGTAAAGGT ACTTTGGGAC      200
GTATTGTCTGA TGTGTTGGGT ACACCTGTTG ATGAAGCAGG TCCGATTGAT      250
ACCGACAAAC ACCGTGCTAT CCATCAGACA GCTCCGAAAT TCGATGAGTT      300
GTCTGCTACT ACCGAGCTGC TGGAAACAGG CATTAAAGTG ATTGACTTGC      350
50 TGTGTCCGTT TGCCAAAGGC GGTAAAGTAG GTCTGTTCGG TGGTGCCGGT      400
GTAGGCAAAA CCGTCAACAT GATGGAATTG ATTAACAACA TCGCCAAAGC      450
GCATAGTGGT TTGTCCGTGT TCGCCGGTGT GGGGGAACGT ACCCGTGAAG      500
GTAACGACTT CTACCACGAG ATGAAAGATT CCAACGTATT GGACAAAGTG      550
GCGATGGTTT ACGGTACAGT GAACGAACCT CCGGGTAACC GTCTGCGTGT      600
55 AGCCTTGACC GGTGTTGACGA TGGCCGAATA CTTCCGTGAT GAAAAAGACG      650
AAAGCGGCAA AGGTCGCGAC GTATTGTTCT TCGTGGACAA CATTTACCGT      700
TACACTCTGG CCGGTACAGA AGTATCCGCA TTGCTCGGTC GTATGCCTTC      750
AGCAGTAGGT TACCAACCGA CATTGGCTGA AGAAATGGGT CGTCTGCAAG      800
AGCGTATTAC CCTCTACTCA AACAGGCTCC ATTACTTCTA                      840

```

60

2) INFORMATION FOR SEQ ID NO: 948

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 15 (B) STRAIN: ATCC 903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948

	GCAGCTGGCG	ACAAGCTACC	TGAGATCAAT	AATGCACTTG	TAGTCTATAA	50
20	AAATGACGAA	AAAAAATCAA	AAATCGTCCT	TGAAGTAGCT	CTTGAGCTTG	100
	GTGATGGAGT	GGTTCGGACC	ATCGCTATGG	AATCAACGGA	TGGGTTGACT	150
	CGTGGCATGG	AAGTGCTAGA	TACTGGCCGT	CCAATTTCTG	TGCCAGTCGG	200
	CAAAGAAACA	CTTGGTCGCG	TCTTTAACGT	TTTGGGAGAT	ACCATTGACT	250
	TGGATGCTCC	TTTTGCGGAT	GATGCAGAGC	GCCAGCCAAT	CCATAAGAAA	300
25	GCTCCAACCT	TTGATGAGTT	GTCTACTTCT	TCAGAGATCT	TAGAGACAGG	350
	TATCAAGGTT	ATCGACCTGT	TAGCCCCTTA	TCTGAAAGGT	GGTAAAGTTG	400
	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAGA	CCGTCCTGAT	TCAAGAATTG	450
	ATCCACAACA	TTGCCCAAGA	ACACGGTGGT	ATTTCTGTAT	TTACTGGCGT	500
	TGGGGAACGT	ACCCGTGAAG	GGAATGACCT	TTATTGGGAA	ATGAAAGAGT	550
30	CTGGTGTTAT	CGAGAAAACA	GCCATGGTCT	TCGGTCAGAT	GAATGAGCCG	600
	CCAGGAGCGC	GTATGCGGGT	TGCTTTGACT	GGTTTGACGA	TTGCAGAATA	650
	CTTCCGTGAT	GTGGAAGGTC	AAGATGTCTT	GCTCTTCATT	GACAACATCT	700
	TCCGTTTCAC	GCAGGCAGGT	TCTGAAGTTT	CTGCCCTTTT	GGGTCGGATG	750
	CCGTCAGCCG	TTGGTTACCA	ACCAACACTT	GCGACAGAAA	TGGGGCAATT	800
35	GCAAGAGCGT	ATCACATCGA	CTAAGAAGGG	TTCTGTAACC	TCT	843

2) INFORMATION FOR SEQ ID NO: 949

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 50 (B) STRAIN: ATCC 49456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GAGATGGTAT	GGTCCGTACT	ATCGCCATGG	AATCAACAGA	TGGTTTGACT	150
	CGTGGAAATG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAATGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GATGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300


```

      GCTCCAACCTT TTGATGAATT GTCTACCTCT TCTGAAATCC TTGAAACAGG 350
      GATTAAGGTT ATCGACCTTC TTGCCCCCTTA CCTTAAAGGT GGTAAGGTTG 400
      GACTTTTCGG TGGTGCCGGA GTTGGTAAAA CCGTCTTAAT CCAAGAATTG 450
      ATTCACAACA TTGCCCAAGA ACACGGTGGT ATTCAGTAT TTACCGGTGT 500
5     TGGGGAACGT ACTCGTGAGG GTAATGACCT TTAGTGGGAA ATGAAAGAAT 550
      CAGGTGTTAT CGAGAAAACA GCCATGGTAT TTGGTCAGAT GAATGAGCCG 600
      CCAGGAGCAC GTATGCGTGT TGCCCTAACT GGTTTGACAA TCGCCGAATA 650
      CTTCCGTGAT GTGGAAGGCC AAGACGTGCT TCTCTTTATC GATAATATCT 700
      TCCGTTTCAC TCAGGCTGGT TCAGAAGTAT CTGCCCTTTT GGGTCGTATG 750
10    CCATCAGCCG TTGGTTACCA ACCAACACTT GCTACGGAAA TGGGTCAATT 800
      GCAAGAGCGT ATTACATCAA CTAAAAAGGG TTCTGTAACC T 841

```

15 2) INFORMATION FOR SEQ ID NO: 950

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950

```

30    GCTACCTGAG ATCAATAATG CACTTGTAGT CTATAAAAAT GACGAAAATA 50
      AATCAAAAAT CGTCCTTGAA GTAGCTCTTG AGCTTGGTGA TGGAGTGGTT 100
      CGGACCATCG CTATGGAATC AACGGATGGG TTGACTCGTG GCATGGAAGT 150
      GCTAGATACT GGTGCTCCAA TTTCTGTGCC AGTCGGCAA GAAACACTTG 200
35    GTCGCGTCTT TAACGTTTTG GGAGATACCA TTGACTTGGA TGCTCCTTTT 250
      GCGGATGATG CAGAGCGCCA GCCAATCCAT AAGAAAGCTC CAACCTTTGA 300
      TGAGTTGTCT ACTTCATCAG AGATCTTAGA GACAGGTATC AAGGTTATCG 350
      ACCTGTTAGC ACCTTATCTG AAAGGTGGTA AAGTCGGACT CTTCGGTGGT 400
      GCCGGAGTTG GTAAGACCGT CCTGATTGAG GAATTGATCC ACAACATTGC 450
40    CCAAGAGCAT GGTGGTATTT CCGTGTTTAC CCGTGTGGG GAACGTACCC 500
      GTGAAGGGAA TGACCTTTAC TGGGAAATGA AGGAGTCTGG CGTTATCGAG 550
      AAAACAGCCA TGGTCTTCGG TCAGATGAAT GAGCCACCAG GAGCGCGTAT 600
      GCGGGTTGCT TTGACTGGTT TGACGATTGC AGAGTACTTC CGTGATGTAG 650
      AAGGTCAAGA TGTCTTGCTC TTCATTGACA ACATCTTCCG TTTCACGCAG 700
45    GCAGGTTCTG AAGTCTCTGC CCTTTTGGGT CGGATGCCAT CAGCCGTTGG 750
      TTACCAACCA ACACTTGCGA CTGAAATGGG ACAACTCCAA GAGCGTATTA 800
      CATCGACTAA GAAAGGTTCT GTAACCT 827

```

50 2) INFORMATION FOR SEQ ID NO: 951

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951

```

GCAGCAGGGG AAACACTTCC TGAGATTAAT AATGCACTTG TCGTCTACAA      50
AAATGACGAA AGAAAAACAA AAATCGTCCT TGAAGTAGCC TTGGAGTTGG      100
GTGATGGTAT GGTCCGTACG ATCGCCATGG AATCAACAGA TGGTTTGACT      150
10 CGTGGAATGG AAGTTTGGGA CACAGGCCGT CCAATCTCTG TACCAGTAGG      200
TAAAGAAACT TTGGGACGTG TCTTCAACGT TTTGGGAGAT ACTATTGACT      250
TGGATGCTCC TTTCGCTGAA GACGCTGAGC GTCAGCCAAT TCATAAGAAA      300
GCTCCAACCT TTGATGAATT GTCTACCTCA TCTGAAATCT TGGAAACAGG      350
GATTAAGGTT ATCGACCTTC TTGCCCCTTA CCTTAAAGGT GGGAAAGTTG      400
15 GACTCTTCGG TGGTGCCGGA GTTGGTAAAA CTGTCTTGAT CCAAGAGTTG      450
ATTCAACAAC TTGCCCAAGA ACATGGTGGT ATTTCAGTAT TTACCGGTGT      500
TGGAGAACGT ACCCGTGAGG GGAACGACCT TTAAGTGGGAA ATGAAAGAAT      550
CAGGCGTTAT CGAGAAAACA GCCATGGTAT TTGGTCAGAT GAATGAGCCA      600
CCTGGAGCAC GTATGCGTGT TGCTCTTACT GGTTTGACAA TCGCCGAATA      650
20 CTTCCGTGAT GTAGAAGGCC AAGATGTGCT TCTCTTTATC GACAATATCT      700
TCCGTTTCAC TCAAGCTGGT TCAGAAGTAT CTGCCCTTTT GGGTCGGATG      750
CCTTCAGCCG TTGGTTACCA ACCAACACTT GCTACGGAAA TGGGTCAATT      800
GCAAGAACGT ATCACATCAA CTAAGAAGGG TTCTGTAACC TCTA          844

```

25

2) INFORMATION FOR SEQ ID NO: 952

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952

```

GCAGCAGGGG AAAA ACTTCC TGAGATTAAC AATGCACTTG TCGTCTACAA      50
AAATGACGAA AGAAAAACAA AAATCGTCCT TGAAGTAGCC TTGGAGTTAG      100
45 GAGATGGTAT GGTTCGTACT ATCGCCATGG AATCAACAGA TGGGTTGACT      150
CGTGGAATGG AAGTATTGGA CACAGGTCGT CCAATCTCTG TACCAGTAGG      200
TAAAGAAACT TTGGGACGTG TCTTCAACGT TTTGGGAGAT ACCATTGATT      250
TGAAGCTCC TTTTACAGAA GACGCAGAGC GTCAGCCAAT TCATAAAAAA      300
GCTCCAACCT TTGATGAGTT GTCTACCTCT TCTGAAATCC TTGAAACAGG      350
50 GATCAAGGTT ATTGACCTTC TTGCCCCTTA CCTTAAAGGT GGTAAAGTTG      400
GACTTTTCGG TGGTGCCGGA GTTGGTAAAA CCGTCTTAAT CCAAGAATTG      450
ATTCAACAAC TTGCCCAAGA GCACGGTGGT ATTTCAGTAT TTAAGTGGTGT      500
TGGGGAACGT ACTCGTGAGG GGAATGACCT TTAAGTGGGAA ATGAAAGAAT      550
CAGGCGTTAT CGAGAAAACA GCCATGGTCT TTGGTCAGAT GAATGAGCCA      600
55 CCAGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TCGCTGAATA      650
CTTCCGTGAT GTGGAAGGCC AAGAGCTGCT TCTCTTTATC GATAATATCT      700
TCCGTTTCAC TCAGGCTGGT TCAGAAGTAT CTGCCCTTTT GGGTCGTATG      750
CCATCAGCCG TTGGTTACCA ACCAACACTT GCTACGGAAA TGGGTCAATT      800
GCAAGAACGT ATCACATCAA CCAAGAAGGG          830

```

60

2) INFORMATION FOR SEQ ID NO: 953

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 15 (B) STRAIN: StrR-11
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953

	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
20	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACCT	300
25	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
	TTGCCCAAGA	GCACGGTGGT	ATTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
30	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAT	TGGGTCAATT	GCAAGAACGT	800
35	ATCACATCAA	CTAAGAAGGG	TTC			823

2) INFORMATION FOR SEQ ID NO: 954

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

```

GCTCCAACCTT TTGATGAGTT GTCTACCTCT TCTGAAATCC TTGAAACAGG 350
GATCAAGGTT ATTGACCTTC TTGCCCCCTTA CCTTAAAGGT GGTAAAGTTG 400
GACTTTTCGG TGGTGCCGGA GTTGGTAAAA CTGTCTTAAT CCAAGAATTG 450
ATTCAACAACA TTGCCCAAGA GCACGGTGGT ATTTTCAGTAT TTGCTGGTGT 500
5 TGGGGAACGT ACTCGTGAGG GGAATGACCT TTAAGGGGAA ATGAAAGAAT 550
CAGGCGTTAT CGAGAAAACA GCCATGGTCT TTGGTCAGAT GAATGAGCCA 600
CCAGGAGCAC GTATGCGTGT TGCCCTTACT GGTTCGACAA TCGCTGAATA 650
CTTCCGTGAT GTGGAAGGCC AAGACGTGCT TCTCTTTATC GATAATATCT 700
TCCGTTTCAC TCAGGCTGGT TCAGAAGTAT CTGCCCTTTT GGGTCGTATG 750
10 CCATCAGCCG TTGGTTACCA ACCAACACTT GCTACGAAA TGGGTCAATT 800
GCAAGAACGT ATCACATCAA CCAAGAAGGG TTCTGTAACC TCTA 844

```

15 2) INFORMATION FOR SEQ ID NO: 955

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Streptococcus pneumoniae
(B) STRAIN: StrR-05

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955

```

30 AAAAACTTCC TGAGATTAAC AATGCACTTG TCGTCTACAA AAATGACGAA 50
AGAAAAACAA AAATCGTCCT TGAAGTAGCC TTGGAGTTAG GAGATGGTAT 100
GGTTCGTACT ATCGCCATGG AATCAACAGA TGGGTTGACT CGTGGAATGG 150
AAGTATTGGA CACAGGTCGT CCAATCTCTG TACCAGTAGG TAAAGAAACT 200
35 TTGGGACGTG TCTTCAACGT TTTGGGAGAT ACCATTGATT TGGAAGCTCC 250
TTTTACAGAA GACGCAGAGC GTCAGCCAAT TCATAAAAAA GCTCCAACCT 300
TTGATGAGTT GTCTACCTCT TCTGAAATCC TTGAAACAGG GATCAAGGTT 350
ATTGACCTTC TTGCCCCCTTA CCTTAAAGGT GGTAAAGTTG GACTTTTCGG 400
TGGTGCCGGA GTTGGTAAAA CCGTCTTAAT CCAAGAATTG ATTCACAACA 450
40 TTGCCCAAGA GCACGGTGGT ATTTTCAGTAT TTAAGGGTGT TGGGGAACGT 500
ACTCGTGAGG GGAATGACCT TTAAGGGGAA ATGAAAGAAT CAGGCGTTAT 550
CGAGAAAACA GCCATGGTCT TTGGTCAGAT GAATGAGCCA CCAGGAGCAC 600
GTATGCGTGT TGCCCTTACT GGTTCGACAA TCGCTGAATA CTTCCGTGAT 650
GTGGAAGGCC AAGACGTGCT TCTCTTTATC GATAATATCT TCCGTTTCAC 700
45 TCAGGCTGGT TCAGAAGTAT CTGCCCTTTT GGGTCGTATG CCATCAGCCG 750
TTGGTTACCA ACCAACACTT GCTACGAAA TGGGTCAATT GCAAGAACGT 800
ATCACATCAA CCAAGAAGGG TTCTGTAACC TCTA 844

```

50 2) INFORMATION FOR SEQ ID NO: 956

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 495 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microti*
 (B) STRAIN: Persing-1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956

	TTGTATATCA	CAGGCACTCA	GCAAATATTC	CGATACTGAC	GTAATTATAT	50
	ACGTGGGTTG	TGGTGAACGT	GGGAATGAAA	TGGCTGAGAT	TCTATGCGAA	100
	TTCCCTGAAC	TATCTACTGT	AGTTAATGAT	GAAAAGGTGG	CCATTATGGA	150
10	ACGTACATGC	TTAGTTGCCA	ATACTTCTAA	TATGCCAGTG	GCCGCTAGAG	200
	AAGCTAGTAT	ATACACTGGT	ATTACAATTG	CTGAATATTT	CCGTGATATG	250
	GGTTACAAC	GCACTCTTAT	GGCCGATTCC	ACTAGCCGAT	GGGCAGAGGC	300
	TCTAAGGGAA	ATTTCTGGTA	GATTGGCTGA	AATGCCTGCA	GATTCTGGCT	350
	ATCCGGCCTA	TTTATCGTCA	AGGTTGTCAG	CTTTTTATGA	ACGTGCAGGT	400
15	GGGATAACTG	TCTAATTAAT	TTAGGCTTGA	TTAAGTGCTT	AGG TTCACCA	450
	ACACGAACCG	GATCTATTAC	GGTTGTAGGA	GCAGTTTCTC	CACCA	495

20 2) INFORMATION FOR SEQ ID NO: 957

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Entamoeba histolytica*
 (B) STRAIN: HM1-1MSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957

35	AGTTATTTC	CAAGCATTA	GTAAATATAG	TAATTCAGAT	GTTATTATTT	50
	ATGTAGGATG	TGGTGAACGA	GGAAATGAAA	TGGCAGAAGT	TCTTCGAGAT	100
	TTTCCAGCTC	TTTCTATTAA	AGTAGGAGAT	AAAGAAGAAT	CTATTATGAC	150
	AAGAACAGCA	CTTGTTGCTA	ATACATCTAA	TATGCCTGTT	GCAGCACGTG	200
40	AAGCATCAAT	TTTACTGGA	ATTACATTAT	CAGAATATTA	TAGAGATATG	250
	GGATATAATG	TTGCTATGAT	GGCAGATTCA	ACATCAAGAT	GGGCTGAAGC	300
	ACTTAGAGAA	ATTTCAGGAC	GTCTTGCAGA	AATGCCAGCT	GATTCTGGAT	350
	ATCCAGCATA	TCTTGCAGCA	CGTTTAGCAT	CATTTTATGA	ACGTGCAGGT	400
	ATGGTTGAAT	GTTTAGGATC	ACCAAAAAGA	ATAGGGTCAG	TTTCTATTGT	450
45	AGGAGCTGTT	TCACCACCT				469

2) INFORMATION FOR SEQ ID NO: 958

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*

(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958

```

5  TACAACACCA ACTTGCTAAA TGGGCAGATG CAGAAGTAGT TGTTTATGTT      50
   GGTGTGTTGGG AACGTGGAAA TGAAATGACC GATGTACTTA TGGAATTCCC      100
   AGAAATTATT GACCCTAAGA CAGGACAATC TTTAATGAAG AGAACAGTTC      150
   TTATAGCTAA TACTTCTAAT ATGCCAGTTG CTGCTCGTGA GGCTTCAATC      200
   TATACTGGTA TAACTATTGC AGAATATTTT AGAGATATGG GATATTCAGT      250
10  GGCACCTTATG GCAGATTCAA CAAGTCGTTG GGCAGAAGCA CTTCGTGAAA      300
   TGTCAGGACG TTTGGAAGAA ATGCCAGGTG ATGAAGGATA TCCAGCATAT      350
   CTATCAAGTA GAATAGCAGA GTTTTATGAA AGAGCAGGGC TTGTTGAATG      400
   TCTAGGTAAT GGAGAAGAAG GAGCATTAAC TGTAATTGGA GCAGTATCTC      450
   CA
15

```

2) INFORMATION FOR SEQ ID NO: 959

```

20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 469 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25
   (ii) MOLECULE TYPE: Genomic DNA
   (vi) ORIGINAL SOURCE:
30  (A) ORGANISM: Leishmania aethiopica
      (B) STRAIN: ATCC 50119

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959

```

35  TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TCGTTCATCT      50
   ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GTCATGGAG      100
   TTCCCGACCC TGACGACCGT GATCAATGGT CGCGAGGAGT CGATCATGAA      150
   GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG      200
   AGGCCTCTAT TTACACCGGC ATCACCTGG CCGAGTACTA CCGTGATATG      250
   GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC      300
40  GCTTCGTGAG ATTTCTGGGTC GTCTGGCGGA GATGCCGGCC GATGGTGGCT      350
   ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC      400
   CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT      450
   CGGTGCCGTG TCTCCGCCG
45

```

2) INFORMATION FOR SEQ ID NO: 960

```

50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 469 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
55
   (ii) MOLECULE TYPE: Genomic DNA
   (vi) ORIGINAL SOURCE:
60  (A) ORGANISM: Leishmania tropica
      (B) STRAIN: ATCC 30815

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
5	TTCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGCA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCCCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTTCGGGTC	GTTTGCGCGA	GATGCCGGCC	GATGGTGGCT	350
10	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

15

2) INFORMATION FOR SEQ ID NO: 961

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 469 bases
20	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Leishmania guyanensis</i>
(B)	STRAIN: ATCC 50126

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961

	TGTCATCAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGTGTCATCT	50
	ATGTCGGCTG	CGGTGAACGC	GGTAACGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACTGT	GATCGATGGT	CGCGAAGAGT	CCATCATGAA	150
35	GCGCACCTGC	CTCGTGCGCA	ACACCTCGAA	CATGCCCGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTATACCGGC	ATCACCCCTTG	CTGAGTACTA	CCGTGATATG	250
	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTGCGTGAG	ATTTTCGGGTC	GATTGGCGGA	GATGCCGGCT	GATGGTGGCT	350
	ACCCTGCCTA	CCTCAGCGCC	CGCCTCGCCT	CCTTCTACGA	GCGCGCCGGT	400
40	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCAGTG	TCTCCACCG				469

45 2) INFORMATION FOR SEQ ID NO: 962

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 469 bases
50	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Leishmania donovani</i>
(B)	STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962

60

```

      TGTCATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAT TCGGTCATCT      50
      ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG      100
      TTCCCGACCC TGACGACCGT GATCGATGGC CGCGAGGAGT CGATCATGAA      150
      GCGCACCTGC CTCGTGGCGA ACACCTCGAA CATGCCAGTC GCAGCCCGTG      200
5     AGGCCTCTAT TTACACCGGC ATCACCTTGG CCGAGTACTA CCGTGATATG      250
      GGCAAGCATA TCGCCATGAT GGCTGACTCG ACGTCTCGCT GGGCCGAGGC      300
      GCTTCGTGAG ATTTCCGGTC GTCTGGCGGA GATGCCGGCC GATGGTGGCT      350
      ACCCCGCCTA CCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC      400
      CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATCGT      450
10    CGGTGCCGTG TCTCCACCG                                469

```

2) INFORMATION FOR SEQ ID NO: 963

```

15    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 469 bases
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
20    (D) TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
25    (A) ORGANISM: Leishmania hertigi
        (B) STRAIN: ATCC 50125

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963

```

```

30    TGTGATCAGT CAGGCCCTTT CCAAGTACTC CAACTCGGAC TCGGTCATCT      50
      ACGTCGGCTG TGGTGAGCGC GGGAACGAGA TGGCCGAGGT GCTCATGGAT      100
      TTCCCGACTT TGACGACTGT GATCGATGGT CGCGAGGAGT CCATCATGAA      150
      GCGCACCTGC CTCGTGGCGA ACACCTCCAA CATGCCAGTT GCAGCCCGTG      200
      AGGCTTCTAT CTATACCGGC ATCACACTGG CTGAGTACTA TCGTGATATG      250
35    GGCAAGCACA TTGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC      300
      GTTGCGTGAG ATTTCCGGTC GGCTGGCGGA GATGCCGGCC GATGGTGGTT      350
      ACCCCGCCTA CCTCAGTGCC CGTCTCGCCT CCTTCTACGA GCGCGCTGGC      400
      CTCGTGACCT GTATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACAATTGT      450
40    TGGTGCGGTG TCTCCACCG                                469

```

2) INFORMATION FOR SEQ ID NO: 964

```

45    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 469 bases
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
50    (D) TOPOLOGY: Linear

        (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
55    (A) ORGANISM: Leishmania mexicana
        (B) STRAIN: ATCC 50156

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964

```

```

60    GGTCATTAGT CAGGCCCTTT CCAAGTACTC CAACTCTGAC TCGGTCATCT      50
      ACGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG      100

```


TTCCCGACCC TGACGACCAT GATCGATGGT CGGGAGGAGT CGATCATGAA 150
 GCGCACCTGC CTCGTGGCGA ACACCTCGAA CATGCCCGTC GCAGCCCGTG 200
 AGGCCTCTAT CTACACCGGC ATCACCCCTCG CCGAGTACTA CCGTGATATG 250
 GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCTGAGGC 300
 5 GCTTCGTGAG ATTTTCGGGTC GTCTGGCGGA GATGCCGGCC GATGGTGGCT 350
 ACCCCGCCTA CCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC 400
 CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATCGT 450
 CCGTGCCGTG TCTCCGCCG 469

10

2) INFORMATION FOR SEQ ID NO: 965

- (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965

TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TCGGTCATCT 50
 ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG 100
 30 TTCCCGACCC TGACGACCGT GATCGATGGT CGCGAGGAGT CGATCATGAA 150
 GCGCACCTGC CTCGTGGCGA ACACCTTCGAA CATGCCAGTC GCAGCCCGTG 200
 AGGCCTCTAT TTACACCGGC ATCACCCCTGG CCGAGTACTA CCGTGATATG 250
 GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC 300
 GCTTCGTGAG ATTTTCGGGTC GTTTGGCGGA GATGCCGGCC GATGGTGGCT 350
 35 ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC 400
 CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT 450
 CCGTGCCGTG TCTCCGCCG 469

40

2) INFORMATION FOR SEQ ID NO: 966

- (i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 449 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966

CACCAGTTCG CCAAGTGGGC AGATGCTCAG ATAGTTGTAT ACGTTGGTTG 50
 TGGAGAACGT GGTAACGAGA TGACAGACGT TCTAAATGAA TTCCAGAAC 100
 TGATTGACCC TCATACAGGC GAATCTCTAA TGAAGAGAAC AGTTCTTATA 150
 60 GCTAATACGT CAAATATGCC AGTTGCAGCC AGAGAGGCAA GTATATATAC 200

	AGGTATTACA	ATAGCTGAAT	ATTTTAGAGA	CATGGGATAT	TCAGTAGCGG	250
	TAATGGCCGA	CTCTACATCA	AGATGGGCAG	AGGCCCTAAG	AGAGATGTCA	300
	GGTCGTCTAG	AAGAAATGCC	TGGTGATGAA	GGTTATCCAG	CCTATCTAGG	350
	TTCTAGAGCT	GCAGAGTTCT	ATGAAAGAGC	AGGTAAGGTA	ATATGTAAGG	400
5	GTAGCGATAA	TAGAGAGGGA	GCCCTTACAA	TAATAGGTGC	CGTGTCCACC	449

2) INFORMATION FOR SEQ ID NO: 967

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*
- (B) STRAIN: ATCC 9797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967

25	CTGGTGGTGT	CGGCCGCAGA	CGGCCCGATG	CCGCAGACGC	GCGAGCACAT	50
	TTTGCTGTCT	CGCCAGGTTG	GCGTGCCGTA	CATCATCGTG	TTCCTGAACA	100
	AGGCGGACAT	GGTTGATGAC	GCGGAGCTGC	TCGAGCTGGT	GAAGATGGAA	150
	GTCCGCGAAC	TGCTGAGCAA	GTACGATTTT	CCGGGCGATG	ACACGCCGAT	200
	CGTGAAGGGT	TCGGCCAAGC	TGGCGCTGGA	AGGCGACAAG	GGCGAACTGG	250
30	GCGAGCAGGC	GATTCTGTCT	CTGGCGCAAG	CGCTGGACAC	GTACATTCCG	300
	ACGCCGGAGC	GCGCGGTCGA	CGGTGCGTTC	CTGATGCCCG	TGGAAGACGT	350
	GTTCTCGATC	TCGGGCCCGT	GCACGGTGGT	GACTGGCCGT	ATCGAGCGCG	400
	GCGTGGTGAA	GGTTGGCGAG	GAAATCGAAA	TCGTGGGCAT	CAAGCCGACG	450
	GTGAAGACGA	CCTGCACGGG	CGTGAGATG	TTCCGCAAGC	TGCTGGACCA	500
35	GGCCAGGCG	GGCGACAACG	TGGGTATCTT	GCTGCGCGGC	ACCAAGCGTG	550
	AAGACGTCGA	GCGTGCCAG	GTGCTGGCCA	AGCCGGGTTC	GATCAACCCG	600
	CACACGGACT	TCACGGCCGA	GGTGATACAT	CTGTCCAAGG	AAGAGGGTGG	650
	CCGTCACACG	CCGTTCTTCA	ACGGCTATCG	TCCGCAGTTC	TACTTCCGCA	700
	CGACGGACGT	GACCGGCACG	ATCGACCTGC	CGCGGGACAA	GGAAATGGTG	750
40	CTGCCGGGCG	ACAACGTGTC	GATGACCGTC	AAGCTGCTGG	CCCCGATCGC	800
	CATGGAAGAA	GGTCTGCGTT	TCGCCA			826

2) INFORMATION FOR SEQ ID NO: 968

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*
- (B) STRAIN: BD180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968

	CGATCCTGGT	GGTGTGCGCC	GCAGACGGCC	CGATGCCGCA	GACGCGCGAG	50
	CACATTTTGC	TGTCGCGCCA	GGTTGGCGTG	CCGTACATCA	TCGTGTTCCCT	100
	GAACAAGGCG	GACATGGTTG	ATGACGCGGA	GCTGCTCGAG	CTGGTGGAGA	150
	TGGAAGTCCC	CGAACTGCTG	AGCAAGTACG	ATTTCCTGGG	CGATGACACG	200
5	CCGATCGTGA	AGGGTTCGGC	CAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
	ACTGGGCGAG	CAGGCGATTC	TGTCGCTGGC	GCAAGCGCTG	GACACGTACA	300
	TTCCGACGCC	GGAGCGCGCG	GTCGACGGTG	CGTTCCTGAT	GCCGGTGGAA	350
	GACGTGTTCT	CGATCTCGGG	CCGTGGCACG	GTGGTGAAGT	GCCGTATCGA	400
	GCGCGGCGTG	GTGAAGGTTG	GCGAGGAAAT	CGAAATCGTG	GGCATCAAGC	450
10	CGACGGTGAA	GACGACCTGC	ACGGGCGTGG	AGATGTTCCG	CAAGCTGCTG	500
	GACCAGGGCC	AGGCGGGCGA	CAACGTGGGT	ATCTTGCTGC	GCGGCACCAA	550
	GCGTGAAAGC	GTCGAGCGTG	GCCAGGTGCT	GGCCAAGCCG	GGTTCGATCA	600
	ACCCGCACAC	GGACTTCACG	GCCGAGGTGT	ACATTCTGTC	CAAGGAAGAG	650
	GGTGGCCGTC	ACACGCCGTT	CTTCAACGGC	TATCGTCCGC	AGTTCTACTT	700
15	CCGCACGACG	GACGTGACCG	GCACGATCGA	CCTGCCGGCG	GACAAGGAAA	750
	TGGTGCTGCC	GGGCGACAAC	GTGTCGATGA	CCGTCAAGCT	GCTGGCCCCG	800
	ATCGCCATGG	AAGAAGG				817

20

2) INFORMATION FOR SEQ ID NO: 969

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 637 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus columbae*
- (B) STRAIN: ATCC 51263

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969

	CCTATGCCAC	AAACTCGTGA	ACACATTCTT	TTATCACGTA	ACGTTGGTGT	50
	GCCATACATC	GTTGTTTTCT	TAAACAAAGT	TGATATGGTT	GACGACGAAG	100
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	AACTGAATAT	150
40	GACTTCCCAG	GAGACGATGT	TCCTGTAATC	GCTGGTTCTG	CATTAAAAGC	200
	TTTAGAAGGC	GACCCTGCTT	ACGAAGAAAA	AATCTTAGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACATCCCA	ACTCCAGAAC	GTGACAACGA	CAAACCATTC	300
	ATGATGCCAG	TTGAAGACGT	GTTCTCAATT	ACTGGTCGTG	GTAAGTTGAC	350
	TACAGGTCGT	GTTGAACGTG	GACAAGTTTC	TGTTGGTGAC	GAAGTTGAAA	400
45	TCGTTGGTAT	CGCTGACGAA	ACTTCTAAAA	CAACAGTTAC	TGGTGTGAA	450
	ATGTTCCGTA	AATTATTAGA	TTACGCTGAA	GCTGGAGACA	ACATCGGTGC	500
	ATTATTACGT	GGTGTGGCTC	GTGAAGACAT	CCAACGTGGT	CAAGTATTAG	550
	CTAAACCAGG	TTCAATCACT	CCACATACAA	AATTCACTGC	TGAAGTGTAC	600
50	GTTTTAACTA	AAGAAGAAGG	TGGACGTCAT	ACTCCAT		637

2) INFORMATION FOR SEQ ID NO: 970

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 634 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: ATCC 49997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970

10	TATGCCTCAA	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	50
	CATACATCGT	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	150
	CTTCCCAGGC	GACGATGTTT	CTGTAATCGC	TGGTTCTGCT	TTGAAAGCTC	200
	TTGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	250
	GTTGACGAAT	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTCAT	300
15	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGAAAC	TGCTAAAACA	ACTGTAACGT	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGTCAT	500
	TGCTACGTGG	GGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTAGCT	550
20	AAAGCTGGTA	CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	600
	TTTAACAAAA	GAAGAAGGTG	GACGTCACAC	TCCA		634

25 2) INFORMATION FOR SEQ ID NO: 971

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 787 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971

40	GGACCAATGC	CACAACTCG	TGAGCACATC	CTTCTTTCAC	GTCAGGTG	50
	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	AGTTGACTTG	GTTGACGACG	100
	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	TCCGTGACCT	ATTGTCAGAA	150
	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	ATCCAAGGTT	CAGCACTTAA	200
45	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	CATCGTTATG	GAATTGATGA	250
	ACACAGTTGA	TGAGTATATC	CCAGAACCAG	AACGTGACAC	TGACAAACCA	300
	TTGCTTCTTC	CAGTCGAGGA	CGTATFTCTA	ATCACTGGAC	GTGGTACAGT	350
	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	TAAAGTCAAC	GACGAAATCG	400
	AAATCGTTGG	TATCAAAGAA	GAAACTCAA	AAGCAGTTGT	TACTGGTGTT	450
50	GAAATGTTCC	GTAACAACCT	TGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	500
	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	AATCGAACGT	GGACAAGTTA	550
	TCGCTAAACC	AGGTTCAATC	AACCCACACA	CTAAATTCAA	AGGTGAAGTC	600
	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	CACACTCCAT	TCTTCAACAA	650
	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	TGACGTTACA	GGTTCAATCG	700
55	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	CTGGTGATAA	CGTGACAATC	750
	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	GAACAAG		787

60 2) INFORMATION FOR SEQ ID NO: 972

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972

```

15 TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA GCACATCCTG      50
   CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC TGAACAAATG      100
   CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA ATGGAAGTTC      150
   GTGAACTTCT GTCTCAGTAC GACTTCCCGG GCGACGACAC TCCGATCGTT      200
20 CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT GGAAGCGAA      250
   AATCCTGGAA CTGGCTGGCT TCCTGGATTG TTACATTCCG GAACCAGAGC      300
   GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT ATTCTCCATC      350
   TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAACGCG GTATCATCAA      400
   AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT CAGAAGTCTA      450
25 CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA AGGCCGTGCT      500
   GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG AAGAAATCGA      550
   ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG CACACCAAGT      600
   TCGAATCTGA AGTGATACAT CTGTCCAAAG ATGAAGGCGG CCGTCATACT      650
   CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA CTACTGACGT      700
30 GACTGGTACC ATCGAACTGC CGGAAGGCGT AGAGATGGTA ATGCCGGGCG      750
   ACAACATCAA AATGGTTGTT ACCCTGATCC ACCCGATCGC GATGGACGAC      800
   GGT

```

2) INFORMATION FOR SEQ ID NO: 973

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973

```

50 ACTGACGGCC CGATGCCGCA GACTCGTGAG CACATCCTGC TGGGTCGTCA      50
   GGTAGGCGTT CCGTACATCA TCGTGTTTCCT GAACAAATGC GACATGGTTG      100
   ATGACGAAGA GCTGCTGGAA CTGGTTGAAA TGGAAGTTTCG TGAACCTCTG      150
55 TCTCAGTACG ACTTCCCGGG CGACGACACT CCGATCGTTC GTGGTTCTGC      200
   TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG GGAAGCGAAA ATCCTGGAAC      250
   TGGCTGGCTT CCTGGATTCC TACATTCCGG AACCAGAGCG TGCRAATTGAC      300
   AAGCCGTTCC TGCTGCCGAT CGAAGACGTA TTCTCCATCT CCGGTCGTGG      350
   TACCGTTGTT ACCGGTCGTG TAGAACGCGG TATCATCAAA GTTGGTGAAG      400
60 AAGTTGAAAT CGTTGGTATC AAAGAGACTC AGAAGTCTAC CTGTACTGGC      450

```

	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	GGCCGTGCTG	GTGAGAACGT	500
	AGGTGTTCTG	CTGCGTGGTA	TCAAACGTGA	AGAAATCGAA	CGTGGTCAGG	550
	TACTGGCTAA	GCCGGGCACC	ATCAAGCCGC	ACACCAAGTT	CGAATCTGAA	600
	GTGTACATTC	TGTCCAAAGA	TGAAGGCGGC	CGTCATACTC	CGTTCTTCAA	650
5	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	TACTGACGTG	ACTGGTACCA	700
	TTGAACTGCC	GGAAGGCGTA	GAGATGGTAA	TGCCGGGCGA	CAACATCAAA	750
	ATGTTTGTTA	CC				762

10

2) INFORMATION FOR SEQ ID NO: 974

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 804 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 11775

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974

	CCTGGTAGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCGGT	ACATCATCGT	GTTCCCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
30	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTCTGGT	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCC	TGGAAGTGGC	TGGCTTCCTG	GATTCCTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
35	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTGGCT	GACGAAGGCC	500
	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GCGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGTCGTC	650
40	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGA					804

45

2) INFORMATION FOR SEQ ID NO: 975

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 804 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975

```

5  GCGATCCTGG TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA 50
   GCACATCCTG CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC 100
   TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA 150
   ATGGAAGTTC GTGAACTTCT GTCTCAGTAC GACTTCCCCG GCGACGACAC 200
   TCCGATCGTT CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT 250
   GGAAGCGAA AATCCTGGAA CTGGCTGGCT TCCTGGATTG YACATTCCG 300
   GAACCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT 350
10 ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAACGCG 400
   GTATCATCAA AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT 450
   CAGAAGTCTA CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA 500
   AGGCCGTGCT GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG 550
   AAGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG 600
15 CACACCAAGT TCGAATCTGA AGTGATACAT CTGTCCAAAG ATGAAGGCGG 650
   TCGTCATACT CCGTTCCTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA 700
   CTACTGACGT GACTGGTACC ATCGAACTGC CGGAAGGTGT AGAGATGGTA 750
   ATGCCGGGCG ACAACATCAA AATGGTTGTT ACCCTGATCC ACCCGATCGC 800
   GATG 804
20

```

2) INFORMATION FOR SEQ ID NO: 976

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 825 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Mycobacterium avium*
 - (B) STRAIN: Mavi-1
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976

```

40 GGCGCGATCC TGGTGGTCGC CGCCACCGAC GGCCCGATGC CGCAGACCCG 50
   TGAGCACGTG CTGCTCGCCC GTCAGGTCGG TGTGCCCTAC ATCCTGGTCG 100
   CCCTGAACAA GGCCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC 150
   GAGATGGAGG TCCGCGAGCT GCTGGCCGCC CAGGAGTTCG ACGAGGACGC 200
   CCCGGTGGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGC GACGCCAAGT 250
   GGGTCGAGTC CGTCGAGCAG CTGATGGAGG CCGTCGACGA GTCGATCCCG 300
45 GACCCGGTCC GCGAGACGGA GAAGCCGTTT CTGATGCCGG TGGAGGACGT 350
   CTTCAACCAT ACCGGGCGTG GCACCGTGGT CACCGGTCGT GTCGAGCGCG 400
   GTGTGATCAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CCGCCCGACC 450
   AGCACCAAGA CCACGGTCAC CGGTGTGGAR ATGTTCCGCA AGCTGCTCGA 500
   CCAGGGCCAG GCCGGTGACA ACGTCGGTCT GCTGCTGCGT GGTATCAAGC 550
50 GTGAGGACGT CGAGCGCGGC CAGGTCGTGA CCAAGCCCGG CACCACCACG 600
   CCGCACACCG AGTTCGAGGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG 650
   CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG TTCTACTTCC 700
   GCACCACCGA CGTGACCGGT GTGGTGACGC TGCCGGAGGG CACCGAGATG 750
   GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGCTGA TCCAGCCCGT 800
55 CGCCATGGAC GACGGTSTGC GGTTC 825

```

2) INFORMATION FOR SEQ ID NO: 977

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977

```

15  TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
    ACATCCTTCT TTCACGTCAG GTTGGTGTGA AACACCTTAT CGTCTTCATG      100
    AACAAAGTTG ACTTGGTTGA CGACGAAGAA TTGCTTGAAT TGGTTGAAAT      150
    GGAAATCCGT GACCTATTGT CAGAATACGA CTTCCCAGGT GACGATCTTC      200
    CAGTTATCCA AGGTCAGCA CTTAAAGCTC TTGAAGGTGA CTCTAAATAC      250
20  GAAGACATCG TTATGGAATT GATGAACACA GTTGATGAGT ATATCCCAGA      300
    ACCAGAACGT GACACTGACA AACCATTGCT TCTTCCAGTC GAGGACGTAT      350
    TCTCAATCAC TGGACGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT      400
    ATCGTTAAAG TCAACGACGA AATCGAAATT GTTGGTATCA AAGAAGAAAC      450
    TCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAACTTGACG      500
25  AAGGTCTTGC TGGAGATAAC GTAGGTGTCC TTCTTCGTGG TGTTCACCGT      550
    GATGAAATCG AACGTGGACA AGTTATCGCT AAACCAGGTT CAATCAACCC      600
    ACACACTAAA TTCAAAGGTG AAGTCTACAT CCTTACTAAA GAAGAAGGTG      650
    GACGTCACAC TCCATTCTTC AACAACTACC GTCCACAATT CTACTTCCGT      700
    ACTACTGACG TTACAGGTTT AATCGAACTT CCAGCAGGTA CTGAAATGGT      750
30  AATGCCTGGT GATAACGTGA CAATCGACGT TGAGTTGATT CACCCAATCG      800
    CCGTAGAACA AGGTACTACA
  
```

2) INFORMATION FOR SEQ ID NO: 978

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
 (B) STRAIN: M-Gor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978

```

50  GGCGCGATCC TGGTGGTCGC CGCCACCGAT GGCCCGATGC CGCAGACCCG      50
    TGAGCACGTG CTGCTCGCCC GTCAGGTGGG CGTGCCCTAC ATCCTGGTGG      100
    CGCTGAACAA GTCCGACGCG GTCGACGACG AGGAGCTGCT CGAGCTCGTC      150
    GAGCTGGAGG TCCGCGAGTT GCTGGCCGCC CAGGACTTCG ACGAGGAAGC      200
55  TCCGGTGGTC CGGGTCTCGG CGCTGAAGGC GCTCGAGGGC GACGCCACCT      250
    GGGTGAAGTC GGTAGAGGAC TTGATGGACG CGGTCGACGA GTCGATTCCG      300
    GACCCGGTCC GCGACACCGA CAAGCCGTTT CTGATGCCCG TCGAGGACGT      350
    CTTACCATC ACCGGTCGTG GCACCGTCGT CACCGGCCGT GTGGAGCGCG      400
    GCGTGGTGAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CAAGCCGACC      450
60  AGCACCAAGA CCACGGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA      500
  
```


	CCAGGGTCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTGTCAAGC	550
	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTCA	TCAAGCCCCG	CACCACCACT	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAACTA	CCGTCCGCAG	TTCTACTTCC	700
5	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAAATG	750
	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCCG	800
	GCCCATGGAC	GACGGTCTGC	GG			822

10

2) INFORMATION FOR SEQ ID NO: 979

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-11

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979

	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
30	TGGAAATCCG	TGACCTATFG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	ACTTAAAGCT	CTTGAAGGTG	ACTCTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TATATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTGC	TTCTTCCAGT	CGAGGACGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
35	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTTGAC	500
	GAAGGTCTTG	CTGGAGATAA	CGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTCTACA	TCCTTACTAA	AGAAGAAGGT	650
40	GGACGTCACA	CTCCATTCTT	CAACAACCTAC	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	A			821

45

2) INFORMATION FOR SEQ ID NO: 980

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: ATCC 25177

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980

```

5  GGTGCGATCC TGGTGGTTCG CGCCACCGAC GGCCCGATGC CCCAGACCCG      50
   CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC ATCCTGGTAG      100
   CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC      150
   GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCG ACGAGGACGC      200
   CCCGGTTGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT      250
   GGGTTGCCTC TGTCGAGGAA CTGATGAACG CCGTCGACGA GTCGATTCCG      300
   GACCCGGTCC GCGAGACCGA CAAGCCGTTC CTGATGCCGG TCGAGGACGT      350
10 CTTCAACCATT ACCGGCCGCG GAACCGTGGT CACCGGACGT GTGGAGCGCG      400
   GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG      450
   ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA      500
   CCAGGGCCAG GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GCGGTCAAGC      550
   GCGAGGACGT CGAGCGTGCG CAGGTTGTCA CCAAGCCCGG CACCACCACG      600
15 CCGCACACCG AGTTCGAAGG CAGGTCTAC ATCCTGTCCA AGGACGAGGG      650
   CGGCCGGCAC ACGCCGTTCT TCAACAAC TA CCGTCCGACG TTCTACTTCC      700
   GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG      750
   GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT      800
   CGCCATGGAC GAAGGTNTGC GTTTCGCG      828
20

```

2) INFORMATION FOR SEQ ID NO: 981

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 819 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30
    (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Staphylococcus warneri
35 (B) STRAIN: CSG 144

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981

```

40 CGGCGGTATC TTAGTAGTAT CTGCTGCAGA TGGCCCAATG CCACAAACTC      50
   GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA      100
   TTCCTTAAACA AAGCTGACAT GGTGACGAC GAAGAATTAT TAGAATTAGT      150
   TGAAATGGAA GTTCGTGACT TATTATCTGA ATACGACTTC CCTGGTGACG      200
   ATGTACCAGT TATCGTTGGT TCTGCATTAA AAGCTTTAGA AGGCGACCCA      250
   GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCTGTAG ATGACTACAT      300
45 CCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG      350
   ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCAACAGG CCGTGTGAA      400
   CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATCACTGA      450
   AGAAAGCAAG AAAACAACAG TTACAGGTGT AGAAATGTTC CGTAAATTAT      500
   TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTT      550
50 GCACGTGAAG ACGTACAACG TGGACAAGTA TTAGCAGCTC CTGGCTCTAT      600
   TACTCCACAC ACAAATTC AAGCTGATGT TTACGTTT TA TCTAAAGAAG      650
   AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC      700
   TTCCGTACTA CTGACGTAAC TGGCGTTGTT CACTTACCAG AAGGTACTGA      750
   AATGGTTATG CCTGGCGATA ACGTAGAAAT GACTGTTGAA TTAATCGCTC      800
55 CAATCGCGAT TGAAGACG      819

```

2) INFORMATION FOR SEQ ID NO: 982

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982

```

15 CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG      50
   CACATCCTTC TTTCACGTCA GGTGTTGGT AAACACCTTA TCGTCTTCAT      100
   GAACAAGATC GACTTGTTTG ATGACGAAGA ATTGCTTGAA TTGGTTGAAA      150
   TGGAAATCCG TGACCTCTTG TCAGAATACG ACTTCCCAGG TGACGATCTT      200
   CCAGTTATCC AAGGTTTCAGC TCTTAAAGCT CTTGAAGGTG AACTAAGTA      250
20 CGAAGACATC ATCATGGAAT TGATGAACAC TGTTGATGAG TACATCCCAG      300
   AACCAGAACG TGATACTGAC AAACCTCTTC TTCTTCCAGT CGAAGACGTA      350
   TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
   TACTGTTCGT GTCAACGATG AAATCGAAAT CGTTGGTATC AAAGAAGAAA      450
   TCCAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAGCTTGAC      500
25 GAAGGTCCTG CAGGGGACAA CGTAGGTGTA CTTCTTCGTG GTATCCAACG      550
   TGATGAAATC GAACGTGGTC AAGTTATCGC TAAACCAGGT TCAATCAACC      600
   CACACACTAA ATTCAAGGGT GAAGTTTACA TCCTTACTAA AGAAGAAGGT      650
   GGACGTCACA CTCCATTCTT CAACAACACT CGTCCACAGT TCTACTTCCG      700
   TACAACGAC GTTACAGGTT CAATCGAACT TCCAGCAGGT ACTGAAATGG      750
30 TAATGCCTGG TGATAACGTA ACTATCGACG TTGAGTTGAT CCACCCAATC      800
   GCCGTTGAAC AAGG                                     814

```

35 2) INFORMATION FOR SEQ ID NO: 983

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: bases
 (B) TYPE: 810 Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 983

```

50 CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG      50
   CACATCCTTC TTTCACGTCA GGTGTTGGT AAACACCTTA TCGTCTTCAT      100
   GAACAAAGTT GACTTGTTTG ACGACGAAGA ATTGCTTGAA TTGGTTGAAA      150
   TGGAAATCCG TGACCTATTG TCAGAATACG ACTTCCCAGG TGACGATCTT      200
55 CCAGTTATCC AAGGTTTCAGC TCTTAAAGCC CTTGAAGGTG AACTAATA      250
   CGAAGACATC GTTATGGAAT TGATGAACAC AGTTGATGAG TACATCCCAG      300
   AACCAGAACG TGACACTGAC AAACATTGTC TTCTTCCAGT CGAAGACGTA      350
   TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
   TATCGTTAAA GTCAACGACG AAATCGAAAT CGTTGGTATC AAAGAAGAAA      450
60 CTCAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC      500

```

	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
5	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC					810

10

2) INFORMATION FOR SEQ ID NO: 984

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
(B) STRAIN: ATCC 903

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984

	TCCTTGTAGT	AGCTTCAACT	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCCTTCTTT	CACGTCAGGT	TGGTGTTAAA	CACCTTATCG	TCTTCATGAA	100
	CAAGATCGAC	TTGGTTGATG	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	150
30	AAATCCGTGA	CCTCTTGTC	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	200
	GTTATCCAAG	GTTTCAGCTCT	TAAAGCTCTT	GAAGGTGATA	CTAAGTACGA	250
	AGACATCATC	ATGGAATTGA	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	300
	CAGAACGTGA	TACTGACAAA	CCTCTTCTTC	TTCCAGTCGA	AGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	400
35	TGTTTCGTGTC	AACGATGAAA	TCGAAATCGT	TGGTATCAAA	GAAGAAATCC	450
	AAAAAGCAGT	TGTTACTGGT	GTTGAAATGT	TCCGTAAACA	GCTTGACGAA	500
	GGTCTTGCA	GGGACAACGT	AGGTGTACTT	CTTCGTGGTA	TCCAACGTGA	550
	TGAAATCGAA	CGTGGTCAAG	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	600
	ACACTAAAT	CAAGGGTGAA	GTTTACATCC	TTACTAAAGA	AGAAGGTGGA	650
40	CGTCACACTC	CATTCTTCAA	CAACTACCGT	CCACAGTTCT	ACTTCCGTAC	700
	AACTGACGTT	ACAGGTTC	TCGAACTTCC	AGCAGGTACT	GAAATGGTAA	750
	TGCCTGGTGA	TAACGTAACT	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	800
	GTTGAACAAG	GTACTAC				817

45

2) INFORMATION FOR SEQ ID NO: 985

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 798 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
(B) STRAIN: ATCC 35037

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985

	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTTCTTT	CACGTCAGGT	50
	TGGTGTAA	CACCTTATTG	TCTTCATGAA	CAAAATTGAC	TTGGTAGACG	100
5	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	AAATCCGTGA	CCTCTTGTCA	150
	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	GTTATCCAAG	G TTCAGCTCT	200
	TAAAGCTCTT	GAAGGTGACT	CTAAATACGA	AGACATCATT	ATGGAATTGA	250
	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	CAGAACGTGA	CACTGAAAAA	300
	CCATTGCTTC	TTCCAGTCTGA	AGACGTATTC	TCAATCACTG	GACGTGGTAC	350
10	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	TGTTCTGTGC	AACGACGAAA	400
	TCGAAATCGT	TGGTATCAAA	GAAGAACTC	AAAAAGCAGT	TGTTACTGGT	450
	GTTGAAATGT	TCCGTAAACA	ACTTGACGAA	GGTCTTGCCG	GAGATAACGT	500
	AGGTGTCTT	CTTCGTGGTG	TTCAACGTGA	CGAAATCGAA	CGTGGACAAG	550
	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	ACACTAAATT	TAAAGGTGAA	600
15	GTCTACATCC	TTACTAAAGA	AGAAGGTGGA	CGTCACACTC	CATTCTTCAA	650
	CAACTACCGT	CCACAATTCT	ACTTCCGTAC	TACTGACGTT	ACAGGTTCAA	700
	TCGAACTTCC	TGCAGGTACT	GAAATGGTAA	TGCCTGGTGA	TAACGTGACT	750
	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	G TAGAACAAG	GTACTACA	798

20

2) INFORMATION FOR SEQ ID NO: 986

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986

	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
	CTTCTTTTAC	GTCAGGTTGG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
40	AGTTGACTTG	GTTGACGACG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	ATTGTCAGAA	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	200
	ATCCAAGGTT	CAGCACTTAA	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	250
	CATCGTTATG	GAATTGATGA	ACACAGTTGA	TGAGTATATT	CCAGAACCAG	300
	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	350
45	ATCACTGGAC	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	400
	TAAAGTCAAC	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTCAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAACAAC	TGACGAAGGT	500
	CTTGCTGGAG	ATAACGTAGG	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	550
	AATCGAACGT	GGACAAGTTA	TCGCTAAACC	AGGTTCAATC	AACCCACACA	600
50	CTAAATTCAA	AGGTGAAGTC	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	700
	TGACGTTACA	GGTTCAATCG	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	GACGTTGAGT	TGATTCAACC	AATCGCCGTA	800
	GAACAAGGTA	CTACA				815

55

2) INFORMATION FOR SEQ ID NO: 987

60 (i) SEQUENCE CHARACTERISTICS:

752

(A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987

15	CGGACAATCT	TGGTTGTTTC	TGCTACGGAT	GGCCCAATGC	CTCAAACCTCG	50
	TGAACACATT	TTACTTTCTC	GCCAAGTAGG	CGTGAAATAT	TTGATTGTTT	100
	TCTTGAACAA	AACAGATTTA	GTCGATGATG	AAGAATTAAT	TGATCTAGTA	150
	GAAATGGAAG	TTCGTGAACT	ATTAAGCGAA	TATGGATTTC	CAGGTGATGA	200
	TACACCTGTT	ATCAAAGGAT	CAGCATTAAA	AGCATTACAA	GGTGATCCTG	250
	ATGCAGAAGC	AGCTATCATG	GAATTGATGG	ACACAGTCGA	TGAATACATC	300
20	CCAACACCAG	AACGTGATAC	GGACAAACCA	TTATTGTTAC	CCGCCGAAGA	350
	TGTATTTTCA	ATTACTGGAC	GTGGAACAGT	AGCATCTGGT	CGGATTGACC	400
	GTGGGGCTGT	TAGAGTCGGT	GACGAAATCG	AAATCGTAGG	GATCAAACCA	450
	GAAACGCATA	GAGCCGTAGT	AACAGGAGTT	GAAATGTTCC	GCAAAAACGCT	500
	TGATTACGGT	GAAGCAGGGG	ATAACGTAGG	TGTGTTATTA	CGTGGGATTC	550
25	AAAGAGAAGA	CATCGAACGT	GGCCAAGTGA	TTGCCAAACC	TGGTTC AATT	600
	ACACCTCATA	CTAAATTCAA	AGCAGAAGTT	TAGGTTTGA	CTAAAGAAGA	650
	AGGCGGACGT	CATACACCAT	TCTTCAATAA	TTATCGACCA	CAATTTTATT	700
	TCCGCACAAC	TGACGTAAAC	GGAACAATTG	TTTTGCCAGA	AGGAACGGAA	750
	ATGGTCATGC	CTGGCGACAA	CGTAACGATC	GATGTAGAAT	TGATTCATCC	800
30	TGTTGCTATT	GAAAACGGGA	CGACTTTCTC	CA		832

2) INFORMATION FOR SEQ ID NO: 988

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988

50	TGGTGCATC	TTAGTTGTTT	CTGCGACAGA	TGGACCAATG	CCTCAAACCTC	50
	GCGAGCATAT	CCTTTTATCA	CGTCAAGTTG	GTGTAAAATA	TTTGATTGTA	100
	TTTTTGAATA	AAGTTGATTT	GGTCGATGAT	GAAGAATTGA	TCGATCTTGT	150
	AGAAATGGAA	GTTCTGTGAAT	TACTGAATGA	ATATGGTTTC	CCAGGTGATG	200
	ACACACCTGT	CATCAAAGGC	TCTGCATTGA	AAGCATTGCA	AGGTGACCCA	250
55	GAAGCAGAAG	CTGCGATCAA	TGAATTGATG	GAAACAGTGG	ATGACTATAT	300
	CCCAACACCA	GAACGTGATA	CCGACAAACC	ATTGCTTTTA	CCAGTTGAAG	350
	ATGTTTTTCTC	AATCACTGGT	CGCGGAACGG	TAGCATCTGG	TCGTATCGAC	400
	CGTGGAGCCG	TTCTGTCTCG	TGATGAAATC	GAGATCATCG	GAATCAAACC	450
	TGAAACGAAA	AAAGCGGTTG	TGACAGGGGT	AGAGATGTTT	CGTAAAACGT	500
60	TAGATTATGG	CGAAGCTGGA	GATAACGTAG	GAATCTTGTT	ACGTGGTATC	550

	CAAAGAGAAG	ATATTGAACG	TGGACAAGTA	ATTGCGAAAC	CTGGTTCAAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGCGGACG	TCATACACCA	TTCTTCAATA	ACTACGCCC	ACAATTTTAT	700
	TTCCGCACAA	CAGATGTAAC	AGGTACGATC	GTGTTGCCAG	AAGGAACAGA	750
5	AATGGTCATG	CCTGGAGACA	ACGTAACCAT	CGAGGTAGAG	TTGATCCATC	800
	CAGTGGCAAT	CGAACAAGGA	ACGACTTTCT	CTATT		835

10 2) INFORMATION FOR SEQ ID NO: 989

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989

25	TGCGATCTTA	GTA GTATCTA	CTACTGATGG	ACCAATGCCT	CAAACACGTG	50
	AGCACATTTT	GTTATCACGC	CAAGTAGGTG	TTAAATACTT	GATCGTCTTC	100
	TTGAACAAAG	TTGATTTAGT	CGACGATGAA	GAATTGATTG	ATTTAGTTGA	150
	AATGGAAGTA	CGTGAGTTAC	TTTCAGAATA	TGGTTTCCCA	GGCGATGATA	200
30	TTCTGTCTCT	TAAAGGTTCA	GCTCTGAAAG	CTTTAGAAGG	CGATCCTGAA	250
	CAAGAACAAG	TAATCATGGA	CCTAATGGAT	ACGGTTGACG	AATATATCCC	300
	AACACCAGAA	CGTGACACTG	ACAAACCATT	CTTGTTACCA	GTGGAAGATG	350
	TTTTCTCAAT	CACAGGACGT	GGGACTGTTG	CATCTGGTCG	TATTGATCGT	400
	GGGGAAGTTA	AAGTCGGTGA	CGAAGTTGAA	ATTATCGGGA	TCAAACCTGA	450
35	AGTTCAAAAG	GCTGTGCTAA	CTGGACTTGA	AATGTTCCGT	AAAACATTGG	500
	ATTATGGTGA	AGCTGGAGAT	AACGTTGGGG	TTCTATTACG	TGGTATTACA	550
	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCTAAACCAG	GTTCAATTAC	600
	ACCACATACG	AAATTCAGTG	CAGAAGTTTA	TGTGTTGACG	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTC	TTTAACAAC	ATCGTCCTCA	ATTCTACTTC	700
40	CGTACAACAG	ACGTTACCGG	TAATATCGTG	TTGCCAGAAG	GTACTGAAAT	750
	GGTCATGCCT	GGCGATAACG	TAACAATCGA	CGTTGAATTA	ATCCATCCAA	800
	TCGCCGTAGA	AAAAGGAACA	ACTTTCTCTA	TT		832

45 2) INFORMATION FOR SEQ ID NO: 990

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 154 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9440

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990

	GGATCCTGTA	TATGCACAAA	AACTAGGTGT	TAACATCGAT	GAATTACTAT	50
	TATCACAACC	TGATACAGGG	GAGCAAGGTT	TAGAAATCGC	AGAAGCACTT	100
	GTACGAAGTG	GTGCGGTTGA	TATTATCGTA	ATTGACTCTG	TAGCAGCTCT	150
5	TGTA					154

2) INFORMATION FOR SEQ ID NO: 991

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991

25	GCCATTGCAG	AGGCACAGAA	GCAGGGCGGT	ATTGCAGCCT	TCATTGATGC	50
	TGAGCACGCC	TTCGACCGTT	TCTATGCAGA	GAAGTTAGGT	GTGGATGTTG	100
	ATAACCTTTG	GGTTTCACAG	CCAGACAATG	GTGAGCAGGC	TTTAGAGATT	150
	GCCGACCAGC	TGATTCGCTC	TTCCGCTATT	GACATTCTCG	TTGTTCGACTC	200
	AGTTGCAGCC	TTGACTCCAA	AGAAGGAGAT	TGAGGGTGAC	ATGGGTGACT	250
30	CTGCAGTAGG	TTTACAAGCA	CGACTGATGA	GTCAGGCATT	GCGTAAACTT	300
	ACCTCAACAA	TCGCAAAAAC	TAATACTTGC	TGCATCTTCA	TCAACCAGTT	350
	GCGTGAGAAG	ATTGGTGTGA	TGTTTGGTAA	TCCA		384

2) INFORMATION FOR SEQ ID NO: 992

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992

	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	CATACATCGT	50
	TGTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	TTACTAGAAT	100
	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	CTTCCCAGGC	150
55	GACGATGTTT	CTGTAATCGC	TGGTTCTGCT	TTGAAAGCTC	TTGAAGGCGA	200
	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	GTTGACGAAT	250
	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTTCAT	GATGCCAGTC	300
	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	CAGGCCGTGT	350
	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	GTTGGTATTG	400
60	CTGAAGAAAC	TGCTAAAACA	ACTGTAAC TG	GTGTTGAAAT	GTTCCGTAAA	450

TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	TGCTACGTGG	500
TGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	AAAGCTGGTA	550
CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	TTTAACAAAA	600
GAAGAAGGTG	GACGTCATAC	ACCA			624

5

2) INFORMATION FOR SEQ ID NO: 993

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 756 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Streptococcus pyogenes*
 (C) ACCESSION NUMBER: extracted from U40453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993

25	ATGGAAAACA	ATAAAAAAGT	ATTGAAGAAA	ATGGTATTTT	TTGTTTtagt	50
	GACATTTCTT	GGACTAACAA	TCTCGCAAGA	GGTATTTGCT	CAACAAGACC	100
	CCGATCCAAG	CCAAC TTCAC	AGATCTAGTT	TAGTTAAAAA	CCTTCAAAAT	150
	ATATATTTTC	TTTATGAGGG	TGACCCTGTT	ACTCACGAGA	ATGTGAAATC	200
	TGTTGATCAA	CTTTTATCTC	ACGATTTAAT	ATATAATGTT	TCAGGGCCAA	250
	ATTATGATAA	ATTAAAAACT	GAAC TTAAGA	ACCAAGAGAT	GGCAACTTTA	300
30	TTTAAGGATA	AAAACGTTGA	TATTTATGGT	GTAGAATATT	ACCATCTCTG	350
	TTATTTATGT	GAAAATGCAG	AAAGGAGTGC	ATGTATCTAC	GGAGGGGTAA	400
	CAAATCATGA	AGGGAATCAT	TTAGAAATTC	CTAAAAAGAT	AGTCGTTAAA	450
	GTATCAATCG	ATGGTATCCA	AAGCCTATCA	TTTGATATTG	AAACAAATAA	500
	AAAAATGGTA	ACTGCTCAAG	AATTAGACTA	TAAAGTTAGA	AAATATCTTA	550
35	CAGATAATAA	GCAACTATAT	ACTAATGGAC	CTTCTAAATA	TGAAACTGGA	600
	TATATAAAGT	TCATACCTAA	GAATAAAGAA	AGTTTTTGGT	TTGATTTTTT	650
	CCCTGAACCA	GAATTTACTC	AATCTAAATA	TCTTATGATA	TATAAAGATA	700
	ATGAAACGCT	TGACTCAAAC	ACAAGCCAAA	TTGAAGTCTA	CCTAACAACC	750
40	AAGTAA					756

2) INFORMATION FOR SEQ ID NO: 994

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994

55 TGGACTAACA ATCTCGCAAG AGG

23

2) INFORMATION FOR SEQ ID NO: 995

60

756

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995

ACATTCTCGT GAGTAACAGG GT

22

2) INFORMATION FOR SEQ ID NO: 996

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996

ACAAATCATG AAGGGAATCA TTTAG

25

2) INFORMATION FOR SEQ ID NO: 997

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997

CTAATTCTTG AGCAGTTACC ATT

23

2) INFORMATION FOR SEQ ID NO: 998

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998

GGAGGGGTAA CAAATCATGA AGG

23

2) INFORMATION FOR SEQ ID NO: 999

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999
15 TTGACCTTGT TGATGACGAA GAG

23

2) INFORMATION FOR SEQ ID NO: 1000

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000
30 TTAGTGTGTG GGTGATTGA ACT

23

35 2) INFORMATION FOR SEQ ID NO: 1001

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001
AAGAGTTGCT TGAATTAGTT GAG

23

50 2) INFORMATION FOR SEQ ID NO: 1002

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: Genomic DNA
60

758

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (B) STRAIN: ATCC 700294

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002

```

AACATGATCA CTGGTGCCGC TCAAATGGAC GGAGCTATCC TTGTAGTTGC      50
TTCAACTGAT GGACCAATGC CACAAACTCG TGAGCACATC CTTCTTTCAC      100
GTCAGGTTGG TGTTAAACAC CTTATCGTGT TCATGAACAA AGTTGACCTT      150
10 GTTGATGACG AAGAGTTGCT TGAATTAGTT GAGATGGAAA TTCGTGACCT      200
TCTTTCAGAA TACGATTTC CAGGTGATGA CCTTCCAGTT ATCCAAGGTT      250
CAGCTCTTAA AGCTCTTGAA GGCGACACTA AATTTGAAGA CATCATCATG      300
GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC      350
TGACAAACCA TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC      400
15 GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTACTGT TCGTGTCAAC      450
GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTAAAA AAGCTGTTGT      500
TACTGGTGTT GAAATGTTCC GTAAACAAC TGAAGAAGGT CTTGCAGGAG      550
ACAACGTAGG TATCCTTCTT CGTGGTGTTT AACGTGACGA AATCGAACGT      600
GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCACACA CTAAATTCAA      650
20 AGGTGAAGTA TATATCCTTT CTAAAGACGA AGGTGGACGT CACTCTCCAT      700
TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACAAC TGACGTAACA      750
GGTTCAATCG AACTTCCAGC AGGTACAGAA ATGGTTATGC CTGGTGATAA      800
CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA GAACAAGGTA      850
CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT          894
25

```

2) INFORMATION FOR SEQ ID NO: 1003

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003

```

AATGGATCCT GTATATGCAC AAAAATTAGG CGTTAACATA GATGAATTAC      50
45 TATTATCACA GCCTGATACA GGGGAGCAAG GATTAGAAAT CGCGGAAGCA      100
CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC      150
TCTTGTACCG AAAGCAGAGA TTGAAGGCGA CATGGGTGAC TCACACGTAG      200
GTTTACAAGC ACGTTTAATG TCACAAGCAC TTCGTAAGCT TTCAGGAGCA      250
ATCAACAAAT CAAAAACAAT TGCAATCTTT ATTAACCAAA TTCGTGAAAA      300
50 AGTTGGGGTT ATGTTCGGAA ACCCAGAAAC AA          332

```

2) INFORMATION FOR SEQ ID NO: 1004

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004

```

10 ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAAC TC GATCAATAC      50
   GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT      100
   TTCAAATGGT AAAGTCATCG CCCAACTTGG AGCTCGTCAC CAAGCAAGTA      150
   ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGA CTGGGGT      200
   TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT      250
15 TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG      300
   GAACAAGCAC ACCTGTCTAC AACTGGGATA GAGCATATTT CGGTAATATT      350
   ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC      400
   TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG      450
   GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTC AAGTAATACA      500
20 ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC      550
   TTATGCTGCC TTTGCAAATG GTGGCACTTA CTATAAACCA ATGTATATCC      600
   ATAAAGTCGT CTTCAAGTAT GGAAGTAAAA AAGAGTTCTC TAATGTCGGA      650
   ACTCGTGCCA TGAAGGAAAC GACAGCCTAT ATGATGACCG ACATGATGAA      700
   AACAGTCTTG ACTTATGGAA CTGGGCGTGG AGCCTATCTT CCTTGGCTTC      750
25 CTCAAGCTGG TAAACACAGGA ACCTCTAACT ATACAGATGA GGAAGTTGAA      800
   AACCACATCA AGAACACTGG CTATGTAGCT CCAGATGAAA TGT TTGTTGG      850
   TTATACTCGT AAGTATTCTA TGGCTGTATG GACAGGTTAT TCGAATCGTT      900
   TAACTCCTAT CGTTGGAGAT GGTTCCTAG TTGCAGCTAA AGTTTATCGC      950
   TCAATGATAA CGTATCTATC AGAAGATACT CATCCAGAAG ACTGGACGAT      1000
30 GCCAGACGGA CTTTTCAGAA ACGGGGAATT TGTATTCAAA AATGGAGCTC      1050
   GCCCAATATG GACTGAACCC TCTACTCAAC AATCCTCAAC AGCTGAAAGT      1100
   TCAAGCTCAT CATCAGATAG TTCAACTTCA CAGTCTAGCT CAACCACTCC      1150
   AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT      1200
   CAAATACAAC CC                                     1212
35

```

2) INFORMATION FOR SEQ ID NO: 1005

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005

```

55 AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA ATACGTCTCT      50
   TACCCTGACG ATGATTGCA AGTCGCATCT ACGGTCGTAG ATGTTTCAAA      100
   TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA AGTAACGTTT      150
   CATTTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGACTG GGGTTCTGCT      200
   ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG GTGTTTATGA      250
   TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT CCGGGAACAA      300
60 GCACACCTGT CTACAACTGG GATAGAGCAT ATTTCCGTAA TATTACTCTG      350

```

	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
5	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
10	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
15	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	TC				1212

20

2) INFORMATION FOR SEQ ID NO: 1006

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1213 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-03
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
40	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
45	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCG	TTTGCCAACG	GTGGAATTTA	CCACAAACCC	ATGTATATCA	600
50	ATAAGGTCGT	CTTCAGTGAC	GGTAGTAAAA	AAGAATTTTC	AGATGTAGGT	650
	ACACGAGCTA	TGAAAGAAAC	AACTGCTTAC	ATGATGACCG	AAATGATGAA	700
	AACTGTCTTG	GCATACGGAA	CTGGTCGTGG	AGCCTATCTC	CCATGGTTAG	750
	CGCAAGCTGG	TAAGACAGGT	ACTTCTAACT	ACACAGATGA	TGAAATTGAA	800
	AAACACATCA	AGAACTCTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTT	850
55	TTTACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTGTC	TGAAGGAAGC	AATCCAGAGG	ATTGGAATAT	1000
	ACCAGAGGGG	CTCTACAGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1050
	GTTCTACGTG	GAGCTCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1100
60	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAACT	CAACCACTCC	1150

AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
 CAAATACAAC CCC 1213

5

2) INFORMATION FOR SEQ ID NO: 1007

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1218 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007

ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAAC	CGATCAATAC	50
GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
GAACAAGCAC	ACCTGTCTAC	AACTGGGGATA	GAGCATATTT	CGGTAATATT	350
ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
ACAGAATCTA	ATAAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAAACCA	ATGTATATCC	600
ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
CAAATACAAC	CCCTGATC				1218

50 2) INFORMATION FOR SEQ ID NO: 1008

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1223 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008

5	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	150
	AGTAACGTTT	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	200
10	GGGTTCTGCT	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	250
	GTGTTTATGA	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	300
	CCGGGAACAA	GCACACCTGT	CTACAACTGG	GATAGAGCAT	ATTTTCGGTAA	350
	TATTACTCTG	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	450
15	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	500
	TACAACAGAA	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	550
	CTGCTTATGC	TGCCTTTGCA	AATGGTGGCA	CTTACTATAA	ACCAATGTAT	600
	ATCCATAAAG	TCGTCTTCAG	TGATGGAAAGT	AAAAAAGAGT	TCTCTAATGT	650
	CGGAACTCGT	GCCATGAAGG	AAACGACAGC	CTATATGATG	ACCGACATGA	700
20	TGAAAACAGT	CTTGACTTAT	GGAAGTGGGC	TGGGAGCCTA	TCTTCCTTGG	750
	CTTCCTCAAG	CTGTGAAAAC	AGGAACCTCT	AACATACAG	ATGAGGAAGT	800
	TGAAAACCCAC	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	850
	TTGGTTATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCGAAT	900
	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
25	TCGCTCAATG	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	1000
	CGATGCCAGA	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	1050
	GCTCGCCCAA	TATGGACTGA	ACCCTCTACT	CAACAATCCT	CAACAGCTGA	1100
	AAGTTCAAGC	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	1150
	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
30	CAATCAAATA	CAACCCCTGA	TCA			1223

2) INFORMATION FOR SEQ ID NO: 1009

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1214 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009

50	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
55	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AAC TGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
60	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550

	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
5	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
10	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCT				1214
15						

2) INFORMATION FOR SEQ ID NO: 1010

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1223 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010

	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	CTACAACTCC	GATCAATACG	50
35	TCTCTTACCC	TGACGATGAT	TTGCAAGTCG	CATCTACGGT	CGTAGATGTT	100
	TCAAATGGTA	AAGTCATCGC	ACAAC TTGGT	GCTCGTCATC	AAGCAAGTAA	150
	TGTTTCATTC	GGTACCAACC	AGGCCGTAGA	AACCAATCGT	GACTGGGGAT	200
	CATCAATGAA	ACCAATCACT	GACTATGCTC	CCGCTTTAGA	ATATGGAGTC	250
	TATGACTCTA	CTGCTTCTAT	TGTACATGAT	GTCCCTTATA	ACTATCCTGG	300
40	CACTGATACT	CCACTCTACA	ACTGGGATCA	TGTCTACTTT	GGAAACATTA	350
	CAATCCAGTA	TGCTCTTCAA	CAATCACGAA	ATGTCACAGC	CGTTGAGACT	400
	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	ACCTTCCTTA	ATGGTCTTGG	450
	TATCGACTAT	CCAAGCATGC	ATTATGCAAA	CGCCATTTCA	AGTAACACAA	500
	CTGAATCCAA	CAAAAAATAT	GGTGCAAGTA	GTGAAAAAAT	GGCTGCTGCC	550
45	TACGCTGCTT	TTGCTAATGG	TGGTATTTAT	CACAAACCAA	TGTATATCAA	600
	TAAATATCGTC	TTTAGTGATG	GTAGCGAAAA	AGAATTTTCT	GATGCTGGTA	650
	CACGAGCTAT	GAAAGAGACT	ACTGCCTATA	TGATGACTGA	AATGATGAAA	700
	ACTGTTTTAA	CTTACGGAAC	AGGACGTGGA	GCCTACCTAC	CATGGCTTCC	750
	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	800
50	AGTATATCAA	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	850
	TATACCCGTA	AATATGCAAT	GGCTGTTTGG	ACAGGATACT	CAAATCGTCT	900
	AACTCCAATC	ATCGGAGATG	GTTTCCTTGT	TGCTGGTAAA	GTCTATCGTT	950
	CAATGATAAC	TTACCTTTCT	GAAGATGACC	AACCTGGAGA	TTGGACAATG	1000
	CCAGATGGCT	TGTATAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	1050
55	TTCTACGTGG	AGCTCACCTG	CTCCACAACA	ACCCCCATCA	ACTGAAAGTT	1100
	CAAGCTCATC	ATCAGATAGT	TCAACTTCAC	AGTCTAACTC	AACCACTCCA	1150
	AGCACAAATA	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	1200
	AAATACAACC	CCTGATCAAC	AAA			1223

60

2) INFORMATION FOR SEQ ID NO: 1011

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1207 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGA CTG	GGGTTCTGCT	200
ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
GCACACCTGT	CTACAAC TGG	GATAGAGCAT	ATTTTCGGTAA	TATTACTCTG	350
CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
TGCCCTTGCA	AATGGTGCCA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
TCGTCTTCAG	TGATGGAAGT	AAAAAAGAGT	TCTCTAATGT	CGGAACTCGT	650
GCCATGAAGG	AAACGACAGC	CTATATGATG	ACCGACATGA	TGAAAACAGT	700
CTTGACTTAT	GGAAGTGGG	GTGGAGCCTA	TCTTCCTTGG	CTTCCTCAAG	750
CTGGTAAAC	AGGAACCTCT	AACTATACAG	ATGAGGAAGT	TGAAAACCAC	800
ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCGAAT	CGTTTAACTC	900
CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGCCCAA	1050
TATGGACTGA	ACCCTCTACT	CAACAATCCT	CAACAGCTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCC					1207

2) INFORMATION FOR SEQ ID NO: 1012

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-09

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012

5 AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA ATACGTCTCT 50
 TACCCTGACG ATGATTTGCA AGTCGCATCT ACGGTCGTAG ATGTTTCAAA 100
 TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA AGTAACGTTT 150
 5 CATTTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGACTG GGGTCTGCT 200
 ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG GTGTTTATGA 250
 TTCCACTGCA ACTATGGTTA ATGATATTC TTATAACTAT CCGGGAACAA 300
 GCACACCTGT CTACAACCTG GATAGAGCAT ATTTCCGTAA TATTACTCTG 350
 10 CAATATGCTC TTCAACAATC ACGAAATGTC ACAGCCGTTG AGACTTTGAA 400
 TAAGGTCGGT CTAGATAGAG CTAAAACCTT CCTTAATGGT CTTGGTATCG 450
 ACTATCCAAG CATGCATTAT GCAAACGCCA TTTCAAGTAA TACAACAGAA 500
 TCTAATAAAC AATACGGAGC AAGTAGTGAA AAAATGGCTG CTGCTTATGC 550
 TGCCTTTGCC AACGGTGGAA TTTACCACAA ACCCATGTAT ATCAATAAGG 600
 TCGTCTTCAG TGACGGTAGT AAAAAAGAAT TTTCAGATGT AGGTACACGA 650
 15 GCTATGAAAG AAACAACCTG TTACATGATG ACCGAAATGA TGAAAACCTGT 700
 CTTGGCATAAC GGAACCTGGT GTGGAGCCTA TCTCCCATGG TTAGCGCAAG 750
 CTGGTAAGAC AGGTACTTCT AACTACACAG ATGATGAAAT TGAAAAACAC 800
 ATCAAGAACA CTGGCTATGT AGCTCCAGAT GAAATGTTTG TTGGTTATAC 850
 TCGTAAGTAT TCTATGGCTG TATGGACAGG TTATTCTGAAT CGTTTAACTC 900
 20 CTATCGTTGG AGATGGTTTC CTAGTTGCAG CTAAAGTTTA TCGCTCAATG 950
 ATAACGTATC TATCAGAAGA TACTCATCCA GAAGACTGGA CGATGCCAGA 1000
 CGGACTTTTC AGAAACGGGG AATTTGTATT CAAAAATGGA GCTCGTTCTA 1050
 CGTGGAACCTC ACCTGCTCCA CAACAACCCC CATCAACTGA AAGTTCAAGC 1100
 TCATCATCAG ATAGTTCAAC TTCACAGTCT AGCTCAACCA CTCCAAGCAC 1150
 25 AAATAATAGT ACGACTACCG ATCCTAACAA TAATACGCAA CAATCAAATA 1200
 C 1201

30 2) INFORMATION FOR SEQ ID NO: 1013

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1220 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013

45 TG TAGACCAA GAAGCTCAAA AACATCTGTG GGATATCTAC AACTCCGATC 50
 AATACGTCTC TTACCCTGAC GATGATTTGC AAGTCGCATC TACGGTCGTA 100
 GATGTTTCAA ATGGTAAAGT CATCGCACAA CTTGGTGCTC GTCATCAAGC 150
 AAGTAATGTT TCATTCCGTA CCAACCAGGC CGTAGAAACC AATCGTGACT 200
 50 GGGGATCATC AATGAAACCA ATCACTGACT ATGCTCCCGC TTTAGAATAT 250
 GGAGTCTATG ACTCTACTGC TTCTATTGTA CATGATGTCC CTTATAACTA 300
 TCCTGGCACT GATACTCCAC TCTACAACCTG GGATCATGTC TACTTTGGAA 350
 ACATTACAAT CCAGTATGCT CTTCAACAAT CACGAAATGT CACAGCCGTT 400
 GAGACTTTGA ATAAGGTCGG TCTAGATAGA GCTAAAACCT TCCTTAATGG 450
 55 TCTTGGTATC GACTATCCAA GCATGCATTA TGCAAACGCC ATTTCAAGTA 500
 ACACAACCTGA ATCCAACAAA AAATATGGTG CAAGTAGTGA AAAAAATGGCT 550
 GCTGCCTACG CTGCTTTTGC TAATGGTGTT ATTTATCACA AACCAATGTA 600
 TATCAATAAA ATCGTCTTTA GTGATGGTAG CGAAAAAGAA TTTTCTGATG 650
 CTGGTACACG AGCTATGAAA GAGACTACTG CCTATATGAT GACTGAAATG 700
 60 ATGAAAACCTG TTTTAACTTA CGGAACAGGA CGTGGAGCCT ACCTACCATG 750

	GCTTCCACAA	GCAGGTAAGA	CAGGTACTTC	TAAGTATACT	GACGAAGAAA	800
	TTGAAAAGTA	TATCAAGAAC	ACTGGCTACG	TAGCTCCAGA	TGAAATGTTT	850
	GTGGGTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTTCGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
5	ATCGCTCTAT	GATGACCTAC	CTGTCTGAAG	GAAGCAATCC	AGAGGATTGG	1000
	AATATACCAG	AGGGGCTCTA	CAGAAATGGA	GAATTCGTAT	TAAAAATGG	1050
	TGCTCGTTCT	ACGTGGAGCT	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAGCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
10	ACAATCAAAT	ACAACCCCTG				1220

2) INFORMATION FOR SEQ ID NO: 1014

15

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 1199 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014

30	CAAAAACATC	TGTGGGATAT	TTACAATACA	GACGAATACG	TTGCCTATCC	50
	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	TGTTGATGTT	TCTAACGGTA	100
	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	TGTTTCCTTC	150
	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GACTGGGGAT	CAACTATGAA	200
	ACCGATCACA	GACTATGCTC	CTGCCTTGGA	GTACGGTGTC	TACGATTCAA	250
35	CTGCTACTAT	CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACC	300
	CCTGTTTATA	ACTGGGATAG	GGGCTACTTT	GGCAACATCA	CCTTGCAATA	350
	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	CGTGGAAACT	CTAAACAAGG	400
	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTCGG	AATCGACTAC	450
	CCAAGTATTC	ACTACTCAA	TGCCATTTCA	AGTAACACAA	CCGAATCAGA	500
40	CAAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	550
	TTGCAAATGG	TGGAACCTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	600
	TTTAGTGATG	GGAGTGAAAA	AGAGTTCTCT	AATGTCCGAA	CTCGTGCCAT	650
	GAAGGAAACG	ACAGCCTATA	TGATGACCGA	CATGATGAAA	ACTGTCCTAG	700
	TATACGGAAT	CGGACGTGGA	GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	750
45	AAAACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	AGTATATCAA	800
	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	TATACCCGCA	850
	AATATGCAAT	GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	900
	GTAGGCGATG	GCCTTACGGT	CGCTGCTAAA	GTTTACCGCT	CTATGATGAC	950
	CTACCTGTCT	GAAGGAAGCA	ATCCAGAGGA	TTGGAATATA	CCAGAGGGGC	1000
50	TCTACAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	TTCTACGTGG	1050
	AACTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	CAAGCTCATC	1100
	ATCAGATAGT	TCAACTTCAC	AGTCTAGCTC	AACCACTCCA	AGCACAAATA	1150
	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	AAATACAAC	1199

55

2) INFORMATION FOR SEQ ID NO: 1015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 bases

60

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
15	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACCACTGG	GATAGAGCAT	ATTTCCGGTAA	TATTACTCTG	350
20	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
25	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTG	700
	CTTGGCATAC	GGAACCTGGC	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
30	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
35	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	T				1211

40

2) INFORMATION FOR SEQ ID NO: 1016

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1222 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016

	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCACAAAC	TTGGTGCTCG	TCATCAAGCA	150
60	AGTAATGTTT	CATTCGGTAC	CAACCAGGCC	GTAAGAAACCA	ATCGTGACTG	200

	GGGATCATCA	ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	250
	GAGTCTATGA	CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	300
	CCTGGCACTG	ATACTCCACT	CTACAACTGG	GATCATGTCT	ACTTTGGAAA	350
	CATTACAATC	CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
5	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	450
	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	500
	CACAACTGAA	TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	550
	CTGCCTACGC	TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	600
	ATCAATAAAA	TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	650
10	TGGTACACGA	GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	700
	TGAAAACGTG	TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	750
	CTTCCACAAG	CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	800
	TGAAAAGTAT	ATCAAGAACA	CTGGCTACGT	AGCTCCAGAT	GAAATGTTTG	850
	TGGGTTATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTGCAAT	900
15	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
	TCGCTCTATG	ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	1000
	ATATACCAGA	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	1050
	GCTCGTTCTA	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	1100
	AAGTTCAAGC	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	1150
20	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
	CAATCAAATA	CAACCCCTGA	TC			1222

25 2) INFORMATION FOR SEQ ID NO: 1017

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1229 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017

40	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	50
	AATACGTTGC	CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	100
	GATGTTTCTA	ACGGTAAAGT	CATTGCCACG	CTAGGAGCAC	GCCATCAGTC	150
	AAGTAATGTT	TCCTTCGGAA	TTAACCAAGC	AGTAGAAACA	AACCGCGACT	200
45	GGGGATCAAC	TATGAAACCG	ATCACAGACT	ATGCTCCTGC	CTTGGAGTAC	250
	GGTGTCTACG	ATTCAACTGC	TACTATCGTT	CACGATGAGC	CCTATAACTA	300
	CCCTGGGACA	AATACCCCTG	TTTATAACTG	GGATAGGGGC	TACTTTGGCA	350
	ACATCACCTT	GCAATACGCC	CTGCAACAAT	CGCGAAACGT	CCCAGCCGTG	400
	GAAACTCTAA	ACAAGGTCGG	ACTCAACCGC	GCCAAGACTT	TCCTAAATGG	450
50	TCTCGGAATC	GACTACCCAA	GTATTCACTA	CTCAAATGCC	ATTTCAAGTA	500
	ACACAACCGA	ATCAGACAAA	AAATATGGAG	CAAGTAGTGA	AAAGATGGCT	550
	GCTGCTTACG	CTGCCTTTGC	AAATGGTGGA	ACTTACTATA	AACCAATGTA	600
	TATCCATAAA	GTCGTCTTTA	GTGATGGGAG	TGAAAAAGAG	TTCTCTAATG	650
	TCGGAACCTG	TGCCATGAAA	GAAACAACCTG	CTTACATGAT	GACCGAAATG	700
55	ATGAAAACCTG	TCCTGGCATA	CGGAAGTGGT	CGTGGAGCCT	ATCTCCCATG	750
	GTTAGCGCAA	GCTGGTAAGA	CAGGTACTTC	TAACCTACACA	GATGATGAAA	800
	TTGAAAAACA	CATCAAGAAC	ACTGGCTATG	TAGCTCCAGA	TGAAATGTTT	850
	GTTGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTTATGGACAG	GTTATTCGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
60	ATCGCTCAAT	GATAACGTAT	CTATCAAAAG	ATACTCATCC	AGAAGACTGG	1000

	ACGATGCCAG	ACGGACTTTT	CAGAAACGGG	GAATTTGTAT	TCAAAAATGG	1050
	AGCTCGTTCT	ACGTGGAAC	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAACTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
5	ACAATCAAAT	ACAACCCCTG	ATCAACAAA			1229

2) INFORMATION FOR SEQ ID NO: 1018

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018

25	ATGTAGACCA	AGAGGCTCAA	AAACGTCTGT	GGGATATCTA	CAACTCCGAT	50
	CAATACGTCT	CTTACCCTGA	CGATGATTTG	CAAGTCGCAT	CTACGGTCGT	100
	AGATGTTTCA	AATGGTAAAG	TCATCGCCCA	ACTTGGAGCT	CGTCACCAAG	150
	CAAGTAACGT	TTCATTTGGT	ACCAACCAAG	CTGTGGAAAC	CAACCGTGAC	200
	TGGGGATCAA	GCATGAAACC	AATCACTGAT	TATGCCCCAG	CCTTAGAATA	250
30	TGGTGTATAT	GATTCCACTG	CAACTATGGT	TAATGATATT	CCTTATAACT	300
	ATCCGGGCAC	AAGCACACCT	GTCTACAAC	GGGATCGAGC	ATATTTTGGT	350
	AATATTAGCC	TGCAATATGC	CCTTCAACAA	TCTCGTAACG	TGCTTGCCGT	400
	TGAAACACTA	AACAAGGTTG	GTTTAGATAG	AGCCAAAAC	TTCCTAAATG	450
	GTTTGGGAAT	TGACTATCCA	AGTATTCACT	ACTCAAATGC	TATTTCAAGT	500
35	AATACAAC	AATCTAGTAA	ACAGTACGGG	GCAAGCAGTG	AGAAAATGGC	550
	TGCGGCTTAC	GCTGCATTCT	CTAATGGCGG	TATTTACCAC	AAACCAATGT	600
	ACATCAATAA	AGTTGTCTTT	AGTGATGGTA	GCGAAAAAGA	ATTTTCTGAT	650
	GCTGGTACAC	GAGCTATGAA	AGAGACTACT	GCCTATATGA	TGACTGAAAT	700
	GATGAAAAC	GTTTTAACTT	ACGGAACAGG	ACGTGGAGCC	TACCTACCAT	750
40	GGCTTCCACA	AGCAGGTAAG	ACAGGTACTT	CTAACTATAC	TGACGACGAA	800
	ATTGAAAAGT	ATATCAAGAA	CACTGGCTAC	GTAGCTCCAG	ATGAAATGTT	850
	TGTGGGTTAT	ACTCGTAAAG	ATTCTATGGC	TGTATGGACT	GGATACTCAA	900
	ATCGTTTAAC	TCCAATCATT	GGAGATGGTT	TCCTAGTTGC	TGCCAAAGTT	950
	TATCGCTCAA	TGATATCGTA	TCTATCAGAA	GATGACCATC	CTGGAGATTG	1000
45	GACAATGCCT	GAGGGAGTAT	ACAGAAAGTG	AGAATTTCGT	TTTAAAAATG	1050
	GTGCTCGTTC	TACGTGGAGC	TCCCCTGCTC	CACAACAACC	CCCATCAACT	1100
	GAAAGTTCAA	GCTCATCATC	AGATAGTTCA	ACTTCACAGT	CTAGCTTAAC	1150
	CACTCCAAGC	ACAAATAATA	GTACGACTAC	CAATCCTAAC	AACAATACGC	1200
	AACAATCAAA	TACAACCCCT	GATCA			1225

2) INFORMATION FOR SEQ ID NO: 1019

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019

```

10 GCCTCTATTT CAAAGGAGAT GCCTGGCATT AGTATTTCTA CTTCTTGGA 50
   TCGAAAGGTT TTGGAAACTT CCCTTTCTTC TATAGTAGGG AGTGATATCCA 100
   GTGAAAAAGC TGGTCTCCCA GCGGAAGAAG CAGAATCCTA TCTTAAAAAA 150
   GGCTATTCTC TAAATGACCG TGTGGAACC TCCTATTTGG AAAAGCAATA 200
   TGAAGAGACC TTACAAGGAA AACGCTCGGT AAAAGAAATC CATCTGGATA 250
   AATATGGCAA TATGGAAAGC GTGGACACAA TTGAGGAAGG TAGTAAGGGA 300
15 AACAAATATCA AACTGACCAT TGATTTGGCC TTCCAAGATA GCGTGGATGC 350
   TTTGCTGAAA AGTTATTTCA ATTCCGAGCT AGGAAATGGT GGAGCTAAAT 400
   ATTCTGAAGG TGTCTATGCA GTCGCCCTTA ACCCAAAAAC AGGTGCTGTT 450
   TTATCCATGT CAGGGATCAA ACATGACCTG AAAACGGGAG AGTTGACTCC 500
   TGATTCCTTG GGAACGGTAA CCAATGTCTT TGTCCCAGGT TCGGTTGTCA 550
20 AGGCTGCGAC CATCAGCTCA GGTGGGAAA ATGGTGT TTT ATCAGGAAAC 600
   CAAACCTTAA CAGATCAGCC TATTGTTTTT CAAGGTTTCA CTCCAATTTA 650
   TTCTTGGTAT AAATTGGCAT ATGGATCTTT TCCTATTACA GCTGTGGAAG 700
   CCTTGAGTA TTCATCCAAT GCTTACATGG TTCAAACCGC TCTTGAATC 750
   ATGGGCCAGA CCTATCAACC AAATATGTTT GTTGAACCA GCAATTGGA 800
25 AACAGCTATG GGAAACTTC GTGCGACCTT TGGCGAATAT GGCTTGGGGG 850
   CTGCGACCGG AATTGACCTA CCAGATGAAT CTAAGGATT TGTTCCTCAA 900
   GAGTATAGCT TTGCTAATTA CATCACC AAT TCCTTTGGGC AGTTTGATAA 950
   CTATACGCC ATGCAAGTTGG CTCAGTATGT AGCAACTATT GCAAATAATG 1000
   GTGTTTCGTG GGTCTCTCGT ATTGTTGAAG GCATTTATGG TAATAATGAT 1050
30 AAGGGAGGAC TGGGTGACTT GATTTCAGCA CTGCAACCGA CAGAGATGAA 1100
   TAAGGTCAAT ATATCCGACT CCGATATGAG CATCTTGCAC CAAGGTTTTT 1150
   ATCAGGTTGC CCATGGTACT AGTGGATTGA CAACTGGACG TGCCTTTTCA 1200
   AATGGTGCCT TGGTATCCAT TAGCGGAAAA ACAGGTACAG CCGAAAGCTA 1250
   TGTGGCAGAT GGTCAGCAAG CAACCAATAC CAATGCGGTG GCCTATGCCC 1300
35 CATCTGATAA TCCCCAAATC GCTGTGCGAC TGGTCTTTCC TCATAATACC 1350
   AATCTAACAA ATGGTGATAG ACCTTCCATT GCGCGTGACA TTATCAATCT 1400
   GTATCAAAAA TACCATCCAA TGAAGTAGAA AGGAAATTA 1439

```

40

2) INFORMATION FOR SEQ ID NO: 1020

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020

```

60 GCCTCTATTT CAAAGGAGAT GCCTGGCATT AGTATTTCTA CTTCTTGGA 50
   TCGAAAGGTT TTGGAAACTT CCCTTTCTTC TATAGTAGGG AGTGATATCCA 100
   GTGAAAAAGC TGGTCTCCCA GCGGAAGAAG CAGAATCCTA TCTTAAAAAA 150
   GGCTATTCTC TAAATGACCG TGTGGAACC TCCTATTTGG AAAAGCAATA 200

```


	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
5	ATTCTGAAGG	TGCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCTTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTT	CAAGGTTTCA	CTCCAATTTA	650
10	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGGAGTA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
	AACAGCTATG	GGAAAACTTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAAA	900
15	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAATAATG	1000
	GTGTTCTGAT	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
	AAGGGAGGAC	TGGGTGACTT	GATTACAGCA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGCAC	CAAGGTTTTT	1150
20	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTCA	1200
	AATGGTGCC	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
	CATCTGATAA	TCCCCAAATC	GCTGTCGCAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
25	GTATCAAAAA	TACCATCCAA	TGAAC TAGAA	AGGAAATTAT	G	1441

2) INFORMATION FOR SEQ ID NO: 1021

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021

45	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
50	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
55	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
60	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800

	TGGAACACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCGA	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
5	AATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
10	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCTCATATA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATT	1396

15

2) INFORMATION FOR SEQ ID NO: 1022

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022

	AAAGGAGATG	CCTGGCATTG	GTATTTCTAC	TTCTTGGGAT	CGAAAGGTTT	50
	TGGAACCTTC	CCTTTCTTCT	ATAGTAGGGA	GTGTATCCAG	TGAAAAAGCT	100
	GGTCTCCCAG	CGGAAGAAGC	AGAATCCTAT	CTTAAAAAAG	GCTATTCTCT	150
35	AAATGACCGT	GTTGGAACCT	CCTATTGGGA	AAAGCAATAT	GAAGAGACCT	200
	TACAAGGAAA	ACGCTCGGTA	AAAGAAATCC	ATCTGGATAA	ATATGGCAAT	250
	ATGGAAAGCG	TGGACACAAT	TGAGGAAGGT	AGTAAGGGAA	ACAATATCAA	300
	ACTGACCATT	GATTTGGCCT	TCCAAGATAG	CGTGGATGCT	TTGCTGAAAA	350
	GTTATTTCAA	TTCCGAGCTA	GGAAATGGTG	GAGCTAAATA	TTCTGAAGGT	400
40	GTCTATGCAG	TCGCCCTTAA	CCCAAAAACA	GGTGCTGTTT	TATCCATGTC	450
	AGGGATCAAA	CATGACCTGA	AAACGGGAGA	GTTGACTCCT	GATTCCCTGG	500
	GAACGGTAAC	CAATGTCTTT	GTCCCAGGTT	CGTTGTGCAA	GGCTGCGACC	550
	ATCAGCTCAG	GTTGGGAAAA	TGGTGTTTTA	TCAGGAAACC	AAACCTTAAC	600
	AGATCAGCCT	ATTGTTTTTC	AAGGTTTCAGC	TCCAATTTAT	TCTTGGTATA	650
45	AATTGGCATA	TGGATCTTTT	CCTATTACAG	CTGTGGAAGC	CTTGGAGTAT	700
	TCATCCAATG	CTTACATGGT	TCAAACCGCT	CTTGGAAATCA	TGGGCCAGAC	750
	CTATCAACCA	AATATGTTTG	TTGGAACCA	CAATTTGGAA	ACAGCTATGG	800
	GAAAACCTCG	TGCGACCTTT	GGCGAATATG	GCTTGGGGGC	TGCGACCGGA	850
	ATTGACCTAC	CAGATGAATC	TACTGGATTT	GTTCCCAAAG	AGTATAGCTT	900
50	TGCTAATTAC	ATCACCAATT	CCTTTGGGCA	GTTTGATAAC	TATACGCCCA	950
	TGCAGTTGGC	TCAGTATGTA	GCAACTATTG	CAAATAATGG	TGTTCTGTGTG	1000
	GCTCCTCGTA	TTGTTGAAGG	CATTTATGGT	AATAATGATA	AGGGAGGACT	1050
	GGGTGACTTG	ATTCAGCAAC	TGCAACCGAC	AGAGATGAAT	AAGGTCAATA	1100
	TATCCGACTC	CGATATGAGC	ATCTTGACAC	AAGGTTTTTA	TCAGGTTGCC	1150
55	CATGGTACTA	GTGGATTGAC	AACCTGGACGT	GCCTTTTCAA	ATGGTGCCCTT	1200
	GGTATCCATT	AGCGGAAAAA	CAGGTACAGC	CGAAAGCTAT	GTGGCAGATG	1250
	GTCAGCAAGC	AACCAATACC	AATGCGGTGG	CCTATGCCCC	ATCTGATAAT	1300
	CCCCAATCG	CTGTGCGAGT	GGTCTTTTCT	CATAATACCA	ATCTAACAAA	1350
	TGGTGTAGGA	CCTTCCATTG	CGCGTGACAT	TATCAATCTG	TATCAAAAAT	1400
60	ACCATCCAAT	GAAGTAGAAA	GGAAATTA			1428

2) INFORMATION FOR SEQ ID NO: 1023

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023

```

20  TGCCTCTATT TCAAAGGAGA TGCCTGGCAT TAGTATTTCT ACTTCTTGGG      50
    ATCGAAAGGT TTTGGAAACT TCCCTTTCTT CTATAGTAGG GAGTGTATCC      100
    AGTGAAAAAG CTGGTCTCCC AGCGGAAGAA GCAGAATCCT ATCTTAAAAA      150
    AGGCTATTCT CTAAATGACC GTGTTGGAAC CTCCTATTTG GAAAAGCAAT      200
    ATGAAGAGAC CTTACAAGGA AAACGCTCGG TAAAAGAAAT CCATCTGGAT      250
25  AAATATGGCA ATATGGAAAG CGTGGACACA ATTGAGGAAG GTAGTAAGGG      300
    AAACAATATC AAACGACCA TTGATTTGGC CTTCCAAGAT AGCGTGGATG      350
    CTTTGCTGAA AAGTTATTTT AATTCCGAGC TAGGAAATGG TGGAGCTAAA      400
    TATTCTGAAG GTGTCTATGC AGTCGCCCTT AACCCTAAAA CAGGTGCTGT      450
    TTTATCCATG TCAGGGATCA AACATGACCT GAAAACGGGA GAGTTGACTC      500
30  CTGATTCCTT GGGAACGGTA ACCAATGTCT TTGTCCCAGG TTCGGTTGTC      550
    AAGGCTGCGA CCATCAGCTC AGGTGGGAA AATGGTGTTT TATCAGGAAA      600
    CCAAACCTTA ACAGATCAGC CTATTGTTTT CCAAGGTTCA GCTCCAATTT      650
    ATTCTTGGTA TAAATTGGCA TATGGATCTT TTCCTATTAC AGCTGTGGAA      700
    GCCTTGGAGT ATTCATCCAA TGCTTACATG GTTCAAACCG CTCTTGGAA      750
35  CATGGGCCAG ACCTATCAAC CAAATATGTT TGTGGAACC AGCAATTG      800
    AAACAGCTAT GGGAAACTT CGTGCGACCT TTGGCGAATA TGGCTTGGGG      850
    GCTGCGACCG GAATTGACCT ACCAGATGAA TCTACTGGAT TTGTTCCCAA      900
    AGAGTATAGC TTTGCTAATT ACATCACCAA TTCCTTTGGG CAGTTTGATA      950
    ACTATACGCC CATGCAGTTG GCTCAGTATG TAGCAACTAT TGCAATAAAT      1000
40  GGTGTTTCGTG TGGCTCCTCG TATTGTTGAA GGCATTTATG GTAATAATGA      1050
    TAAGGGAGGA CTGGGTGACT TGATTCAGCA ACTGCAACCG ACAGAGATGA      1100
    ATAAGGTCAA TATATCCGAC TCCGATATGA GCATCTTGCA CCAAGGTTTT      1150
    TATCAGGTTG CCCATGGTAC TAGTGGATTG ACAACTGGAC GTGCCTTTTC      1200
    AAATGGTGCC TTGGTATCCA TTAGCGGAAA AACAGGTACA GCCGAAAGCT      1250
45  ATGTGGCAGA TGGTCAGCAA GCAACCAATA CCAATGCGGT GGCCATATGCC      1300
    CCATCTGATA ATCCCCAAAT CGCTGTGCGA GTGGTCTTTC CTCATAATAC      1350
    CAATCTAACA AATGGTGTAG GACCTTCCAT TGCGCGTGAC ATTATCAATC      1400
    TGTATCAAAA ATACCATCCA ATGAAGTAGA AAGGAAATTA TG              1442

```

2) INFORMATION FOR SEQ ID NO: 1024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTGGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACTGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTGCTGA	AAAGTTATTT	CAATTCGAG	CTAGGAAATG	GTGGAGCTAA	400
	ATATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCTG	450
	TTTTATCCAT	GTCAGGGATC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGTGTT	TTATCAGGAA	600
20	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTT	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAACT	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCTA	900
	AAGAGTATAG	CTTTGCTAAT	TACATCACC	ATTCCTTTGG	GCAGTTTGAT	950
	AACATATAC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAAATA	1000
	TGGTGTTTCG	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTTCAG	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	TTCCGATATG	AGCATCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCCCATGGTA	CTAGTGGATT	GACAACTGGA	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACAGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGCA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTGCG	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AATGAACTAG	AAAGGAAATT	ATGCT	1445

40 2) INFORMATION FOR SEQ ID NO: 1025

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025

55	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAGA	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTGGGAA	CCTCGTATTT	GGAAAAGCAA	200
60	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250

	TAAATATGGC	AATATGGAAA	CGGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACTGACC	ATTGATTGG	CCTTCCAAGA	TAGCGTGGAT	350
	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCCAA	400
	GTATTCTGAG	GGTGTGTATG	CAGTCGCCCT	TAACCCCAAA	ACAGGTGCTG	450
5	TTTTGTCTAT	GTCAGGACTC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTCCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CTGGCTGGGA	AAATGGTGTG	TTATCAGGAA	600
	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTT	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
10	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GTTCAAACC	GCTCTTGGA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTG	800
	GAAACAGCTA	TGGGAAAAC	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCTCA	900
	AAGACTATAG	CTTTGCTAAT	TACATCACCA	ATGCCTTTGG	GCAGTTTGAT	950
15	AACTATACGC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTTCAGC	AACTGCAACC	GACAGAGATG	1100
	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTATCTTGC	ACCAAGGATT	1150
	TTACCAAGTA	TCGCATGGAA	CTAGTCCCCT	TACGACAGGA	CGGGCGTTTT	1200
20	CAGATGGCGC	CACTGTTTCT	ATCAGTGGTA	AGACCGGTAC	AGGTGAAAGC	1250
	TATGTAGCTG	GTGGTCAAGA	AGCTAATAAT	ACCAATGCCG	TGGCCTATGC	1300
	TCCAACAGAA	AATCCTCAA	TTGCAGTTGC	AGTAGTCTTT	CCTCATAATA	1350
	CCAATTTAAC	CAAAAATGTT	GGGCCAGCAA	TTGCTCGCGA	CATTATCAAT	1400
	TTATATAACC	AACACCATCC	AATGAATTAG	AAAGGAAGCC	A	1441
25						

2) INFORMATION FOR SEQ ID NO: 1026

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-08
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
45	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CCTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTGTT	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
50	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
55	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
60	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850

	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
5	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
10	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTA	1443

15

2) INFORMATION FOR SEQ ID NO: 1027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-09

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
35	AAAAGGCTAT	TCTCTAAATG	ATCGTGTAGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCTTTCCAA	GATAGCGTGG	350
	ATGCTTTTACT	GAAAAGTTAT	TTCAATTCCG	AGCTAGAAAA	TGGTGGAGCC	400
40	AAGTATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGGA	TTAAACATGA	CTTGAAAACG	GGAGATTTAA	500
	CACCTGATTC	CTTGGAACA	GTAACCAATG	TCTTTGTCCC	GGGTCTGTGT	550
	GTCAAGGCGG	CGACCATCAG	CTCTGGTTGG	GAGAATGGAG	TCTTATCAGG	600
	AAATCAGACC	TTGACAGACC	AACCGATTGT	CTTCCAAGGT	TCAGCTCCGA	650
45	TTAATTCTTG	GTACACTCAG	GCTTACGATT	CATTTCCGAT	TACAGCGGTG	700
	GAAGCCTTGG	AGTATTCTTC	TAATGCCTAT	ATGGTCCAAA	CAGCTCTAGG	750
	TCTTATGGGG	CAGACCTACC	AACCCAATAT	GTTTGTCGGC	ACCAGCAATC	800
	TAGAGTCTGC	TATGGGGAAA	TTGCGTTCAA	CCTTTGGTGA	ATATGGCTTG	850
	GGCTCTGCGA	CTGGGATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
50	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTG	GAAGGCATTT	ATGGCAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
55	TTTTATCAGG	TTGCTCATGG	GACTAGCGGA	TTGACAACAG	GTCGTGCCTT	1200
	TTCCAATGGT	GCAGCTGTAT	CCATTAGTGG	AAAAACAGGT	ACCGCCGAAA	1250
	GTTATGTAGC	AGGTGGCCAA	GAAGCCAACA	ATACTAATGC	TGTAGCCTAT	1300
	GCACCATCAG	ATAATCCTCA	AATAGCTGTT	GCTGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GATATTATCA	1400
60	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAT	TTA	1443

2) INFORMATION FOR SEQ ID NO: 1028

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028

```

20  TATTGCCTCT ATTTCAAAGG AGATGCCTGG CATTAGTATT TCTACCTCTT      50
    GGGATAGAAA GGTTTTGGAA ACTTCTCTTT CTTCTATAGT AGGGAGTGTA      100
    TCCAGTGAAA AAGCTGGTCT CCCAGCGGAA GAAGCAGAAG CCTATCTTAA      150
    AAAAGGCTAT TCTCTAAATG ACCGTGTTGG GACTTCTTAC CTGGAAAAAC      200
    AATACGAGGA AACCTTACAA GGAAAACGCT CGGTAAAAGA AATCCATCTG      250
25  GATAAATATG GCAATATGGA AAGCGTGGAT ACAATTGAGG AAGGTAGTAA      300
    GGGAAACAAT ATCAAACCTGA CCATTGATTT GGCCTTCCAA GATAGCGTGG      350
    ATGCTTTGCT GAAAAGTTAT TTCAATTCCG AGCTAGGAAA TGGTGGAGCT      400
    AAGTATTCTG AAGGCGTGTA TGCAGTCGCC CTTAACCCCA AAACAGGTGC      450
    TGTTTTGTCT ATGTCAGGAC TCAAACATGA CCTGAAAACG GGAGACTTGA      500
30  CGCCTGATTC CTTGGGAACG GTAACCAATG TCTTTGTCCC AGGGTCAGTA      550
    GTTAAGGCCG CTACCATCAG CTCAGGTTGG GAAAATGGTG TTTTATCAGG      600
    AAACCAAACC TTAACAGATC AGCCTATTGT TTTCCAAGGT TCAGCTCCAA      650
    TTTATTCTTG GTATAAATTG GCATATGGAT CTTTTCTTAT TACAGCTGTG      700
    GAAGCCTTGG AGTATTCATC TAATGCTTAC ATGGTTCAAA CCGCTCTTGG      750
35  AATCATGGGC CAGACCTATC AACCAAATAT GTTTGTGGA ACCAGCAATT      800
    TGGAAACAGC TATGGGAAAA CTTCGTGCGA CCTTTGGCGA ATATGGCTTG      850
    GGGGCTGCGA CCGGAATTGA CCTACCAGAT GAATCTACTG GATTGTGTTCC      900
    CAAAGAGTAT AGCTTTGCTA ATTACATTAC TAATGCCTTT GGGCAGTTTG      950
    ATAACATATC GCCGATGCAG TTGGCTCAGT ATGTAGCAAC TATTGCAAAAT      1000
40  GATGGTGTTC GTGTGGCTCC TCGTATTGTT GAAGGCATTT ATGGTAATAA      1050
    TGATAAGGGA GGACTGGGTG ACTTGATTCA GCAACTGCAA CCGACAGAGA      1100
    TGAATAAGGT CAATATATCC GACTCCGATA TGAGCATCTT GCACCAAGGT      1150
    TTTTATCAGG TTGCCCATGG TACTAGTGGA TTGACAACTG GACGTGCCTT      1200
    TTCAAATGGC GCCTTGGTAT CCATTAGCGG AAAAAACAGGT ACAGCCGAAA      1250
45  GCTATGTGGC AGATGGTCAG CAAGCAACCA ATACCAATGC GGTGGCCTAT      1300
    GCCCCATCTG ATAATCCCCA AATCGCTGTT GCAGTGGTCT TTCCTCATAA      1350
    TACCAATCTA ACAAATGGTG TAGGACCTTC CATTGCGCGT GACATTATCA      1400
    ATCTGTATCA AAAATACCAT CCAATGAACT AGAAAGGAAA TTATGC          1446

```

2) INFORMATION FOR SEQ ID NO: 1029

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029

```

5      TTGCCTCTAT TTCAAAGGAG ATGCCTGGCA TTAGTATTTT TACTTCTTGG      50
      GATAGAAAGG TTTTGGAAC TTCCCTTTCT TCTATAGTTG GGAGTGTATC      100
10     CAGTGAAAAA GCTGGTCTCC CAGCGGAAGA AGCAGAAGCC TATCTTAAAA      150
      AAGGCTATTC TCTAAATGAC CGTGTAGGAA CCTCCTATTT GGAAAAGCAA      200
      TATGAAGAGA CCTTACAAGG AAAACGCTCG GTAAAAGAAA TCCATCTGGA      250
      TAAATATGGC AATATGGAAA GCGTGGATAC AATTGAGGAA GGTAGTAAGG      300
      GAAACAATAT CAAACTGACC ATTGATTTGG CCTTCCAAGA TAGCGTGGAT      350
15     GCTTTACTGA AAAGTTATTT CAATTCTGAG CTAGAAAATG GTGGAGCCAA      400
      GTATTCTGAA GGTGTCTATG CAGTCGCCCT TAACCCAAAA ACAGGTGCGG      450
      TTTTGTCTAT GTCAGGGATT AAACATGACT TGAAAACGGG AGAGTTGACG      500
      CCTGATTCCT TGGGAACGGT AACCAATGTC TTTGTTCCAG GTTCGGTTGT      550
      CAAGGCGGCG ACCATCAGCT CAGGTTGGGA AAATGGAGTC TTGTCAGGAA      600
20     ACCAGACCTT GACAGACCAG TCCATTGTCT TCCAAGGTTT AGCTCCCATC      650
      AATTCTTGGT ATACTCAGGC TTACGGTTCA TTCCCTATCA CAGCGGTCCA      700
      AGCTCTGGAG TATTCATCCA ATGCTTATAT GGTCCAAACA GCCTTAGGTC      750
      TTATGGGGCA GACCTATCAA CCCAATATGT TTGTCGGCAC CAGCAATCTA      800
      GAGTCTGCTA TGGGTAAATT GCGTTCAACC TTTGCGCAAT ATGGCTTGGG      850
25     GGCTGCGACT GGGATTGATC TACCAGATGA ATCTACTGGA TTTGTTCCCA      900
      AAGACTATAA CTTTGCCAAT TTCATTACCA ATGCCTTTGG GCAGTTTGAT      950
      AACTATACCC CAATGCAATT GGCTCAGTAT GTAGCAACTA TTGCAAATGA      1000
      TGGTGTTTCG GTGGCTCCTC GTATTGTTGA AGGCATTTAT GGTAATAATG      1050
      ATAAGGGAGG ACTGGGTGAC TTGATTCAGC AACTGCAACC GACAGAGATG      1100
30     AATAAGGTCA ATATATCCGA CTCCGATATG AGTGTCTTGC ACCAAGGTTT      1150
      TTATCAGGTT GCTCATGGGA CTAGTGGGTT GACAACTGGC CGTGCCTTTT      1200
      CAAATGGTGC CTTGGTATCC ATTAGCGGAA AAACGGGTAC AGCCGAAAGC      1250
      TATGTGGCAG ATGGTCAGGA AGCAACCAAT ACCAATGCGG TGGCCTATGC      1300
      CCCATCTGAT AATCCCCAAA TCGCTGTTCG AGTGGTCTTT CCTCATAATA      1350
35     CCAATCTAAC AAATGGTGTA GGACCTTCCA TTGCGCGTGA CATTATCAAT      1400
      CTGTATCAAA AATACCATCC AAT      1423

```

2) INFORMATION FOR SEQ ID NO: 1030

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1447 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030

```

55     TATTGCCTCT ATTTCAAAGG AGATGCCTGG CATTAGTATT TCTACTTCTT      50
      GGGATCGAAA GGTTTTGGAA ACTTCCCTTT CTTCTATAGT AGGGAGTGTA      100
      TCCAGTGAAA AAGCTGGTCT CCCAGCGGAA GAAGCAGAAT CCTATCTTAA      150
      AAAAGGCTAT TCTCTAAATG ACCGTGTTGG AACCTCCTAT TTGGAAAAGC      200
60     AATATGAAGA GACCTTACAA GGAAAACGCT CGGTAAAGA AATCCATCTG      250

```


	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
5	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
10	GAAGCCTTGG	AGTATTTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
15	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
20	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCTTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGCT	1447
25						

2) INFORMATION FOR SEQ ID NO: 1031

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACCTCTTG	50
45	GGATAGAAAG	GTTTTGGAAA	CTTCTCTTTC	TTCTATAGTA	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
	AAAGGCTATT	CTCTAAATGA	CCGTGTTGGG	ACTTCTTACC	TGGAAAAACA	200
	ATACGAGGAA	ACCTTACAAG	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
50	GGAAACAATA	TCAAACCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCTA	400
	AGTATTCTGA	AGGCGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGACTTGAC	500
	GCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGGTCAGTAG	550
55	TTAAGGCCGC	TACCATCAGC	TCAGGTTGGG	AAAATGGTGT	TTTATCAGGA	600
	AACCAAACCT	TAACAGATCA	GCCTATTGTT	TTCCAAGGTT	CAGCTCCAAT	650
	TTATTCTTGG	TATAAATTGG	CATATGGATC	TTTTCCTATT	ACAGCTGTGG	700
	AAGCCTTGGA	GTATTCATCT	AATGCTTACA	TGGTTCAAAC	CGCTCTTGGA	750
	ATCATGGGCC	AGACCTATCA	ACCAAATATG	TTTGTTGGAA	CCAGCAATTT	800
60	GGAAACAGCT	ATGGGAAAAC	TTCGTGCGAC	CTTTGGCGAA	TATGGCTTGG	850

	GGGCTGCGAC	CGGAATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
	AAAGAGTATA	GCTTTGCTAA	TTACATTACT	AATGCCTTTG	GGCAGTTTGA	950
	TAACATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	1050
5	GATAAGGGAG	GACTGGGTGA	CTTGATTTCAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	1150
	TTTATCAGGT	TGCCCATGGT	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CCTTGGTATC	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	1250
	CTATGTGGCA	GATGGTCAGC	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	1300
10	CCCCATCTGA	TAATCCCCAA	ATCGCTGTTG	CAGTGGTCTT	TCCTCATAAT	1350
	ACCAATCTAA	CAAATGGTGT	AGGACCTTCC	ATTGCGCGTG	ACATTATCAA	1400
	TCTGTATCAA	AAATACCATC	CAATGAACTA	GAAAGGAAAT	TATGCT	1446

15

2) INFORMATION FOR SEQ ID NO: 1032

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	50
	GGATAGAAAG	GTTTTGGAAG	CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
35	AAAGGCTATT	CTCTAAATGA	TCGTGTTGGA	ACCTCCTATT	TGGAAAAGCA	200
	ATATGAAGAG	ACCTTACAAG	GGAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGTGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
	GGAAACAATA	TCAAGCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCCA	400
40	AGTATTCTGA	GGGTGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGAGTTGAC	500
	TCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	550
	TCAAGGCTGC	GACCATCAGC	TCTGGCTGGG	AAAATGGAGT	CTTATCAGGA	600
	AACCAGACCT	TGACAGACCA	GTCCATTGTC	TTTCAAGGTT	CAGCTCCCAT	650
45	CAATTCTTGG	TATACTCAGG	CTTACGGTTC	ATTCCCTATC	ACAGCAGTCC	700
	AAGCTCTGGA	GTATTCATCT	AATGCCTATA	TGGTCCAAAC	AGCTTTAGGT	750
	CTTATGGGGC	AGACCTACCA	ACCTAATATG	TTTGTGCGCA	CCAGCAACCT	800
	AGAGTCTGCT	ATGGGGAAAT	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	850
	GTTCTGCGAC	CGGGATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
50	AAAGACTATA	GCTTTGCTAA	TTACATCACC	AATGCCTTTG	GGCAGTTTGA	950
	TAACATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGAAATAAT	1050
	GATAAGGGAG	GCCTAGGCGA	CTTGATTTCAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCTGATAT	GAGTATTTTG	CACCAAGGTT	1150
55	TTTATCAGGT	TGCTCATGGG	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CAGCGGTATC	CATTAGTGGA	AAAACAGGTA	CTGCCGAAAG	1250
	TTATGTTGAG	GGTGGTCAAG	AAGCTAACAA	TACTAATGCT	GTGGCCTATG	1300
	CACCATCAGA	TAATCCTCAA	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	1350
	ACCAACCTTA	CAAATGGTGT	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	1400
60	CCTCTATAAC	CAACATCATC	CAATGAATTA	GAAAGGAACA	TATGCT	1446

2) INFORMATION FOR SEQ ID NO: 1033

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033

```

20 TATTGCCTCT ATTTCAAAGG AGATGCCTGG CATTAGTATT TCTACTTCTT      50
   GGGATAGAAA GGTTTTGGAA ACTTCCCTTT CTTCTATAGT TGGGAGTGTA      100
   TCCAGTGAAA AAGCTGGTCT CCCAGCGGAA GAAGCAGAAG CCTATCTTAA      150
   AAAAGGCTAT TCTCTAAATG ACCGTGTTGG AACCTCGTAT TTGGAAAAGC      200
   AATATGAAGA GACCTTACAA GGAAAACGCT CGGTAAAAGA AATCCATCTG      250
   GATAAATATG GCAATATGGA AAGCGTGGAT ACAATTGAGG AAGGTAGTAA      300
   GGGAAACAAT ATCAAGCTGA CCATTGATTT GGCCTTCCAA GATAGCGTGG      350
   ATGCTTTGCT GAAAAGTTAT TTCAATTCCG AGCTAGGAAA TGGTGGAGCC      400
   AAGTATTCTG AGGGTGTGTA TGCAGTCGCC CTTAACCCCA AAACAGGTGC      450
   TGTTTTGTCT ATGTCAGGAC TCAAACATGA CCTGAAAACG GGAGAGTTGA      500
   CTCCTGATTC CTTGGGAACG GTAACCAATG TCTTTGTCCC AGGTTTCGGTT      550
   GTTAAGGCCG CTACCATCAG CTCAGGTTGG GAAAATGGTG TTTTATCAGG      600
   AAACCAAACC TTAACAGATC AGCCTATTGT TTTCCAAGGT TCAGCTCCAA      650
   TTTATTCTTG GTATAAATTG GCATATGGAT CTTTTCCTAT TACAGCTGTG      700
   GAAGCCTTGG AGTATTCATC CAATGCTTAC ATGGTTCAAA CCGCTCTTGG      750
   AATCATGGGC CAGACCTATC AACCAAATAT GTTTGTTGGA ACCAGCAATT      800
   TGGAAACAGC TATGGGAAAA CTTTCGTGCGA CCTTTGGCGA ATATGGCTTG      850
   GGGGCTGCGA CCGGAATTGA CCTACCAGAT GAATCTACTG GATTTGTTCC      900
   CAAAGAGTAT AGCTTTGCTA ATTACATCAC CAATGCCTTT GGGCAGTTTG      950
   ATAAC TATAC GCCCATGCAG TTGGCTCAGT ATGTAGCAAC TATTGCAAAT      1000
   GATGGTGTTC GTGTGGCTCC TCGTATTGTT GAAGGCATTT ATGGTAATAA      1050
   TGATAAGGGA GGACTGGGTG ACTTGATTCA GCAACTGCAA CCGACAGAGA      1100
   TGAATAAGGT CAATATATCC GACTCCGATA TGAGTATCTT GCACCAAGGT      1150
   TTTTATCAGG TTGCTCATGG GACTAGTGGA TTGACAAC TGACGTGCTTT      1200
   TTCAAATGGT GCCTTGGTAT CCATTAGTGG GAAAACAGGT ACTGCCGAAA      1250
   GTTATGTTGC AGGTGGTCAA GAAGCCAACA ATACCAACGC GGTGGCCTAT      1300
   GCCCCATCAG ATAATCCTCA AATCGCTGTT GCCGTTGTCT TCCCTCATAA      1350
   CACCAATCTA ACAAATGGTG TTGGACCTTC TATTGCACGC GATATTATCA      1400
   ACCTCTATAA CCAACACCAT CCAATGAATT AGAAAGGAAC TTATGC          1446

```

2) INFORMATION FOR SEQ ID NO: 1034

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

782

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034

```

5      GGAAACTGCA GAGGTCAAGG GGATTGATTT TACAACCAGT CCCAATCGTA      50
      GTTATCCAAA CGGACAATTT GCTTCTAGTT TTATCGGACT AGCTCAGCTC      100
10     CATGAAAATG AAGATGGCAG CAAGAGCTTA CTGGGAACCT CTGGAATGGA      150
      GAGTTCCTTG AACAGTATTC TTGCAGGGAC AGACGGTATT ATTACCTATG      200
      AAAAAGACCG TGTAGGAAAT ATCGTACCAG GTACAGAACT GGTATCGCAA      250
      CAAACTGTGG ATGGCAAGGA TGTTTATACA ACATTGTCTA GTCCGCTACA      300
      ATCTTTCATG GAAACTCAGA TGGATGCCTT TCTAGAAAAA GTAAAAGGTA      350
15     AGTATATGAC CGCGACCTTG GTCAGTGCAA AGACCGGTGA AATCCTCGCT      400
      ACCACCCAAC GACCTACCTT TAATGCAGAT ACTAAAGAAG GAATCACTGA      450
      GGACTTTGTT TGGCGTGATA TTCTTTATCA AAGTAACTAT GAACCAGGAT      500
      CAGCCATGAA GGTATGACG TTAGCTTCTT CTATTGATAA TAATACCTTC      550
      CCAAGTGGAG AATACTTCAA TAGCAGTGAA TTCAAATAG CGGATGCGAC      600
20     GACTCGAGAT TGGGATGTTA ATGATGGTTT GACTACTGGT GGGATGATGA      650
      CTTTCTTACA AGGTTTCGCT CACTCCAGTA ATGTTGGAAT GAGTCTACTT      700
      GAACAAAAAA TGGGAGATGC TACTTGGTTG GATTATCTAA AACGCTTTAA      750
      ATTTGGGGTT CCAACTCGCT TTGGCTTGAC AGATGAATAC GCTGGTCAAC      800
      TTCCAGCTGA TAATATTGTT AGTATTGCTC AAAGCTCATT TGGGCAAGGA      850
25     ATTTCAGTGA CACAAACACA AATGCTTCGT GCCTTTACAG CTATTGCTAA      900
      TGATGGAGTT ATGCTGGAGC CAAAATTTAT AAGTGCTATT TATGATACTA      950
      ACAATCAGTC TGTACGTAAG TCACAAAAAG AAATAGTAGG AAATCCTGTT      1000
      TCCAAAGAGG CAGCAAGCAC AACTCGAAAT CACATGATCT TAGTTGGGAC      1050
      GGACCCTCTA TATGGAAC TAATAATCA CTACACAGGA AAGCCAATTA      1100
30     TAACAGTTCC TGGACAAAAT GTAGCAGTTA AATCCGGTAC GGCTCAAATC      1150
      GCTGATGAGA AAAATGGAGG ATACTTGCTT GGTCTACCA ATTATATTTT      1200
      CTCAGTTGTG ACTATGAATC CTGCTGAAA TCGTGATTTT ATCTTGATG      1250
      TAACGGTTCA ACAGCCTGAG CATTATTGAG GTATCCAGTT GGGAGAATTT      1300
      GCCACCCCAA TCTTGGAGCG GGCTTCAGCT ATGAAAGAAT CTCTCAATCT      1350
35     TCAATCTCCA GCCAAAATT TAGATAAAGT TACGACAGAA TCTTCTTATG      1400
      CAATGCCTAG CATCAAGGAT ATTTACCTG GTGAGTTGGC GGAAGCCTTA      1450
      CGCCGAAATA TTGTGCAACC AATCGTTGTA GGTACTGGAA CAAAGATTAA      1500
      AGAGACTTCT GTAGAAGAAG GGACCAATCT TGCACCAAAC CAACAAGTTC      1550
      TCCTTTTATC GGATAAGGTA GAAGAAATTC CAGACATGTA TGGCTGGAAA      1600
40     AAAGAGACTG CCGAGACCTT TGCTAAATGG TTGGATATTG AACTGGAATT      1650
      TGAAGGTTCA GGTTCCGTTG      1670
  
```

45 2) INFORMATION FOR SEQ ID NO: 1035

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1683 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035

	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	CAACCAGTCC	50
	CAATCGTAGT	TACCCAAATG	GACAATTGCG	TTCTAGTTTT	ATCGGTCTAG	100
	CTCAGCTCCA	TGAAAATGAA	GATGGAAGCA	AGAGTTTGCT	GGGAACCTCT	150
	GGAATGGAGA	GTTCCTTGAA	CAGTATTCTT	GCAGGGACAG	ACGGCATTAT	200
5	TACCTATGAA	AAGGATCGTC	TGGGCAATAT	TGTACCCGGA	ACAGAACAAG	250
	TTTCCCAACA	AACGGTGGAT	GGCAAGGATG	TTTACACAAC	CATTTCCAGC	300
	CCCCTCCAGT	CCTTCATGGA	AACTCAGATG	GATGCCTTTC	TAGAAAAAGT	350
	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	ACCGGTGAAA	400
	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	TAAAGAAGGA	450
10	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	GTAACATGA	500
	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	ATTGATAATA	550
	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	CAAAATAGCG	600
	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	CTACTGGTGG	650
	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	GTTGGAATGA	700
15	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGGTTGGA	TTATCTAAAA	750
	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	ATGAATACGC	800
	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	AGCTCATTTG	850
	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	CTTTACAGCT	900
	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	GTGCTATTTA	950
20	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	ATAGTAGGAA	1000
	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	CATGATCTTA	1050
	GTTGGGACGG	ACCCTCTATA	TGGAACATATG	TATAATCACT	ACACAGGAAA	1100
	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	TCCGGTACGG	1150
	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	TTCTACCAAT	1200
25	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	CTGATTTTAT	1250
	CTTGATATGA	ACGGTTCAAC	AGCCTGAGCA	TTATTTCAGGT	ATCCAGTTGG	1300
	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	GAAAGAATCT	1350
	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	CGACAGAATC	1400
	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	GAGTTGGCGG	1450
30	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	TACTGGAACA	1500
	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	CACCAAACCA	1550
	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	GACATGTATG	1600
	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	GGATATTGAA	1650
	CTGGAATTTG	AAGGTTTCAGG	TTCCGTTGTT	CAG		1683

2) INFORMATION FOR SEQ ID NO: 1036

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - (B) STRAIN: StrR-03
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036

	TCAAAAAAGA	ATTGGAAACT	GCAGAGGTCA	AGGGGATTGA	TTTTACAACC	50
55	AGTCCCAATC	GTAGTTACCC	AAATGGACAA	TTTGCTTCTA	GTTTTATCGG	100
	TCTAGCTCAG	CTCCATGAAA	ATGAAGATGG	AAGCAAGAGT	TTGCTGGGAA	150
	CCTCTGGAAT	GGAGAGTTCC	TTGAACAGTA	TTCTTGCAGG	GACAGACGGC	200
	ATTATTACCT	ATGAAAAGGA	TCGTCTGGGC	AATATTGTAC	CCGGAACAGA	250
	ACAAGTTTCC	CAACAAACGG	TGGATGGCAA	GGATGTTTAC	ACAACCATTT	300
60	CCAGCCCCCT	CCAGTCCTTC	ATGGAAACTC	AGATGGATGC	CTTCTAGAA	350

	AAAGTAAAAG	GTAAGTATAT	GACCGCGACC	TTGGTCAGTG	CAAAGACCGG	400
	TGAAATCCTC	GCTACCACCC	AACGACCTAC	CTTTAATGCA	GATACTAAAG	450
	AAGGAATCAC	TGAGGACTTT	GTTTGGCGTG	ATATTCTTTA	TCAAAGTAAC	500
	TATGAACCAG	GATCAGCCAT	GAAGGTTATG	ACGTTAGCTT	CTTCTATTGA	550
5	TAATAATACC	TTCCCAAGTG	GAGAATACTT	CAATAGCAGT	GAATTCAAAA	600
	TAGCGGATGC	GACGACTCGA	GATTGGGATG	TTAATGATGG	TTTGACTACT	650
	GGTGGGATGA	TGACTTTCTT	ACAAGGTTTC	GCTCACTCCA	GTAATGTTGG	700
	AATGAGTCTA	CTTGAACAAA	AAATGGGAGA	TGCTACTTGG	TTGGATTATC	750
	TAAAACGCTT	TAAATTTGGG	GTTCCAACCTC	GCTTTGGCTT	GACAGATGAA	800
10	TACGCTGGTC	AACTTCCAGC	TGATAATATT	GTTAGTATTG	CTCAAAGCTC	850
	ATTTGGGCAA	GGAATTTTCAG	TGACACAAAC	ACAAATGCTT	CGTGCCCTTA	900
	CAGCTATTGC	TAATGATGGA	GTTATGCTGG	AGCCAAAATT	TATAAGTGCT	950
	ATTTATGATA	CTAACAATCA	GTCTGTACGT	AAGTCACAAA	AAGAAATAGT	1000
	AGGAAATCCT	GTTTCCAAAG	AGGCAGCAAG	CACAACTCGA	AATCACATGA	1050
15	TCTTAGTTGG	GACGGACCCCT	CTATATGGAA	CTATGTATAA	TCACTACACA	1100
	GGAAAGCCAA	TTATAACAGT	TCCTGGACAA	AATGTAGCAG	TTAAATCCGG	1150
	TACGGCTCAA	ATCGCTGATG	AGAAAAATGG	AGGATACTTG	GTTGGTTCTA	1200
	CCAATTATAT	TTTCTCAGTT	GTGACTATGA	ATCCTGCTGA	AAATCCTGAT	1250
	TTTATCTTGT	ATGTAACGGT	TCAACAGCCT	GAGCATTATT	CAGGTATCCA	1300
20	GTTGGGAGAA	TTTGCCACCC	CAATCTTGGA	GCGGGCTTCA	GCTATGAAAG	1350
	AATCTCTCAA	TCTTCAATCT	CCAGCCAAAA	ATTTAGATAA	AGTTACGACA	1400
	GAATCTTCTT	ATGCAATGCC	TAGCATCAAG	GATATTTTAC	CTGGTGAGTT	1450
	GGCGGAAGCC	TTGACCCGAA	ATATTGTGCA	ACCAATCGTT	GTAGGTACTG	1500
	GAACAAAGAT	TAAAGAGACT	TCTGTAGAAG	AAGGGACCAA	TCTTGCACCA	1550
25	AACCAACAAG	TTCTCCTTTT	ATCGGATAAG	GTAGAAGAAA	TTCCAGACAT	1600
	GTATGGCTGG	AAAAAAGAGA	CTGCCGAGAC	CTTTGCTAAA	TGGTTGGATA	1650
	TTGAACTGGA	ATTTGAAGGT	TCAGGTTCCG	TT		1682

30

2) INFORMATION FOR SEQ ID NO: 1037

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037

	CAAAAAAGAA	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAATCG	TAGTTATCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAA	TGAAGATGGC	AGCAAGAGCT	TACTGGGAAC	150
50	CTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGTA	200
	TTATTACCTA	TGAAAAAGAC	CGTGTAGGAA	ATATCGTACC	AGGTACAGAA	250
	CTGGTATCGC	AACAAACTGT	GGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
55	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
60	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700

	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
5	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
10	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTAGATAAAA	GTTACGACAG	1400
15	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
20	TGAACCTGGAA	TTTGAAGGTT	CAGGTTCCGT	T		1681

2) INFORMATION FOR SEQ ID NO: 1038

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038

40	AAAAAAGAAT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCAATCGT	AGTTATCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	ACTGGGAACC	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGTAT	200
	TATTACCTAT	GAAAAAGACC	GTGTAGGAAA	TATCGTACCA	GGTACAGAAC	250
45	TGGTATCGCA	ACAAACTGTG	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
	AGTCCGCTAC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
50	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
55	AAACGCTTTA	AATTTGGGGT	TCCAACCTCGC	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	TATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
60	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050

```

TTAGTTGGGA CGGACCCTCT ATATGGAAC TGTATAATC ACTACACAGG 1100
AAAGCCAATT ATAACAGTTC CTGGACAAAA TGTAGCAGTT AAATCCGGTA 1150
CGGCTCAAAAT CGCTGATGAG AAAAATGGAG GATACTTGGT TGGTTCTACC 1200
AATTATATTT TCTCAGTTGT GACTATGAAT CCTGCTGAAA ATCCTGATTT 1250
5 TATCTTGTAT GTAACGGTTC AACAGCCTGA GCATTATTCA GGTATCCAGT 1300
TGGGAGAATT TGCCACCCCA ATCTTGGAGC GGGCTTCAGC TATGAAAGAA 1350
TCTCTCAATC TTCAATCTCC AGCCAAAAAT TTAGATAAAG TTACGACAGA 1400
ATCTTCTTAT GCAATGCCTA GCATCAAGGA TATTTACCT GGTGAGTTGG 1450
CGGAAGCCTT ACGCCGAAAT ATTGTGCAAC CAATCGTTGT AGGTACTGGA 1500
10 ACAAAGATTA AAGAGACTTC TGTAAGAGAA GGGACCAATC TTGCACCAAA 1550
CCAACAAGTT CTCCTTTTAT CGGATAAGGT AGAAGAAAT CCAGACATGT 1600
ATGGCTGGAA AAAAGAGACT GCCGAGACCT TTGCTAAATG GTTGGATATT 1650
GAAC TGGAA TTTGAAGGTT AGGTTCCGTT GTTCA 1685

```

15

2) INFORMATION FOR SEQ ID NO: 1039

```

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 1679 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Streptococcus pneumoniae
    (B) STRAIN: StrR-06

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039

```

AAAAGAATTG GAAACTGCAG AGGTCAAGGG GATTGATTTT ACAACCAGTC 50
CCAATCGTAG TTATCCAAAC GGACAATTG CTCTAGTTT TATCGGACTA 100
35 GCTCAGCTCC ATGAAAATGA AGATGGCAGC AAGAGCTTAC TGGGAACCTC 150
TGGAATGGAG AGTTCCTTGA ACAGTATTCT TGCAGGGACA GACGGTATTA 200
TTACCTATGA AAAAGACCGT GTAGGAAATA TCGTACCAGG TACAGAACTG 250
GTATCGCAAC AAAGTGTGGA TGGCAAGGAT GTTTATACAA CATTGTCTAG 300
TCCGCTACAA TCTTTCATGG AAAGTCAGAT GGATGCCTTT CTAGAAAAAG 350
40 TAAAGGTAA GTATATGACC GCGACCTTGG TCAGTGCAA GACCGGTGAA 400
TACCTCGCTA CCACCAACG ACCTACCTTT AATGCAGATA CTAAAGAAGG 450
AATCAGTGAG GACTTTGTTT GCGGTGATAT TCTTTATCAA AGTAACTATG 500
AACCAGGATC AGCCATGAAG GTTATGACGT TAGCTTCTTC TATTGATAAT 550
AATACCTTCC CAAGTGGAGA ATACTTCAAT AGCAGTGAAT TCAAAATAGC 600
45 GGATGCGACG ACTCGAGATT GGGATGTTAA TGATGGTTT ACTACTGGTG 650
GGATGATGAC TTTCTTACAA GGTTTCGCTC ACTCCAGTAA TGTGGAATG 700
AGTCTACTTG AACAAAAAAT GGGAGATGCT ACTTGGTTGG ATTATCTAAA 750
ACGCTTTAA TTTGGGGTTC CAAGTCGCTT TGGCTTGACA GATGAATACG 800
CTGGTCAACT TCCAGCTGAT AATATTGTTA GTATTGCTCA AAGCTCATTT 850
50 GGGCAAGGAA TTTCAGTGAC ACAAACACAA ATGCTTCGTG CCTTTACAGC 900
TATTGCTAAT GATGGAGTTA TGCTGGAGCC AAAATTTATA AGTGCTATTT 950
ATGATACTAA CAATCAGTCT GTACGTAAGT CACAAAAGA AATAGTAGGA 1000
AATCCTGTTT CCAAAGAGGC AGCAAGCACA ACTCGAAATC ACATGATCTT 1050
AGTTGGGACG GACCCTCTAT ATGGAACAT GTATAATCAC TACACAGGAA 1100
55 AGCCAATTAT AACAGTTCTT GGACAAAATG TAGCAGTTAA ATCCGGTACG 1150
GCTCAAAATCG CTGATGAGAA AAATGGAGGA TACTGGTTG GTTCTACCAA 1200
TTATATTTTC TCAGTTGTGA CTATGAATCC TGCTGAAAAT CCTGATTTTA 1250
TCTTGATATG AACGGTTCAA CAGCCTGAGC ATTATTCAGG TATCCAGTTG 1300
GGAGAATTTG CCACCCCAAT CTTGGAGCGG GCTTCAGCTA TGAAAGAATC 1350
60 TCTCAATCTT CAATCTCCAG CCAAAAATTT AGATAAGTT ACGACAGAAT 1400

```


	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
	AAAGATTAAA	GAGACTTCTG	TAGAAAGAAG	GACCAATCTT	GCACCAAACC	1550
	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
5	GGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1650
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTG			1679

10 2) INFORMATION FOR SEQ ID NO: 1040

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1685 bases
	(B) TYPE: Nucleic acid
15	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Streptococcus pneumoniae</i>
	(B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040

25	TAAAAAGGAT	CTAAAAGACG	CTAGTGTTGA	AGGAATTGAC	TTCACAAC TA	50
	GCCCTAATAG	AAGCTATCCA	AATGGACAAT	TCGCTTCTAG	TTTTATTGGT	100
	TTGGCCCCAAC	TCCATGAAAA	TGAGGATGGT	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGGATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
30	TTATTACCTA	TGAAAAGATG	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
35	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGAAGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCCTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
40	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTC	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
45	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAAC TCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
50	CAATTATATT	TTCTCAGCTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTTACC	TGGTGAGTTG	1450
55	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCAACAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAAG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
60	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	CGTTC		1685

2) INFORMATION FOR SEQ ID NO: 1041

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041

20	GTCTATCAAA	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	50
	CAACCACTCC	CAATCGTAGT	TATCCAAACG	GACAATTTGC	TTCTAGTTTT	100
	ATCGGACTAG	CTCAGACTCCA	TGAAAATGAA	GATGGCAGCA	AGAGCTTACT	150
	GGGAACCTCT	GGAATGGAGA	GTTCCCTTGA	CAGTATTCTT	GCAGGGACAG	200
	ACGGTATTAT	TACCTATGAA	AAAGACCGTG	TAGGAAATAT	CGTACCAGGT	250
	ACAGAACTGG	TATCGCAACA	AACTGTGGAT	GGCAAGGATG	TTTATACAAC	300
25	ATTGTCCTAGT	CCGCTACAAT	CTTTCATGGA	AACTCAGATG	GATGCCTTTC	350
	TAGAAAAAGT	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	400
	ACCGGTGAAA	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	450
	TAAAGAAGGA	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	500
	GTAACCTATGA	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	550
30	ATTGATAATA	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	600
	CAAAATAGCG	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	650
	CTACTGGTGG	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	700
	GTTGGAATGA	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGTTTGA	750
	TTATCTAAAA	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	800
35	ATGAATACGC	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	850
	AGCTCATTTG	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	900
	CTTTACAGCT	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	950
	GTGCTATTTA	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	1000
	ATAGTAGGAA	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	1050
40	CATGATCTTA	GTGGGGACGG	ACCCTCTATA	TGGAACCTATG	TATAATCACT	1100
	ACACAGGAAA	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	1150
	TCCGGTACGG	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	1200
	TTCTACCAAT	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	1250
	CTGATTTTAT	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	1300
45	ATCCAGTTGG	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	1350
	GAAAGAATCT	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	1400
	CGACAGAATC	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	1450
	GAGTTGGCGG	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	1500
	TACTGGAACA	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	1550
50	CACCAAACCA	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	1600
	GACATGTATG	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	1650
	GGATATTGAA	CTGGAATTTG	AAGGTTTCAGG	TTCCGTTGTT	CAGAAG	1696

2) INFORMATION FOR SEQ ID NO: 1042

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-09

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	GCTGGGAACC	150
15	TCTGGAATGG	AGAGTTCCCT	GAACAGTATT	CTTGCAGGGA	CAGACGGCAT	200
	TATTACCTAT	GAAAAGGATC	GTCTGGGAAA	TATTGTCCCC	GGAACGGAAC	250
	AAGTTTCCCA	ACAAACTGTA	GATGGCAAGG	ATGTTTATAC	GACTATTTCC	300
	AGCACCTTTC	AGTCCTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
20	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
25	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AAATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTTCAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
30	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAAATTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
	TTAGTTGGGA	CGGACCCTCT	ATATGGAACT	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
35	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAC	1350
	TCTCTCAATC	TTCAAACAAC	AGCTAAAGCT	TTGGAGCAAG	TAAGTCAACA	1400
40	AAGTCCTTAT	CCTATGCCTA	GTGTCAAGGA	TATTTACCTT	GGTGATTTAG	1450
	CAGAAGAATT	GCGTCGCAAT	CTTGTAACAAC	CCATCGTTGT	GGGAACAGGA	1500
	ACGAAGATTA	AAAACAGTTC	TGCTGAAGAA	GGGAAGAATC	TTGCCCCGAA	1550
	TCAGCAAGTC	CTTATCTTAT	CTGATAAAGT	AGAGGAAGTT	CCAGATATGT	1600
	ATGGTTGGAC	AAAGGAGACT	GCTGAGACCC	TTGCTAAGTG	GCTCAATATA	1650
45	GAACTTGAAT	TTCAAGGTTT	GGGTTCTACT	GTGCAGAAG		1689

2) INFORMATION FOR SEQ ID NO: 1043

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1690 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043

5	CAAAAAAGAG	TTGGAAACTG	CAGAGGTC	GGGGATTGAT	TTTACAACCA	50
	GTCCTAATCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGT	100
	CTAGCTCAAC	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
	TTATTACTTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
10	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTC	CAATCTTTTC	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
15	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	ACGGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCCTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
20	AAAACGCTTT	AAATTGGGGG	TTCCAACCTG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
25	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTCTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
30	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTCAAC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
35	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
	TGAACCTGGA	TTTGAAGGTT	CAGGTTCCGT	TGTTCAGAAG		1690

40

2) INFORMATION FOR SEQ ID NO: 1044

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044

	AGTTGGAAAC	TGCAGAGGTC	AAGGGGATTG	ATTTTACAAC	CAGTCCTAAT	50
	CGTAGTTACC	CAAACGGACA	ATTTGCTTCT	AGTTTATATCG	GACTAGCTCA	100
60	GCTCCATGAA	AATGAAGATG	GCAGCAAGAG	CTTGCTGGGA	ACCTCTGGGA	150

	TGGAGAGTTC	TTTAAATAGA	ATTCTTGCAG	GGACAGACGG	CATTATTACC	200
	TATGAAAAGG	ATCGTCTGGG	AAATATTGTC	CCCGGAACGG	AACAAGTTTC	250
	CCAACAAACG	GTAGATGGCA	AGGATGTTTA	TACGACTATT	TCCAGCACCC	300
	TTCAGTCCTT	CATGGAGACC	CAGATGAATG	CCTTTCAAGA	AAAAGTAAAA	350
5	GGCAAGTATA	TGACGGCTAC	CTTGGTCAGT	GCTAAAACAG	GGGAAATTCT	400
	TGCAACAACG	CAACGGCCGA	CCTTCGATGC	TGATACTAAG	GAAGGACTTA	450
	CCAAGGACTT	TGTTTGGCGT	GATATCCTCT	ATCAAAGTAA	CTATGAGCCA	500
	GGGTCAACCA	TGAAGGTCAT	GACGCTTGCT	GCTGCTATTG	ATAATAACAC	550
	TTTCCCAGGA	GGAGAAGTTT	TCAATAGTAG	TGAATTAAAA	ATAGCGGATG	600
10	CGACAATTCG	AGATTGGGAT	GTTAATGATG	GTTTGACGAC	TGGTGGGATG	650
	ATGACTTTCT	TACAAGGTTT	CGCTCACTCC	AGTAATGTTG	GAATGAGTCT	700
	ACTTGAACAA	AAAATGGGAG	ATGCTACTTG	GTTGGATTAT	CTAAACCGCT	750
	TTAAGTTTGG	GGTGCCGACG	CGTTTTGGTC	TGACTGATGA	GTATTCAGGT	800
	CAATTGCCTG	CAGATAATAT	TGTTAATATT	GCCATGAGTG	CATTTGGTCA	850
15	GGGGATTTCA	GTGACCCAGA	CGCAAATGAT	TCGTGCCTTT	ACAGCTATTG	900
	CTAATGATGG	TGTTATGCTG	GAGCCTAAAT	TTATTAGTGC	CATTTATGAT	950
	CCAAATGATC	AAACTGCTCG	GAAATCTCAA	AAAGAAATTG	TGGGAAATCC	1000
	TGTTTCTAAA	GATGCAGCTA	GTCTAACTCG	GACTAACATG	ATTTTGGTAG	1050
	GGACGGATCC	GGTTTATGGA	ACCATGTATA	ACCACAGCAC	AGGTAAGCCA	1100
20	ACTGTAAC TG	TTCTTG GGC A	AAATGTAGCC	CTCAAGTCTG	GTACGGCTCA	1150
	GATTGCTGAC	GAGAAAAATG	GTGGTTATCT	AGTCGGGTTA	ACCAACTATA	1200
	TTTTCTCGCG	TGTATCGATG	AATCCGGCTG	AAAATCCTGA	TTTTATCTTG	1250
	TATGTAACGG	TACAGCAACC	TGAACATTAT	TCAGGTATCC	AGTTGGGAGA	1300
	ATTTGCCACC	CCAATCTTGG	AGCGGGCTTC	AGCTATGAAA	GAATCTCTCA	1350
25	ATCTTCAATC	TCCAGCCAAG	AATTTAGATA	AAGTTACGAC	AGAATCTTCT	1400
	TATGCAATGC	CTAGCATCAA	GGATATTTCA	CCTGGTGAGT	TGGCGGAAGC	1450
	CTTACGCCGA	AATATTGTGC	AACCAATCGT	TGTAGGTACT	GGAACAAAGA	1500
	TTAAAGAGAC	TTCTGTAGAA	GAAGGGACCA	ATCTTGCACC	AAACCAACAA	1550
	GTTCTCCTTT	TATCGGATAA	GGTAGAAGAA	ATTCCAGACA	TGTATGGCTG	1600
30	GAAAAAAGAG	ACTGCTGAAA	CCTTTGCTAA	ATGGTTGAT	ATTGAGCTGG	1650
	AATTTGAAGG	GTCAGGTT				1668

35 2) INFORMATION FOR SEQ ID NO: 1045

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1680 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045

50	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	GTCCCAATCG	50
	TAGTTACCCA	AATGGACAAT	TTGCTTCTAG	TTTTATCGGT	CTAGCTCAGC	100
	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	CTCTGGAATG	150
	GAGAGTTTCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	TTATTACCTA	200
55	TGAAAAGGAT	CGTCTGGGCA	ATATTGTACC	CGGAACAGAA	CAAGTTTCCC	250
	AACAAACGGT	GGATGGCAAG	GATGTTTACA	CAACCATTTC	CAGCCCCCTC	300
	CAGTCCTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	AAGTAAAAGG	350
	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	GAAATCCTCG	400
	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	AGGAATCACT	450
60	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	ATGAACCAGG	500

	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	AATAATACCT	550
	TCCCAAGTGG	AGAATACCTC	AATAGCAGTG	AATTCAAAAT	AGCGGATGCG	600
	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	GTGGGATGAT	650
	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	ATGAGTCTAC	700
5	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	AAAACGCTTT	750
	AAATTTGGGG	TTCCAACCTC	CTTTGGCTTG	ACAGATGAAT	ACGCTGGTCA	800
	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	TTTGGGCAAG	850
	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	AGCTATTGCT	900
	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	TTTATGATAC	950
10	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	GGAAATCCTG	1000
	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	CTTAGTTGGG	1050
	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACACACAG	GAAAGCCAAT	1100
	TATAACAGTT	CCTGGACAAA	ATGTACAGAT	TAAATCCGGT	GCGGCTCAAA	1150
	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	CAATTATATT	1200
15	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	TTATCTTGTA	1250
	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	TTGGGAGAAT	1300
	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	ATCTCTCAAT	1350
	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	AATCTTCTTA	1400
	TGCAATGCCT	AGCATCAAGG	ATATTTACC	TGGTGAGTTG	GCGGAAGCCT	1450
20	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	AACAAAGATT	1500
	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	ACCAACAAGT	1550
	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	TATGGCTGGA	1600
	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	TGAACTGGAA	1650
	TTTGAAGGTT	CAGGTTCCGT	TGTTTCAGAAG			1680

2) INFORMATION FOR SEQ ID NO: 1046

30 (i) SEQUENCE CHARACTERISTICS: _____

(A) LENGTH: 1689 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

40 (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
45	TCCTAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGTC	100
	TAGCTCAACT	CCATGAAAAT	GAAGATGGAA	GCAAGAGTTT	GCTGGGAACT	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	AAGACGGTAT	200
	TATTACTTAT	GAAAAGGATC	GTCTGGGTAA	TATTGTCCCT	GGAACAGAAC	250
	AAGTTTCCCA	ACAAACGGTA	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
50	AGTCCGCTCC	AATCTTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
55	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
60	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850

	TTGGGCAAGG	AATTTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
5	TTAGTTGGGA	CGGACCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAA	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
10	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
15	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAACTGGAAT	TTGAAGGTTT	AGGTTCCGTT	GTTTACAAG		1689

20

2) INFORMATION FOR SEQ ID NO: 1047

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 1690 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047

	CAAAAAAGAA	TTGGAAGCTG	CAGAGGTC	GGGGATTGAT	TTTACAACCA	50
	GTCCCAACCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TGCTGGGAAC	150
40	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	200
	TTATTACCTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTACC	CGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTACA	CAACCATTTC	300
	CAGCCCCCTC	CAGTCCTTTA	TGGAAACCCA	GATGGATGCT	TTTCAAGAGA	350
	AGGTAAAAGG	AAAGTACACG	ACAGCGACTT	TGGTCAGTGC	TAAAACAGGG	400
45	GAAATTCTGG	CAACAACGCA	ACGACCGACC	TTTGATGCAG	ATACAAAAGA	450
	AGGCATTACA	GAGGACTTTG	TTTGGCGTGA	TATCCTTTAC	CAAAGTAACT	500
	ATGAGCCAGG	TTCCCCTATG	AAAGTGATGA	TGTTGGCTGC	TGCTATTGAT	550
	AATAATACCT	TTCCAGGGGG	AGAAGTCTTC	AATAGTAGTG	AGTTAAAAAT	600
	TGCAGATGTC	ACGATTCGAG	ATTGGGACGT	CAATGAAGGA	TTGACTGGTG	650
50	GCAGAATGAT	GACCTTTTCT	CAAGGGTTTC	CTCACTCAAG	TAACGTTGGG	700
	ATGACGCTTC	TTGAGCAAAA	GATGGGAGAT	GCTACATGGC	TTGATTATCT	750
	AAATCGCTTT	AAATTTGGTG	TTCCGACTCG	TTTTGGCTTG	ACGGATGAAT	800
	ATGCAGGCCA	ACTTCCAGCT	GACAATATCG	TAAATATTGC	TCAGAGTTCA	850
	TTTGGACAAG	GGATTTCAGC	GACCCAGACG	CAAATGATTC	GTGCCTTCAC	900
55	GGCTATTGCC	AACGATGGAG	TCATGTTAGA	ACCTAAATTT	ATCAGTGCCA	950
	TTTATGATCC	AAATGATCAA	ACTGCTCGGA	AATCACAAAA	AGAAGTTGTG	1000
	GGAAATCCTG	TGTCTAAAGA	TGCAGCGAGC	TTGACGCGAA	CGCATATGGT	1050
	TTTAGTCGGT	ACCGATCCAG	TATATGGAAC	TATGTATAAT	CATAAGACAG	1100
	GGAAACCAAC	TGTAACGTGT	CCTGGGCAAA	ATGTAGCCCT	CAAGTCTGGT	1150
60	ACGGCTCAGA	TTGCCGATGA	GAAAAATGGA	GGTTACTTAG	TTGGTACGAC	1200

	CAATTACATT	TTTTCGGCTG	TATCGATGAA	CCCTGCTGAA	AATCCTGATT	1250
	TTATTCTCTA	TGTGACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATTCAG	1300
	TTGGGGGAAT	TTGCCAATCC	TATCTTGGAA	AGGGCAGTGG	CTATGAAAGA	1350
5	TTCCCTTAAC	CTCCAATCTA	CCGCTAAAAC	GTTAAATCAG	GTAACCAATC	1400
	AAAGCGCTTA	TGCCATGCCT	AGCATCAAGG	ACATTTCAAC	TGGCGATTTG	1450
	GCGGAAGCCT	TACGTGCGAA	TATTGTGCAA	CCAATCGTTG	TAGGAACAGG	1500
	AACAAAAATT	AAAGAATCAT	CTGTAGAAGA	AGGGACGGAT	CTTGCACCTA	1550
	ACCAGCAAGT	TCTTCTCTTA	TCTGATAAAG	CAGAGGAAGT	TCCAGATATG	1600
	TATGGTTGGA	CAAAAGAGAC	TGCTGAGACC	TTTGCTAAGT	GGCTCAATAT	1650
10	AGAACTTGAA	TTTGAAGGTT	CGGGCTCTAC	TGTGCAGAAG		1690

2) INFORMATION FOR SEQ ID NO: 1048

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048

30	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTACCCAAAC	GGACAATTTG	CTTCTAGCTT	TATTGGCTTA	100
	GCCCAACTTC	ATGAAAATGA	GGATGGTAGT	AAGAGTTTGT	TAGGGACTTC	150
	TGGTTTGGAG	AGTTCTTTAA	ATACCATTCT	TGCTGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
35	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
40	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAAGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GTTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
45	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
50	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAACATAT	GTATAATCAC	TACACAGGAA	1100
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
55	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTAAGTGAAC	1500
60	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550


```

AACAAAGTTCT CTTTTTATCG GATAAGGTAG AAGAAATTCC AGACATGTAT 1600
GGCTGGAAAAA AAGAGACTGC TGAAACCTTT GCTAAATGGT TGGATATTGA 1650
GTTGGAATTT GAAGGTCAG GTTCCGTCGT TC 1682

```

5

2) INFORMATION FOR SEQ ID NO: 1049

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1241 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R690

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049

```

GCAGCGTTGC GTGATACCGT TGAAAAAACC ATTAAAAACT GTTTGGATTT 50
TGAAAGGAGA CAGGAGCATG AATAGAATAA AAGTTGCAAT ACTGTTTGGG 100
25 GGTGCTCAG AGGAGCATGA CGTATCGGTA AAATCTGCAA TAGAGATAGC 150
CGCTAACATT AATAAAGAAA AATACGAGCC GTTATACATT GGAATTACGA 200
AATCTGGTGT ATGGAAAATG TCGGAAAAC CTTGCGCGGA ATGGGAAAAC 250
GACAATTGCT ATTCAGCTGT ACTCTCGCCG GATAAAAAAA TGCACGGATT 300
ACTTGTTAAA AAGAACCATG AATATGAAAT CAACCATGTT GATGTAGCAT 350
30 TTTCAGCTTT GCATGGCAAG TCAGGTGAAG ATGGATCCAT ACAAGGTCTG 400
TTTGAATTGT CCGGTATCCC TTTTGTAGGC TGCATATTC AAAGCTCAGC 450
AATTTGTATG GACAAATCGT TGACATACAT CGTTGCGAAA AATGCTGGGA 500
TAGCTACTCC CGCCTTTTGG GTTATTAATA AAGATGATAG GCCGGTGGCA 550
GCTACGTTTA CCTATCCTGT TTTTGTAAAG CCGGCGCGTT CAGGCTCATC 600
35 CTTCGGTGTG AAAAAAGTCA ATAGCGCGGA CGAATTGGAC TACGCAATTG 650
AATCGGCAAG ACAATATGAC AGCAAAATCT TAATTGAGCA GGCTGTTTCG 700
GGCTGTGAGG TCGGTGTGTC GGTTATGGGA AACAGTGCCG CGTTAGCTGT 750
TGGCGAGGTG GACCAATCA GGCTGCAGTA CGGAATCTTT CGTATTCATC 800
AGGAAGTCGA GCCGGAAAAA GGCTCTGAAA ACGCAGTTAT AACCGTTCCC 850
40 GCAGACCTTT CAGCAGAGGA GCGAGGACGG ATACAGGAAA CGGCAAAAAA 900
AATATATAAA GCGCTCGGCT GTAGAGGTCT AGCCCGTGTG GATATGTTTT 950
TACAAGATAA CGGCCGCATT GTACTGAACG AAGTCAATAC TCTGCCCGGT 1000
TTCACGTCAT ACAGTCGTTA TCCCCGTATG ATGGCCGCTG CAGGTATTGC 1050
ACTTCCCGAA CTGATTGACC GCTTGATCGT ATTAGCGTTA AAGGGGTGAT 1100
45 AAGCATGGAA ATAGGATTTA CTTTTTTAGA TGAAATAGTA CACGGTGTTT 1150
GTTGGGACGC TAAATATGCC ACTTGGGATA ATTTACCGG AAAACCGGTT 1200
GACGGTTATG AAGTAAATCG CATTGTAGGG ACATACGAAT T 1241

```

50

2) INFORMATION FOR SEQ ID NO: 1050

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1249 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
10	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
15	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
20	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
25	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCGTGTTG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
30	TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCG	1249

35 2) INFORMATION FOR SEQ ID NO: 1051

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1272 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R481

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051

	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAACTG	50
	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	100
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	150
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	200
55	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	250
	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	300
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	350
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	400
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	450
60	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	500

```

ATGCTGGGAT AGCTACTCCC GCCTTTTGGG TTATTAATAA AGATGATAGG 550
CCGGTGGCAG CTACGTTTAC CTATCCTGTT TTTGTTAAGC CGGCGCGTTC 600
AGGCTCATCC TTCGGTGTGA AAAAAGTCAA TAGCGCGGAC GAATTGGACT 650
ACGCAATTGA ATCGGCAAGA CAATATGACA GCAAAATCTT AATTGAGCAG 700
5 GCTGTTTCGG GCTGTGAGGT CGGTTGTGCG GTATTGGGAA ACAGTGCCGC 750
GTTAGTTGTT GGCGAGGTGG ACCAAATCAG GCTGCAGTAC GGAATCTTTC 800
GTATTCATCA GGAAGTCGAG CCGGAAAAAG GCTCTGAAAA CGCAGTTATA 850
ACCGTTCCCG CAGACCTTTC AGCAGAGGAG CGAGGACGGA TACAGGAAAC 900
GGCAAAAAAA ATATATAAAG CGCTCGGCTG TAGAGGTCTA GCCCGTGTGG 950
10 ATATGTTTTT ACAAGATAAC GGCCGCATTG TACTGAACGA AGTCAATACT 1000
CTGCCCCGTT TCACGTCATA CAGTCGTTAT CCCCCTATGA TGGCCGCTGC 1050
AGGTATTGCA CTTCCCGAAC TGATTGACCG CTTGATCGTA TTAGCGTTAA 1100
AGGGGTGATA AGCATGGAAA TAGGATTTAC TTTTTTAGAT GAAATAGTAC 1150
ACGGTGTTTCG TTGGGACGCT AAATATGCCA CTTGGGATAA TTTCACCGGA 1200
15 AAACCGGTTG ACGGTTATGA AGTAAATCGC ATTGTAGGGA CATACGAATT 1250
GGCTTGAATC GCTTTTTGAA GG 1272

```

20 2) INFORMATION FOR SEQ ID NO: 1052

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1237 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052

```

35 TCCCCCGGCA TACGGCCTAT TATACCGAGC AAGCGTTGCG TGATACCGTT 50
GAAAAAACCA TTA AAAACTG TTTGGATTTT GAAAGGAGAC AGGAGCATGA 100
ATAGAATAAA AGTTGCAATA CTGTTTGGGG GTTGCTCAGA GGAGCATGAC 150
GTATCGGTAA AATCTGCAAT AGAGATAGCC GCTAACATTA ATAAAGAAAA 200
40 ATACGAGCCG TTATACATTG GAATTACGAA ATCTGGTGTA TGGAAAATGT 250
GCGAAAAACC TTGCGCGGAA TGGGAAAACG ACAATTGCTA TTCAGCTGTA 300
CTCTCGCCGG ATAAAAAAT GCACGGATTA CTTGTTAAAA AGAACCATGA 350
ATATGAAATC AACCATGTTG ATGTAGCATT TTCAGCTTTG CATGGCAAGT 400
CAGGTGAAGA TGGATCCATA CAAGGTCGTG TTGAATTGTC CGGTATCCCT 450
45 TTTGTAGGCT GCGATATTCA AAGCTCAGCA ATTTGTATGG ACAAATCGTT 500
GACATACATC GTTGCGAAAA ATGCTGGGAT AGCTACTCCC GCCTTTTGGG 550
TTATTAATAA AGATGATAGG CCGGTGGCAG CTACGTTTAC CTATCCTGTT 600
TTTGTTAAGC CGGCGCGTTC AGGCTCATCC TTCGGTGTGA AAAAAGTCAA 650
TAGCGCGGAC GAATTGGACT ACGCAATTGA ATCGGCAAGA CAATATGACA 700
50 GCAAAATCTT AATTGAGCAG GCTGTTTCGG GCTGTGAGGT CGGTTGTGCG 750
GTATTGGGAA ACAGTGCCCG GTTAGCTGTT GGCGAGGTGG ACCAAATCAG 800
GCTGCAGTAC GGAATCTTTC GTATTCATCA GGAAGTCGAG CCGGAAAAAG 850
GCTCTGAAAA CGCAGTTATA ACCGTTCCCG CAGACCTTTC AGCAGAGGAG 900
CGAGGACGGA TACAGGAAAC GGCAAAAAAA ATATATAAAG CGCTCGGCTG 950
55 TAGAGGTCTA GCCCGTGTGG ATATGTTTTT ACAAGATAAC GGCCGCATTG 1000
TACTGAACGA AGTCAATACT CTGCCCCGTT TCACGTCATA CAGTCGTTAT 1050
CCCCGTATGA TGGCCGCTGC AGGTATTGCA CTTCCCGAAC TGATTGACCG 1100
CTTGATCGTA TTAGCGTTAA AGGGGTGATA AGCATGGAAA TAGGATTTAC 1150
TTTTTTAGAT GAAATAGTAC ACGGTGTTTCG TTGGGACGCT AAATATGCCA 1200
60 CTTGGGATAA TTTCACCGGA AAACCGGTTG ACGGTTA 1237

```

2) INFORMATION FOR SEQ ID NO: 1053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053

20	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	TTGAAAAAAC	50
	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	GAATAGAATA	100
	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	ACGTATCGGT	150
	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	AAATACGAGC	200
	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	GTGCGAAAAA	250
25	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	TACTCTCGCC	300
	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	GAATATGAAA	350
	TCAACCATGT	TGATGTAGCA	TTTTTCAGCTT	TGCATGGCAA	GTCAGGTGAA	400
	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	CTTTTGTAGG	450
	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	TTGACATACA	500
30	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	GGTTATTAAT	550
	AAAGATGATA	GGCCGGTGCG	AGCTACGTTT	ACCTATCCTG	TTTTTGTAA	600
	GCCGCGCGCT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	AATAGCGCGG	650
	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAAATATGA	CAGCAAAATC	700
	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	CGGTATTGGG	750
35	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	AGGCTGCAGT	800
	ACGGAATCTT	TCGTATTTCAT	CAGGAAGTCG	AGCCGGAAAA	AGGCTCTGAA	850
	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	AGCGAGGACG	900
	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	TGTAGAGGTC	950
	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	TGTACTGAAC	1000
40	GAAGTCAATA	CTCTGCCCCG	TTTCACGTCA	TACAGTCGTT	ATCCCCGTAT	1050
	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	CGCTTGATCG	1100
	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	ACTTTTTTTAG	1150
	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	CACTTGGGAT	1200
	AATTTACCG	GAAAACCGGT	TGACGGGTAT	GAAAGTAAAT	CGCATTGTAG	1250
45	GGACATTCTGA	ATT				1263

2) INFORMATION FOR SEQ ID NO: 1054

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1054

5	CGGCCTATTA	TNCCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCATT	50
	AAAAACTGTT	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAG	100
	TTGCAATACT	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	150
	TCTGCAATAG	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	200
	ATACATTGGA	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	250
10	GCGCGGAATG	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	300
	AAAAAAATGC	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	350
	CCATGTTGAT	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	400
	GATCCATACA	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	450
	GATATTCAAA	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	500
15	TGCGAAAAAT	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	550
	ATGATAGGCC	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	600
	GCGCGTTCAG	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	650
	ATTGGACTAC	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	700
	TTGAGCAGGC	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	750
20	AGTGCCGCGT	TAGTTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	800
	AATCTTTTCG	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	850
	CAGTTATAAC	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	900
	CAGGAAACGG	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	950
	CCGTGTGGAT	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	1000
25	TCAATACTCT	GCCCCGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	1050
	GCCGCTGCAG	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	1100
	AGCGTTAAAG	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	1150
	AATAGTACAC	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	1200
30	TCACCGGAAA	ACCGGTTGAC	GGTTATAAGT	AA		1232

2) INFORMATION FOR SEQ ID NO: 1055

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055

50	TACCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCATT	AAAAACTGTT	50
	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAG	TTGCAATACT	100
	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	TCTGCAATAG	150
	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	ATACATTGGA	200
	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	GCGCGGAATG	250
	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	AAAAAAATGC	300
55	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	CCATGTTGAT	350
	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	GATCCATACA	400
	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	GATATTCAAA	450
	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	TGCGAAAAAT	500
	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	ATGATAGGCC	550
60	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	GCGCGTTCAG	600

	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	ATTGGACTAC	650
	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	TTGAGCAGGC	700
	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	AGTGCCGCGT	750
	TAGCTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	AATCTTTCGT	800
5	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	CAGTTATAAC	850
	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	CAGGAAACGG	900
	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	CCGTGTGGAT	950
	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	TCAATACTCT	1000
	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	GCCGCTGCAG	1050
10	GTATTGCACT	TCCCGAAGTG	ATTGACCGCT	TGATCGTATT	AGCGTTAAAG	1100
	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	AATAGTACAC	1150
	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	TCACCGGAAA	1200
	ACCGGTTGAC	GGTTAGAA				1218

15

2) INFORMATION FOR SEQ ID NO: 1056

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R688
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056

	AATCACACCG	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	50
	TTGAAAAAAC	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	100
35	GAATAGAATA	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	150
	ACGTATCGGT	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	200
	AAATACGAGC	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGAAAAAT	250
	GTGCGAAAAA	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	300
	TACTCTCGCC	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	350
40	GAATATGAAA	TCAACCATGT	TGATGTAGCA	TTTTTCAGCTT	TGCATGGCAA	400
	GTCAGGTGAA	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	450
	CTTTTGTAGG	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	500
	TTGACATACA	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	550
	GGTTATTAAT	AAAGATGATA	GGCCGGTGCG	AGCTACGTTT	ACCTATCCTG	600
45	TTTTTGTAA	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	650
	AATAGCGCGG	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	700
	CAGCAAAATC	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	750
	CGGTATTGGG	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	800
	AGGCTGCAGT	ACGGAATCTT	TCGTATTCAT	CAGGAAGTCG	AGCCGGAAAA	850
50	AGGCTCTGAA	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	900
	AGCGAGGACG	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	950
	TGTAGAGGTC	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	1000
	TGTACTGAAC	GAAGTCAATA	CTCTGCCCGG	TTTCACGTCA	TACAGTCGTT	1050
	ATCCCCGTAT	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	1100
55	CGCTTGATCG	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	1150
	ACTTTTTTAG	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	1200
	CACTTGGGAT	AATTTACCCG	GAAAACCGGT	TGACGGTTAT	GAAGTAAATC	1250
	GCATTGTAGG	GACAT				1265

60

2) INFORMATION FOR SEQ ID NO: 1057

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
20	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
25	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
30	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGAAAAAAG	850
35	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCCGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
40	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	1250
	ATTGTAGGGA	CATACGAAT				1269

2) INFORMATION FOR SEQ ID NO: 1058

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058

	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
5	ATTCTCCAGA	ATACTCAGTG	TCACTAACCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTAACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
10	CTTGCAATGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
15	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750
	TTGACGATTG	GTGCTTGTGA	TGCGATTTCT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
20	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTTCGTCAC	950
	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
25	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCGCGAC	TTAGTGCTA				1169

30 2) INFORMATION FOR SEQ ID NO: 1059

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1166 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059

45	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
	ATTCTCCAGA	ATACTCAGTG	TCACTAGCCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTGACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
50	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
	CTTGCAATGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
55	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
60	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750

10
 5
 TTGACGATTG GTGCTTGTGA TGC GATTCTCT CTTGTCGACG GTTTTTTTTGA 800
 TTTTGAAGAG AAATACCAAT TAATCAGCGC CACGATCACT GTCCCAGCAC 850
 CATTGCCTCT CGCGCTTGAA TCACAGATCA AGGAGCAGGC ACAGCTGCTT 900
 TATCGAAACT TGGGATTGAC GGGTCTGGCT CGAATCGATT TTTTCGTCAC 950
 CAATCAAGGA GCGATTTATT TAAACGAAAT CAACACCATG CCGGGATTTA 1000
 CTGGGCACTC CCGCTACCCA GCTATGATGG CGGAAGTCGG GTTATCCTAC 1050
 GAAATATTAG TAGAGCAATT GATTGCACTG GCAGAGGAGG ACAAACGATG 1100
 AACACATTAC AATTGATCAA TAAAACCAT CCATTGAAAA AAAATCAAGA 1150
 GCCCCCGCAC TTAGTG 1166

2) INFORMATION FOR SEQ ID NO: 1060

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1028 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus casseliflavus*
 25 (B) STRAIN: ATCC 25788
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060

30 AACATGAAAA AAATCGCCTT ATTTTGGAG GCAATTCACC GGAATACACC 50
 GTTTCCTTTAG CTTTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC 100
 CTATGACTAC GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT 150
 GGTACTTGTA TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG 200
 TTGGATACGA AACATAAACA GAAAATACAG CCGCTATTCG AAGGAAACGG 250
 CTTTGGCTA AGTGAAGAGC AGCAAACGTT GGTACCTGAT GTTTTATTTT 300
 35 CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT 350
 GAATTGATGA AGCTGCCTTA TGTAGGCTGC GGGGTGGCAG GTTCTGCCTT 400
 ATGTATGAAC AAATGGCTGC TGCATCAAGC TGCAGCAGCC ATTGGCGTAC 450
 AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGAACAA 500
 ATCGAAGCTT TTATCCAGAC CCATGGCTTC CCAGTTTCTT TTAAGCCTAA 550
 40 TGAAGCGGGC TCCTCAAAG GGATCACTAA AGTCACCTGC GTTGAAGAAA 600
 TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTCCGC AGTGCTCCTA 650
 CAAAAAATA TTGCCGGTGT TGAGATCGGT TGCGGTATTT TGGGCAACGA 700
 CTCTTTGACT GTCGGTGCTT GTGACGCCAT TTCATTAGTA GACGGCTTTT 750
 TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAAAT CACCGTCCCT 800
 45 GCGCCATTGC CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT 850
 GCTCTATCGT AGTCTTGGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTTG 900
 TCACGGAGCG AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC 950
 TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGG TCGGCTTATC 1000
 CTATCAAGAA CTACTACAAA AACTGCTT 1028
 50

2) INFORMATION FOR SEQ ID NO: 1061

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061

```

10  AATATGAAAA AAATCGCCTT ATTTTGGAG GCAATTCACC GGAGTACGCC      50
    GTTTCCTTTAG CCTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC      100
    CGATGACTAT  GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT      150
    GGTATTTGTA  TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG      200
    TTGGATACGA  AACATAAACA GAAAATCCAG CCGCTTTTGT AAGGAAACGG      250
    CTTTTGGCTA  AGTGAAGAGC AACAAACGTT GGTTCCTGAT GTTTTATTTT      300
15  CCATTATGCA  TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT      350
    GAATTGATGA  AACTACCTTA TGTAGGCTGC GGGGTGGCAG CCTCTGCCTT      400
    ATGTATGAAC  AAATGGCTGC TGCATCAAGC AGCAGAAGCG ATTGGCGTAC      450
    AAAGTGCTCC  TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGATCAA      500
    ATCGAAGCTT  TTATCCAGAC CCATGGCTTT CCGGTTTTTT TTAAGCCTAA      550
20  TGAAGCGGGC  TCCTCAAAAG GGATCACTAA AGTCACCTGC GTTGAAGAAA      600
    TCGCTTCTGC  CTTAAAAGAA GCCTTTACTT ATTGTTTCAGC AGTGCTCCTA      650
    CAAAAAATA  TTGCCGGTGT TGAGATCGGT TCGCGTATTT TGGGCAACGA      700
    CTCTTTGACT  GTCGGTGCTT GTGACGCTAT TTCATTAGTA GACGGCTTTT      750
    TCGATTTTGA  AGAAAAGTAC CAGCTGATCA GCGCCAAGAT CACCGTTCCT      800
25  GCACCATTGC  CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT      850
    GCTCTATCGT  AGTCTTTGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTT      900
    TCACGGATCA  AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC      950
    TTTACGAGTC  ACTCCCGCTA TCCTGCCATG ATGGCAGCGA TCGGCTTATC     1000
    CTATCAAGAA  CTACTACAAA AACTGCTTGT      1030
30

```

2) INFORMATION FOR SEQ ID NO: 1062

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1031 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062

```

50  AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
    CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
    CCCTATGACT  ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
    TTGGTACTTG  TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
    TGTTGGATAC  GAAACATAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
    GGCTTTTGGC  TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTATT      300
55  TCCCATTATG  CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
    TTGAATTGAT  GAAGCTGCCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
    TTATGTATGA  ACAAATGGCT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
    ACAAAGTGCT  CCTACGATTC TCTTGACAAA TCAAGCCAAC CAGCAAGAAC      500
    AAATCGAAGC  TTTTATCCAG ACCCATGGCT TCCCAGTTTT CTTTAAGCCT      550
60  AATGAAGCGG  GCTCCTCAAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600

```

```

AATCGCTTCT GCCTTAAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC 650
TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC 700
GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATFTCATAG TAGACGGCTT 750
TTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCGTCC 800
5 CTGCGCCATT GCCTGAAACG ATTGAAACCA AGGTCAAAGA ACAAGCTCAG 850
CTGCTCTATC GTAGTCTTGG TCTTAAAGGT CTTGCTCGCA TCGACTTTTT 900
TGTCACGGAG CGAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG 950
GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTCGGCTTA 1000
10 TCCTATCAAG AACTACTACA AAAACTGCTT G 1031

```

2) INFORMATION FOR SEQ ID NO: 1063

```

15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1030 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Enterococcus casseliflavus
25 (B) STRAIN: R775

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063

```

AACATGAAAA AAATCGCCAT TATTTTTGGA GGCAATTCAC CGGAATACAC 50
30 CGTTTCTTTA GCTTCAGCAA CTAGCGCAAT CGAAGCACTC CAATCATCTC 100
CCTATGACTA CGACCTCTCT TTGATCGGGA TCGCCCCAGA TGCTATGGAT 150
TGGTACTTGT ATACAGGAGA ACTGGAAAAC ATCCGACAAG ACACGTGGTT 200
GTTGGATACG AAACATAAAC AGAAAATACA GCCGCTATTT GAAGGAAACG 250
GCTTTTGGCT AAGTGAAGAG CAGCAAACGT TAGTACCTGA TATTTTATTT 300
35 CCCATTATGC ATGGCAAATA CGGGGAAGAT GGCAGTATCC AAGGATTGTT 350
TGAATTGATG AAATACCTT ATGTAGGTTG CGGGGTGGCA GGTTCGCTT 400
TATGTATGAA CAAATGGCTG CTGCATCAAG CTGCAGCAGC CATTGGCGTA 450
CAAAGTGCTC CTACGATTCT CTTGACAAAT CAAGCCAACC AGCAAGAACA 500
AATCGAAGCT TTTATCCAGA CCCATGGCTT CCCAGTTTTC TTTAAGCCTA 550
40 ATGAAGCGGG CTCTTCAAAA GGGATCACTA AAGTCACCTG CGTTGAAGAA 600
ATCGCTTCTG CCTTAAAAAA AGCCTTTACT TATTGTTCCG CAGTGCTCCT 650
ACAAAAAAT ATTGCCGGTG TTGAGATCGG TTGCGGTATT TTTGGGCAACG 700
ACTCTTTGAC TGTCGGTGCT TGTGACGCCA TTTTATTAGT AGACGGCTTT 750
TTCGATTTTG AAGAAAAGTA CCAGCTGATC AGCGCCAAAA TCACCGTCCC 800
45 TGCGCCATTG CCTGAAACGA TTGAAACCAA GGTCAAAGAA CAAGCTCAGC 850
TGCTCTATCG TAGTCTTGGT CTTAAAGGTC TTGCTCGCAT CGACTTTTTT 900
GTCACGGATC AAGGAGAACT AACTTTGAAT GAAATCAATA CTATGCCGGG 950
CTTTACGAGT CACTCCCGTT ATCCTGCCAT GATGGCAGCG GTCGGCTTAT 1000
50 CCTATCAAGA ACTACTACAA AAATGCTTG 1030

```

2) INFORMATION FOR SEQ ID NO: 1064

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1032 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064

10	AAACATGAAA	AAAATCGCCA	TTATTTTTTG	AGGCAATTCA	CCGGAATACA	50
	CCGTTTCTTT	AGCTTCAGCA	ACTAGCGCAA	TCGAAGCACT	CCAATCATCT	100
	CCCTATGACT	ACGACCTCTC	TTTGATCGGG	ATCGCCCCAG	ATGCTATGGA	150
	TTGGTACTTG	TATACAGGAG	AACTGGAAAA	CATCCGACAA	GACACGTGGT	200
	TGTTGGATAC	GAAACAGAAA	CAGAAAATAC	AGCCGCTATT	CGAAGGAAAC	250
	GGCTTTTGGT	TAAGTGAAGA	GCAGCAAACG	TTGGTACCTG	ATGTTTATT	300
15	TCCCATTATG	CATGGCAAAT	ACGGGGAAGA	TGGCAGTATC	CAAGGATTGT	350
	TTGAATTGAT	GAAGCTACCT	TATGTAGGCT	GCGGGGTGGC	AGGTTCTGCC	400
	TTATGTATGA	ACAAATGGTT	GCTGCATCAA	GCTGCAGCAG	CCATTGGCGT	450
	ACAAAGTGCT	CCTACGATTC	TCTTGACAAA	TCACGCCAAC	CAGCAAGAAC	500
	AAATCGAAGC	TTTTATCCAG	ACCCATGGCT	TTCCAGTTTT	CTTTAAGCCT	550
20	AATGAAGCGG	GTTCCTCAAA	AGGGATCACT	AAAGTCACCT	GCGTTGAAGA	600
	AATCGCTTCT	GCCTTAAAG	AAGCCTTTAC	TTATTGTTCC	GCAGTGCTCC	650
	TACAAAAAAA	CATTGCCGGT	GTTGAGATCG	GTTGCCGTAT	TTTGGGCAAC	700
	GACTCTTTGA	CTGTCCGGTG	TTGTGACGCC	ATTTCATTAG	TAGACGGCTT	750
	TTTCGATTTT	GAAGAAAAGT	ACCAGCTGAT	CAGCGCCAAA	ATCACCGTCC	800
25	CTGCGCCATT	GCCTGAAACG	ATTGAAACTA	AGGTCAAAGA	ACAAGCTCAG	850
	CTGCTCTATC	GTAGTCTTGG	ACTTAAAGGT	CTTGCTCGCA	TCGACTTTTT	900
	TGTCACGGAT	CAAGGAGAAC	TATACTTGAA	TGAAATCAAT	ACTATGCCCG	950
	GCTTTACGAG	TCACTCCCGC	TATCCTGCCA	TGATGGCAGC	GGTCGGGTTA	1000
30	TCCTATCAAG	AACTACTACA	AAAACACTTT	GT		1032

2) INFORMATION FOR SEQ ID NO: 1065

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

(B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065

50	AAAAACATGA	AAAAAATCGC	CATTATTTTT	GGAGGCAATT	CACCGGAATA	50
	CACCGTTTCT	TTAGCTTCAG	CAACTAGCGC	AATCGAAGCA	CTCCAATCAT	100
	CTCCCTATGA	CTACGACCTC	TCTTTGATCG	GGATCGCCCC	AGATGCTATG	150
	GATTGGTACT	TGTATACAGG	AGAACTGGAA	AACATCCGAC	AAGACACGTG	200
	GTTGTTGGAT	ACGAAACATA	AACAGAAAAT	ACAGCCGCTA	TTCGAAGGAA	250
	ACGGCTTTTG	GCTAAGTGAA	GAGCAGCAAA	CGTTGGTACC	TGATGTTTTA	300
55	TTTCCCATT	TGCATGGCAA	ATACGGGGAA	GATGGCAGTA	TCCAAGGATT	350
	GTTTGAATTG	ATGAAGCTGC	CTTATGTAGG	CTGCGGGGTG	GCAAGTTCTG	400
	CCTTATGTAT	GAACAAATGG	CTGCTGCATC	AAGCTGCAGC	AGCCATTGGC	450
	GTACAAAGTG	CTCCTACGAT	TCTCTTGACA	AATCAAGCCA	ACCAGCAAGA	500
	ACAAATCGAA	GCTTTTATCC	AGACCCATGG	CTTTCCAGTT	TTCTTTAAGC	550
60	CTAATGAAGC	GGGCTCCTCA	AAAGGGATCA	CTAAAGTCAC	CTGCGTTGAA	600

```

GAAATCGCTT CTGCCTTAAA AGAAGCCTTT ACTTATTGTT CCGCAGTGCT 650
CCTACAAAAA AATATTGCCG GTGTTGAGAT CGGTTGCGGT ATTTTGGGCA 700
ACGACTCTTT GACTGTCGGT GCTTGTGACG CCATTTTCATT AGTAGACGGC 750
TTTTTCGATT TTGAAGAAAA GTACCAGCTG ATCAGCGCCA AAATCACCGT 800
5 CCCTGCGCCA TTGCCTGAAA CGATTGAAAC CAAGGTCAAA GAACAAGCTC 850
AGCTGCTCTA TCGTAGTCTT GGTCTTAAAG GTCTTGCTCG CATCGACTTT 900
TTTGTACACG ATCAAGGAGA ACTATACTTG AATGAAATCA ATACTATGCC 950
GGGCTTTACG AGTCACTCCC GCTATCCTGC CATGATGGCA GCGGTCGGCT 1000
TATCCTATCA AGAACTACTA CAAAACTGC TTGT 1034

```

10

2) INFORMATION FOR SEQ ID NO: 1066

```

15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1012 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Enterococcus flavescens
25 (B) STRAIN: R760

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066

```

CATGAAAAAA ATCGCCATTA TTTTGGAGG CAATTCACCG GAATACACCG 50
30 TTTCTTTAGC CTCAGCAACT AGCGCAATCG AAGCACTCCA ATCATCTCCC 100
TATGATTACG ACCTCTCTTT GATCGGGATC GCCCCAGATG CTATGGATTG 150
GTACTTGAT ATCAGGAGAAC TGGAAAACAT CCGACAAGAC ACGTGGTTGT 200
TGGATACGAA ACATACACAG AAAATCCAGC CACTTTTTGA AGGAAACGGC 250
TTTTGGATAA GTGAAGCGCA GCAAACGTTG GTACCTGATG TTTTATTTCC 300
35 CATTATGCAT GGTAAATACG GGAAGATGG CAGTATCCAA GGATTGTTTG 350
AATTGATGAA GCTGCCTTAT GTAGGCTGTG GGGTGGCAGC CTCTGCCTTA 400
TGTATGAACA AATGGTTATT GCATCAAGCA GCAGCAGCGA TTGGCGTACA 450
AAGCGCTCCT ACGATTCTCT TGACAAATCA AGCCAACCAG CAAAGACAAA 500
TCGAAGCCTT ATCCAGACC ATGGGCTTTC CAGTTTTCTT TAAGCCTAAT 550
40 GAAGCGGGCT CCTCAAAAGG GATCACAAA GTAACCTGTG TTGAAGAAAT 600
CGCTCCTGCC TTGAAGGAAG CCTTCGCTTA TTGTTCCGCA GTGCTCTTAC 650
AAAAAATAT CGCTGGCGTT GAGATTGGTT GCGGTATCTT AGGCAACGAC 700
TCTTTGACTG TCGGTGCTTG TGACGCTATT TCATTAGTAG ACGGCTTTTT 750
CGATTTTGAA GAAAAGTACC AGTTGATCAG CGCCAAAATC ACCGTTCTTG 800
45 CGCCATTGCC TGAAACGATT GAAACCAAAG TCAAAGAACA AGCTCAGCTG 850
CTCTATCACA GTCTTGGTCT TAAAGGACTT GCTCGCATCG ACTTTTTTGT 900
CACGGATCAA GGAGAACTAT ACTTGAATGA AATCAATACT ATGCCGGGCT 950
TTACGAGTCA CTCCCGCTAT CCTGCCATGA TGGCAGCGGT CGGCTTATCC 1000
TATCAAGAAT TA 1012

```

50

2) INFORMATION FOR SEQ ID NO: 1067

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 721 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067

```

10 CTTACGCTTT ATCGATTAGA CACGGGNAGC TTGTCCAATG GGRAGCCGAT      50
   TTGATTTTAT GGATGAACGC TCTCATCATG CGGCAAATGG AATATCATGC      100
   AATGAAGCGC AAAATCGCAG ACGTTTGCGC TCCATCATGG AAAACAGTGG      150
   GTTTGAAGCA TATAGCCTCG AATGGTGGCA CTATGTATTA AGAGACGAAC      200
   CATACCCCAA TAGCTATTTT GATTTCCCCG TTAAATAAAC TTTTAACCGT      250
   TGCACGGACA AACTATATAA GCTAACTCTT TCGGCAGGAA ACCCGACGTA      300
15 TGTAAGTGGT TCTTAGGGAA TTTATATATA GTAGATAGTA TTGAAGATGT      350
   AAGGCAGAGC GATATTGCGG TCATTATCTG CGTGCCTGCT GCAGAGATAG      400
   CCTGATAATA AGACTGATCG CATAGAGGGG TGGTATTTCA CACCGCCCAT      450
   TGTCACAGAG CAGTTCAGCC TCGTTAAATT CAGCATGGGT ATCACTTATG      500
   AAAATTCATC TACATTGGTG ATAATAGTAA ATCCAGTAGG GCGAAATAAT      550
20 TGACTGTAAT TTACGGGGCA AAACGGCACA ATCTCAAACG AGATTGTGCC      600
   GTTTAAGGGG AAGATTCTAG AAATATTTCA TACTTCCAAC TATATAGTTA      650
   AGGAGGAGAC TGAAAATGAA GAAGTTGTTT TTTTATTGTT TATTGTTATT      700
   CTTAATATAC TTAGGTTATT G                                     721

```

25

2) INFORMATION FOR SEQ ID NO: 1068

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

```

45 ATTTTTAAGG ATGAACGCTC TTCATCATGC GGCAAATGGA ATATCATGCA      50
   ATGAAGCGCA AAATCGCAGA CGTTTGCGCT CCATCATGGA AAACAGTGGG      100
   TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC TATGTATTAA GAGACGAACC      150
   ATACCCCAAT AGCTATTTTG ATTTCCCCGT TAAATAAACT TTTAACCGTT      200
   GCACGGACAA ACTATATAAG CTAACCTCTT CCGCAGGAAA CCCGACGTAT      250
   GTAAGTGGTT CTTAGGGAAT TTATATATAG TAGATAGTAT TGAAGATGTA      300
   AGGCAGAGCG ATATTGCGGT CATTATCTGC GTGCGCTGCG GCAAGATAGC      350
50 CTGATAATAA GACTGATCGC ATAGAGGGGT GGTATTTTCA ACCGCCCAT      400
   GTCAACAGGC AGTTCAGCCT CGTTAAATTC AGCATGGGTA TCACTTATGA      450
   AAATTCATCT ACATTGGTGA TAATAGTAAA TCCAGTAGGG CGAAATAAAT      500
   GACTGTAATT TACGGGGCAA AACGGCACAA TCTCAAACGA GATTGTGCCG      550
   TTTAAGGGGA AGATTCTAGA AATATTTTCA ACTTCCAAC ATATAGTTAA      600
55 GGAGGAGACT GAAAATGAAG AAGTTGTTTT TTTTATTGTT ATTGTTATTC      650
   TTAATATACT TAGGTTAT                                     668

```

60 2) INFORMATION FOR SEQ ID NO: 1069

ATTTACACACC GCCCATTTGTC AACAGGCAGT TCAGCCTCGT TAAATTCAGC 550
 ATGGGTATCA CTTATGAAAA TTCATCTACA TTGGTGATAA TAGTAAATCC 600
 AGTAGGGCGA AATAATTGAC TGTAATTTAC GGGGCAAAAC GGCACAATCT 650
 CAAACGAGAT TGTGCCGTTT AAGGGGAAGA TTCTAGAAAT ATTTCATACT 700
 5 TCCAACTATA TAGTTAAGGA GGAGACTGAA AATGAAGAAG TTGTTTTTTT 750
 TTATTGTTAT TGTTATTCTT AATATACTTA GGTTATGACT ACGTTAATGA 800
 A 801

10

2) INFORMATION FOR SEQ ID NO: 1071

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 711 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R684

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071

TTGTACCAAT GGGGAGCCGA TTTGATTTTA TGGATGAACG CTCTCATCAT 50
 GCGGCAAATG GAATATCATG CAATGAAGCG CAAAATCGCA GACGTTTGCG 100
 CTCCATCATG GAAAACAGTG GGTTTGAAGC ATATAGCCTC GAATGGTGGC 150
 30 ACTATGTATT AAGAGACGAA CCATACCCCA ATAGCTATTT TGATTTCCCC 200
 GTTAAATAAA CTTTTAACCG TTGCACGGAC AACTATATA AGCTAACTCT 250
 TTCGGCAGGA AACCCGACGT ATGTAACCTG TTCTTAGGGA ATTTATATAT 300
 AGTAGATAGT ATTGAAGATG TAAGGCAGAG CGATATTGCG GTCATTATCT 350
 GCGTGCGCTG CCGCAAGATA GCCTGATAAT AAGACTGATC GCATAGAGGG 400
 35 GTGGTATTTT ACACCGCCCA TTGTCAACAG GCAGTTCAGC CTCGTAAAT 450
 TCAGCATGGG TATCACTTAT GAAAATTCAT CTACATTGGT GATAATAGTA 500
 AATCCAGTAG GCGGAAATAA TTGACTGTAA TTTACGGGGC AAAACGGCAC 550
 AATCTCAAAC GAGATTGTGC CGTTTAAGGG GAAGATTCTA GAAATATTTC 600
 ATACTTCCAA CTATATAGTT AAGGAGGAGA CTGAAAATGA AGAAGTTGTT 650
 40 TTTTTTATTG TTATTGTTAT TCTTAATATA CTTAGGTTAT GACTACGTTA 700
 ATGAAGCACT G 711

45 2) INFORMATION FOR SEQ ID NO: 1072

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R688

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072


```

GCCATTGATC TTACGCTTTA TCGATTAGAC ACGGGTNAGC TTGTACCAAT      50
GGGGAGCCGA TTTGATTTTA TGGATGAACG CTCTCATCAT GCGGCAAATG      100
GAATATCATG CAATGAAGCG CAAAATCGCA GACGTTTGCG CTCCATCATG      150
GAAAACAGTG GGTTTGAAGC ATATAGCCTC GAATGGTGGC ACTATGTATT      200
5  AAGAGACGAA CCATACCCCA ATAGCTATTT TGATTTCCCC GTTAAATAAA      250
CTTTTAACCG TTGCACGGAC AAACATATA AGCTAACTCT TTCGGCAGGA      300
AACCCGACGT ATGTAAGTGG TTCTTAGGGA ATTTATATAT AGTAGATAGT      350
ATTGAAGATG TAAGGCAGAG CGATATTGCG GTCATTATCT GCGTGCGCTG      400
CGGCAAGATA GCCTGATAAT AAGACTGATC GCATAGAGGG GTGGTATTTT      450
10 ACACCGCCCA TTGTCAACAG GCAGTTCAGC CTCGTTAAAT TCAGCATGGG      500
TATCACTTAT GAAAATTCAT CTACATTGGT GATAATAGTA AATCCAGTAG      550
GGCGAAATAA TTGACTGTAA TTTACGGGGC AAAACGGCAC AATCTCAAAC      600
GAGATTGTGC CGTTTAAGGG GAAGATTCTA GAAATATTTT AACTTCCAA      650
CTATATAGTT AAGGAGGAGA CTGAAAATGA AGAAGTTGTT TTTTATTATT      700
15 TTATTGTTAT TCTTAATATA CTTAGGTTAT GACTACGTTA ATGAAGCACT      750
G

```

20 2) INFORMATION FOR SEQ ID NO: 1073

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073

```

35 ATTTGATTTT ATGGATGAAC GCTCTCATCA TGCGGCAAAT GGAATATCAT      50
GCAATGAAGC GCAAAATCGC AGACGTTTGC GCTCCATCAT GGAAAACAGT      100
GGGTTTGAAG CATATAGCCT CGAATGGTGG CACTATGTAT TAAGAGACGA      150
ACCATACCCC AATAGCTATT TTGATTTCCC CGTTAAATAA ACTTTTAACC      200
40 GTTGCACGGA CAAACTATAT AAGCTAACTC TTTCGGCAGG AAACCCGACG      250
TATGTAAGTGT GTTCTTAGGG AATTTATATA TAGTAGATAG TATTGAAGAT      300
GTAAGGCAGA GCGATATTGC GGTCATTATC TGCGTGCGCT GCGGCAAGAT      350
AGCCTGATAA TAAGACTGAT CGCATAGAGG GGTGGTATTT CACACCGCCC      400
ATTGTCAACA GGCAGTTCAG CCTCGTTAAA TTCAGCATGG GTATCACTTA      450
45 TGAAAATTCA TCTACATTGG TGATAATAGT AAATCCAGTA GGGCGAAATA      500
ATTGACTGTA ATTTACGGGG CAAAACGGCA CAATCTCAA CGAGATTGTG      550
CCGTTTAAGG GGAAGATTCT AGAAATATTT CATACTTCCA ACTATATAGT      600
TAAGGAGGAG ACTGAAAATG AAGAAGTTGT TTTTATTATT GTTATTGTGA      650
50 TTCTTAATAT ACTTAGGTTA TGACTACGTT AATGA
685

```

2) INFORMATION FOR SEQ ID NO: 1074

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074

```

10 ATCGATTAGA CACGGGTGAG CTTGTACCAA TGGGGAGCCG ATTTGATTTT 50
   ATGGATGAAC GCTCTCATCA TGCGGCAAAT GGAATATCAT GCAATGAAGC 100
   GCAAAATCGC AGACGTTTGC GCTCCATCAT GGAAAACAGT GGGTTTGAAG 150
   CATATAGCCT CGAATGGTGG CACTATGTAT TAAGAGACGA ACCATACCCC 200
   AATAGCTATT TTGATTTCCC CGTTAAATAA ACTTTTAACC GTTGCACGGA 250
   CAACTATAT AAGCTAACTC TTTCGGCAGG AAACCCGACG TATGTAAGTG 300
15 GTTCTTAGGG AATTTATATA TAGTAGATAG TATTGAAGAT GTAAGGCAGA 350
   GCGATATTGC GGTCATTATC TGCCTGCGCT GCGGCAAGAT AGCCTGATAA 400
   TAAGACTGAT CGCATAGAGG GGTGGTATTT CACACCGCCC ATTGTCAACA 450
   GGCAGTTCAG CCTCGTTAAA TTCAGCATGG GTATCACTTA TGAAAATTCA 500
   TCTACATTGG TGATAATAGT AAATCCAGTA GGGCGAAATA ATTGACTGTA 550
20 ATTTACGGGG CAAAACGGCA CAATCTCAAA CGAGATTGTG CCGTTTAAGG 600
   GGAAGATTCT AGAAATATTT CATACTTCCA ACTATATAGT TAAGGAGGAG 650
   ACTGAAAATG AAGAAGTTGT TTTTTTTATT GTTATTGTTA TTCTTAATAT 700
   ACTTAGGTTA TGACTACGTT AATGAAGCAC TG 732

```

25

2) INFORMATION FOR SEQ ID NO: 1075

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 670 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075

```

45 TCTCATCATG CGGCAAATGG AATATCATGC AATGAAGCGC AAAATCGCAG 50
   ACGTTTGCGC TCCATCATGG AAAACAGTGG GTTTGAAGCA TATAGCCTCG 100
   AATGGTGGCA CTATGTATTA AGAGACGAAC CATACCCCAA TAGCTATTTT 150
   GATTTCCTCG TTAAATAAAC TTTTAACCGT TGCACGGACA AACTATATAA 200
   GCTAACTCTT TCGGCAGGAA ACCCGACGTA TGTAAGTGGT TCTTAGGGAA 250
   TTTATATATA GTAGATAGTA TTGAAGATGT AAGGCAGAGC GATATTGCGG 300
   TCATTATCTG CGTGCGCTGC GGCAAGATAG CCTGATAATA AGACTGATCG 350
50 CATAGAGGGG TGGTATTTCA CACCGCCCAT TGTCAACAGG CAGTTCAGCC 400
   TCGTTAAATT CAGCATGGGT ATCACTTATG AAAATTTCATC TACATTGGTG 450
   ATAATAGTAA ATCCAGTAGG GCGAAATAAT TGACTGTAAT TTACGGGGCA 500
   AAACGGCACA ATCTCAAACG AGATTGTGCC GTTTAAGGGG AAGATTCTAG 550
   AAATATTTCA TACTTCCAAC TATATAGTTA AGGAGGAGAC TGAAAATGAA 600
55 GAAGTTGTTT TTTTATTGT TATTGTTATT CTTAATATAC TTAGGTTATG 650
   ACTACGTTAA TGAAGCACTG 670

```

60 2) INFORMATION FOR SEQ ID NO: 1076

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: DG131/3 serotype OX3:H8
 (C) ACCESSION NUMBER: extracted from Z36901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076

```

TTGTGTAATA TGAAAATAAT AATTTTTAGA GTGCTAACTT TTTTCTTTGT      50
TATCTTTTCT GTTAATGTGG TTGCGAAGGA ATTTACCTTA GATTTCCTCGA    100
CAGCAAAGAC GTATGTAGAT TCGCTGAATG TCATTGCTC TGCAATAGGT      150
ACTCCATTAC AGACTATTTT ATCAGGAGGT ACGTCTTTAC TGATGATTGA      200
TAGTGGCACA GGGGATAAAT TGTTTGCAGT TGATGTCAGA GGGATAGATC      250
CAGAGGAAGG GCGGTTTAAT AATCTACGGC TTATTGTTGA ACGAAATAAT      300
TTATATGTGA CAGGATTTGT TAACAGGACA AATAATGTTT TTTATCGCTT      350
TGCTGATTTT TCACATGTTA CCTTTCCTGG TACAACGCG GTTACATTGT      400
CTGGTGACAG TAGCTATAAC ACGTTACAGC GTGTTGCGGG GATCAGTCGT      450
ACGGGGATGC AGATAAATCG CCATTGCTTG ACTACTTCTT ATCTGGATTT      500
AATGTCGCAT AGCGGAACCT CACTGACGCA GTCTGTGGCA AGAGCGATGT      550
TACGGTTTGT TACTGTGACA GCTGAAGCTT TACGTTTTCG GCAAATTCAG      600
AGGGGATTTT GTACAACACT TGATGATCTC AGTGGGCGTT CTTATGTAAT      650
GACTGCTGAA GATGTTGATC TTACGTTGAA CTGGGGAAGG TTGAGTAGTG      700
TCCTGCCTGA CTATCATGGA CAAGACTCTG TTCGTGTTGG AAGAATTTCT      750
TTTGGAAGTG TTAATGTAACT TCTGGGTAGC GTGGCATTAA TACTGAATTG      800
TCATCATCAT GCATCGCGAG TTGCCAGAAT TGTACCTAAT GAGTTTCCTT      850
CTATGTGCCC GGTAGATGGA AGAGTGCGTG GGATTACGCA CAATAAAATA      900
TTGTGGGACT CATCCACTCT GGGGGCAATT TTGATACGCA GGGCTATTAG      950
CAGTTGAGGG GGGTAAAATG AAAAAAATAT TATTAATAGC TGCATCACTT    1000
TCATTTTTTT CAGCAAGTGT GCTGGCTGCG CCAGATTGTG TAACTGGGAA    1050
GGTGGAGTAT ACAAATATA ATGATGACGA TACCTTTACA GTTAAAGTGG    1100
GAGATAAAGA ATTATTTACT AACAGATGGA ATCTTCAGTC TCTTCTTCTC    1150
AGTGCACAAA TTACGGGGAT GACGGTAACC ATTAAACTA ATGCCTGTCA    1200
TAATGGAGGG GGATTCAGCG AGGTTATTTT CCGTTGACTC AGAATA      1246

```

2) INFORMATION FOR SEQ ID NO: 1077

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: 94C serotype O48:H21
 (C) ACCESSION NUMBER: extracted from Z37725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077

CACCTGTATA TGAAGTGTAT ATTATTTAAA TGGGTACTGT GCCTGT TACT 50
 GGGTTTTTCT TCGGTATCCT ATTCCCGGGA GTTTACGATA GACTTTTCGA 100
 CCCAACAAAG TTATGTCTCT TCGTTAAATA GTATACGGAC AGAGATATCG 150
 5 ACCCCTCTTG AACATATATC TCAGGGGACC ACATCGGTGT CTGTTATTAA 200
 CCACACCCCA CCGGGCAGTT ATTTTGCTGT GGATATACGA GGGCTTGATG 250
 TCTATCAGGC GCGTTTTGAC CATCTTCGGC TGATTATTGA GCAAAATAAT 300
 TTATATGTGG CCGGGTTCGT TAATACGGCA ACAAATACTT TCTACCGTTT 350
 TTCAGATTTT ACACATATAT CAGTGCCCCG TGTGACAACG GTTTCCATGA 400
 10 CAACGGACAG CAGTTATACC ACTCTGCAAC GTGTGCGAGC GCTGGAACGT 450
 TCCGGAATGC AAATCAGTCG TCACTCACTG GTTTCATCAT ATCTGGCGTT 500
 AATGGAGTTC AGTGGTAATA CAATGACCAG AGATGCATCC AGAGCAGTTC 550
 TGCGTTTTGT CACTGTCACA GCAGAAGCCT TACGCTTCAG GCAGATACAG 600
 AGAGAATTTT GTCAGGCACT GTCTGAAACT GCTCCTGTGT ATACCATGAC 650
 15 GCCGGGAGAC GTGGACCTCA CTCTGAACTG GGGGCGAATC AGCAATGTGC 700
 TTCCGGAGTA TCGGGGAGAG GATGGTGTCA GAGTGGGGAG AATATCCTTT 750
 AATAATATAT CAGCGATACT GGGTACTGTG GCCGTTATAC TGAATTGCCA 800
 TCATCAGGGG GCGCGTTCGT TTCGCGCCGT GAATGAAGAG AGTCAACCAG 850
 AATGTCAGAT AACTGGCGAC AGGCCCGTTA TAAAAATAAA CAATACATTA 900
 20 TGGGAAAGTA ATACAGCTGC AGCGTTTCTG AACAGAAAGT CACAGTTTTT 950
 ATATACAACG GGTAATAATA GGAGTTAAGT ATGAAGAAGA TGTTTATGGC 1000
 GGTTTTATTT GCATTAGTTT CTGTTAATGC AATGGCGGCG GATTGTGCTA 1050
 AAGGTAAAT TGAGTTTTC AAGTATAATG AGGATGACAC ATTTACAGTG 1100
 AAGGTTGACG GGAAAGAATA CTGGACCAGT CGCTGGAATC TGCAACCGTT 1150
 25 ACTGCAAAGT GCTCAGCTGA CAGGAATGAC TGTCACAATC AAATCCAGTA 1200
 CCTGTGAATC AGGCTCCGGA TTTGCTGAAG TGCAGTTTAA TAATGACTGA 1250
 GGCATAACC 1259

30

2) INFORMATION FOR SEQ ID NO: 1078

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078

AGTTCTGCGT TTTGTCACTG TC

22

45

2) INFORMATION FOR SEQ ID NO: 1079

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079

CGGAAGCACA TTGCTGATT

60

19

2) INFORMATION FOR SEQ ID NO: 1080

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080
15 TATAGCTACT GTCACCAGAC AATGT 25

2) INFORMATION FOR SEQ ID NO: 1081

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081
30 ATGTCAGAGG GATAGATCCA 20

2) INFORMATION FOR SEQ ID NO: 1082

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082
TTGARCRAAA TAATTTATAT GTG 23

2) INFORMATION FOR SEQ ID NO: 1083

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083

TGATGATGRC AATTCAGTAT

20

5

2) INFORMATION FOR SEQ ID NO: 1084

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084

CCACGCCGCT TTGCTGATTT TTCACATGTT ACCGCGTGG

39

20

2) INFORMATION FOR SEQ ID NO: 1085

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085

CCACGCCACT GTCTGAAACT GCTCCTGTGC GTGG

34

35

2) INFORMATION FOR SEQ ID NO: 1086

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086

CTACTCCCGC CTTTGGGTT

20

50

55 2) INFORMATION FOR SEQ ID NO: 1087

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087

CTCACAGCCC GAAACAGCCT

20

10

2) INFORMATION FOR SEQ ID NO: 1088

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

15

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088

TGCCGTTTCC TGTATCCGTC

20

25

2) INFORMATION FOR SEQ ID NO: 1089

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089

ATCCACACGG GCTAGACCTC

20

40

2) INFORMATION FOR SEQ ID NO: 1090

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090

55 AATAGCGCGG ACGAATTGGA C

21

60

2) INFORMATION FOR SEQ ID NO: 1091

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091

AACGCGGCAC TGTTTCCCAA

20

2) INFORMATION FOR SEQ ID NO: 1092

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092

TCGGCAAGAC AATATGACAG C

21

2) INFORMATION FOR SEQ ID NO: 1093

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSsa-165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093

TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
CGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACCTGCTT	200
TTTTAAAGTA	TAGGTATAAA	ATACAATTGA	TTAAAATAGT	AAAGGAAATG	250
AATCATGAAA	CAATTAACTA	AGCCTTTATA	CTTTTACCTA	TTACTTTTTA	300
TTACAACAAC	ACTGATTGGC	GCGTTACTAT	TATATTTGCC	AATCACAGGT	350
AAACATCCTA	TTGATTTTGT	GGACGCCCGT	T		381

2) INFORMATION FOR SEQ ID NO: 1094

(i) SEQUENCE CHARACTERISTICS:

819

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094

10 GGTAACACAG GTACTTCTAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1095

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095

25

CGATAGAAGC AGCAGGACAA

20

30 2) INFORMATION FOR SEQ ID NO: 1096

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096

CTGATGGATG CGGAAGATAC

20

45

2) INFORMATION FOR SEQ ID NO: 1097

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097

TCYTCAAAAG GGATCACWAA AGTMAC

26

60

2) INFORMATION FOR SEQ ID NO: 1098

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098
15 TCTTCAAAAT CGAAAAAGCC GTC

23

2) INFORMATION FOR SEQ ID NO: 1099

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099
30 TCAAAAGGGA TCACWAAAGT MAC

23

2) INFORMATION FOR SEQ ID NO: 1100

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100
45 GTAAAKCCCG GCATRGTRTTGATTTC

26

50 2) INFORMATION FOR SEQ ID NO: 1101

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101

GACGGYTTTT TYGATTTTGAAGA

23

5

2) INFORMATION FOR SEQ ID NO: 1102

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102

AAAAARTCGA TKCGAGCMAGACC

23

20

2) INFORMATION FOR SEQ ID NO: 1103

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103

ATCCCGCTAT GAAAACGATC

20

35

2) INFORMATION FOR SEQ ID NO: 1104

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104

50 GGATCAACAC AGTAGAACCG

20

55

2) INFORMATION FOR SEQ ID NO: 1105

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105

5

CTCCTACGAT TCTCTTGAYA AATCA

25

10 2) INFORMATION FOR SEQ ID NO: 1106

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106

CAACCGATCT CAACACCGGC AAT

23

25

2) INFORMATION FOR SEQ ID NO: 1107

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107

CTCATTTGAC TTCCTCCTTT GCT

23

40

2) INFORMATION FOR SEQ ID NO: 1108

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108

GTAAGAATCG GAAAAGCGGA AGG

23

55

2) INFORMATION FOR SEQ ID NO: 1109

(i) SEQUENCE CHARACTERISTICS:

60

823

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109

10 ACATCGTGAT CGCTAAAAGG AGC

23

2) INFORMATION FOR SEQ ID NO: 1110

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110

25

ACGAGAAAGA CAACAGGAAG ACC

23

30 2) INFORMATION FOR SEQ ID NO: 1111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111

40

CTTTTCCGG CTCGWYTTCC TGATG

25

45

2) INFORMATION FOR SEQ ID NO: 1112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112

55

GGCTGYGATA TTCAAAGCTC

20

60

2) INFORMATION FOR SEQ ID NO: 1113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113

ACCGACCTCA CAGCCCGAAA

20

2) INFORMATION FOR SEQ ID NO: 1114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114

TCWGAGCCTT TTTCCGGCTC G

21

2) INFORMATION FOR SEQ ID NO: 1115

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115

TTTCGGGCTG TGAGGTCGGB TGHGCG

26

2) INFORMATION FOR SEQ ID NO: 1116

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116

TTTCGGGCTG TGAGGTCGGB TGHGCGG

27

5

2) INFORMATION FOR SEQ ID NO: 1117

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 801 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: 94
(C) ACCESSION NUMBER: U94526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117

25	AAATTCGATC	CGCACTACAT	CGGAATTACA	AAAAACGGTG	TATGGAAGCT	50
	ATGCAAGAAG	CCATGTACGG	AATGGGAAGC	CGACAGTCTC	CCCGCCATAC	100
	TCTCCCCGGA	TAGGAAAACG	CATGGGCTGC	TTGTCATGAA	AGAAAGCGAA	150
	TACGAAACAC	GGCGTATTGA	TGTGGCTTTC	CCGGTTTTGC	ATGGCAAATG	200
	CGGGGAGGAT	GGTGCATAC	AGGGGCTGTT	TGTATTGTCT	GGTATCCCCT	250
	ATGTGGGCTG	TGATATTCAA	AGCTCCGCAG	CTTGCATGGA	CAAATCACTG	300
30	GCCTACATTC	TTACAAAAAA	TGCGGGCATC	GCCGTTCCCG	AATTTCAAAT	350
	GATTGATAAA	GGTGACAAGC	CGGAGGCGGG	TGCGCTTACC	TACCCTGTCT	400
	TTGTGAAGCC	GGCACGGTCA	GGTTCGTCCT	TTGGCGTAAC	CAAAGTAAAC	450
	GGTACGGAAG	AACTTAACGC	TGCGATAGAA	GCGGCAGGAC	AATATGATGG	500
	AAAAATCTTA	ATTGAGCAAG	CGATTTCCGG	CTGTGAGGTC	GGGTGTGCGG	550
35	TCATGGGGAA	CGAGGATGAT	TTGATTGTCG	GCGAAGTGGA	TCAAATCCGG	600
	CTGAGCCACG	GTATCTTCCG	CATCCATCAG	GAAAACGAGC	CGGAAAAAGG	650
	CTCAGAAAAT	GCGATGATTA	CAGTTCCCGC	AGACATTCCG	GTCGAGGAAC	700
	GAAATCGGGT	GCAGGAAACG	GCAAAGAAAG	TATATCGGGT	GCTTGGATGC	750
	AGAGGGCTTG	CCCCTGTTGA	TCTTTTTTTG	CAGGAGGATG	GCGGCATCGT	800
40	T					801

2) INFORMATION FOR SEQ ID NO: 1118

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118

55

TTTTCWGAGC CTTTTTCCGG CTCG

24

60 2) INFORMATION FOR SEQ ID NO: 1119

826

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119
TTTCGGGCTG TGAGGTCGGB TGHGC 25

15 2) INFORMATION FOR SEQ ID NO: 1120

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120
TTTCGGGCTG TGAGGTCGGB TGHG 24

30 2) INFORMATION FOR SEQ ID NO: 1121

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121
TGTTTGWATT GTCYGGYATC CC 22

45 2) INFORMATION FOR SEQ ID NO: 1122

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122

TGGTGCATTG CTACGTGG

18

5 2) INFORMATION FOR SEQ ID NO: 1123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123

TTTCGGGCTG TGAGGTCGGB TG

22

20 2) INFORMATION FOR SEQ ID NO: 1124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124

GATTTGRTCC ACYTCGCCRA CA

22

35 2) INFORMATION FOR SEQ ID NO: 1125

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125

ACTCACAAC TGGGATGGATG

20

50 2) INFORMATION FOR SEQ ID NO: 1126

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

828

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126

TTATGGTTGT GCTGGTTGAG G

21

2) INFORMATION FOR SEQ ID NO: 1127

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127

KCAAAYGCCA TTTCAAGTAA

20

2) INFORMATION FOR SEQ ID NO: 1128

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128

GACGACYTTA TKGATATACA

20

2) INFORMATION FOR SEQ ID NO: 1129

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129

ATGATGACCG AMATGATGAA AAC

23

2) INFORMATION FOR SEQ ID NO: 1130

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130
10 GACTATCCAA GCATGCATTA TG 22

15 2) INFORMATION FOR SEQ ID NO: 1131

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131
 CATCTGGAGC TACRTARCCA GT 22

30 2) INFORMATION FOR SEQ ID NO: 1132

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132
 AGTGAAAARA TGGCTGCTGC 20

45 2) INFORMATION FOR SEQ ID NO: 1133

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133
 CATCAAGAAC ACTGGCTAYG TAG 23

2) INFORMATION FOR SEQ ID NO: 1134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134

CTAGATAGAG CTAAAACCTT CCT

23

2) INFORMATION FOR SEQ ID NO: 1135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135

CATTATGCAA ACGCCATTTT AAG

23

2) INFORMATION FOR SEQ ID NO: 1136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136

ACTTGTCCAC GTTSGATRTC T

21

2) INFORMATION FOR SEQ ID NO: 1137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137

AATTAATGGC TGCWGTGAY GAA

23

2) INFORMATION FOR SEQ ID NO: 1138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
- (C) ACCESSION NUMBER: M75132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138

25	GAGCTCTTCC	TTCAACGCAC	TTCTGTACCA	AGAGTTGTTG	TCCATTTGAT	50
	CACTAACAAT	AGCTTCCCCT	GCTTTCTTCA	AGCCCTTTGT	CATAAAATCG	100
	TTAGATTTTC	ATCATAAAAA	TACGAGAAAG	ACAACAGGAA	GACCGCAAAT	150
	TTTCTTTTCT	TTTCCTAGGT	ACACTGAATG	TAACCTTAAA	AGAAAAAAGG	200
	AAAGGAAGAA	AATGATGAAA	AAAATTGCCG	TTTTATTTGG	AGGGAATTCT	250
	CCAGAATACT	CAGTGTCACT	AACCTCAGCA	GCAAGTGTGA	TCCAAGCTAT	300
30	TGACCCGCTG	AAATATGAAG	TAATGACCAT	TGGCATCGCA	CCAACAATGG	350
	ATTGGTATTG	GTATCAAGGA	AACCTCGCGA	ATGTTTCGCA	TGATACTTGG	400
	CTAGAAGATC	ACAAAACTG	TCACCAGCTG	ACTTTTCTTA	GCCAAGGATT	450
	TATATTAGGA	GAAAAACGAA	TCGTCCCTGA	TGTCCTCTTT	CCAGTCTTGC	500
	ATGGGAAGTA	TGGCGAGGAT	GGCTGTATCC	AAGGACTGCT	TGAACATAATG	550
35	AACCTGCCTT	ATGTTGGTTG	CCATGTCGCT	GCCTCCGCAT	TATGTATGAA	600
	CAAATGGCTC	TTGCATCAAC	TTGCTGATAC	CATGGGAATC	GCTAGTGCTC	650
	CCACTTTGCT	TTTATCCCGC	TATGAAAACG	ATCCTGCCAC	AATCGATCGT	700
	TTTATTCAAG	ACCATGGATT	CCCGATCTTT	ATCAAGCCGA	ATGAAGCCGG	750
	TTCTTCAAAA	GGGATCACAA	AAGTAACTGA	CAAAACAGCG	CTCCAATCTG	800
40	CATTAACGAC	TGCTTTTGCT	TACGGTTCTA	CTGTGTTGAT	CCAAAAGGCG	850
	ATAGCGGGTA	TTGAAATTGG	CTGCGGCATC	TTAGGAAATG	AGCAATTGAC	900
	GATTGGTGCT	TGTGATGCGA	TTTCTCTTGT	CGACGGTTTT	TTTGATTTTG	950
	AAGAGAAATA	CCAATTAATC	AGCGCCACGA	TCACTGTCCC	AGCACCATTG	1000
	CCTCTCGCGC	TTGAATCACA	GATCAAGGAG	CAGGCACAGC	TGCTTTATCG	1050
45	AAACTTGGGA	TTGACGGGTC	TGGCTCGAAT	CGATTTTTTC	GTCACCAATC	1100
	AAGGAGCGAT	TTATTTAAAC	GAAATCAACA	CCATGCCGGG	ATTTACTGGG	1150
	CACTCCCGCT	ACCCAGCTAT	GATGGCGGAA	GTCGGGTTAT	CCTACGAAAT	1200
	ATTAGTAGAG	CAATTGATTG	CACTGGCAGA	GGAGGACAAA	CGATGAACAC	1250
	ATTACAATTG	ATCAATAAAA	ACCATCCATT	GAAAAAAAAT	CAAGAGCCCC	1300
50	CGCACTTAGT	GCTAGCTCCT	TTTAGCGATC	ACGATGTTTA	CCTGCAG	1347

2) INFORMATION FOR SEQ ID NO: 1139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1768 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: BM4147

(C) ACCESSION NUMBER: X56895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139

```

10  GATATCGTTA CGCTTCATGT GCCGCTCAAT ACGGATACGC ACTATATTAT 50
    CAGCCACGAA CAAATACAGA GAATGAAGCA AGGAGCATTT CTTATCAATA 100
    CTGGGCGCGG TCCACTTGTA GATACCTATG AGTTGGTTAA AGCATTAGAA 150
    AACGGGAAAC TGGGCGGTGC CGCATTGGAT GTATTGGAAG GAGAGGAAGA 200
15  GTTTTTCTAC TCTGATTGCA CCCAAAACC AATTGATAAT CAATTTTAC 250
    TTAAACTTCA AAGAATGCCT AACGTGATAA TCACACCGCA TACGGCCTAT 300
    TATACCGAGC AAGCGTTGCG TGATACCGTT GAAAAAACCA TTAAAAACTG 350
    TTTGGATTTT GAAAGGAGAC AGGAGCATGA ATAGAATAAA AGTTGCAATA 400
    CTGTTTGGGG GTTGCTCAGA GGAGCATGAC GTATCGGTAA AATCTGCAAT 450
20  AGAGATAGCC GCTAACATTA ATAAAGAAAA ATACGAGCCG TTATACATTG 500
    GAATTACGAA ATCTGGTGTA TGGAAAATGT GCGAAAAACC TTGCGCGGAA 550
    TGGGAAAAACG ACAATTGCTA TTCAGCTGTA CTCTCGCCGG ATAAAAAAT 600
    GCACGGATTA CTTGTAAAAA AGAACCATGA ATATGAAATC AACCATGTTG 650
    ATGTAGCATT TTCAGCTTTG CATGGCAAGT CAGGTGAAGA TGGATCCATA 700
25  CAAGGTCTGT TTGAATTGTC CGGTATCCCT TTTGTAGGCT GCGATATTCA 750
    AAGCTCAGCA ATTTGTATGG ACAAATCGTT GACATACATC GTTGCGAAAA 800
    ATGCTGGGAT AGCTACTCCC GCCTTTTGGG TTATTAATAA AGATGATAGG 850
    CCGGTGGCAG ATACGTTTAC CTATCCTGTT TTTGTTAAGC CGGCGCGTTC 900
    AGGCTCATCC TTCGGTGTGA AAAAAGTCAA TAGCGCGGAC GAATTGGACT 950
30  ACGCAATTGA ATCGGCAAGA CAATATGACA GCAAATCTT AATTGAGCAG 1000
    GCTGTTTCGG GCTGTGAGGT CGGTTGTGCG GTATTGGGAA ACAGTGCCGC 1050
    GTTAGTTGTT GGCGAGGTGG ACCAAATCAG GCTGCAGTAC GGAATCTTTC 1100
    GTATTCATCA GGAAGTCGAG CCGGAAAAAG GCTCTGAAAA CGCAGTTATA 1150
    ACCGTTCCCC CAGACCTTTC AGCAGAGGAG CGAGGACGGA TACAGGAAAC 1200
35  GGCAAAAAAA ATATATAAAG GCCTCGGCTG TAGAGGTCTA GCCCGTGTGG 1250
    ATATGTTTTT ACAAGATAAC GGCCGCATTG TACTGAACGA AGTCAATACT 1300
    CTGCCCCGGT TCACGTCATA CAGTCGTTAT CCCCCTATGA TGGCCGCTGC 1350
    AGGTATTGCA CTTCCCGAAC TGATTGACCG CTTGATCGTA TTAGCGTTAA 1400
    AGGGGTGATA AGCATGGAAA TAGGATTTAC TTTTTTAGAT GAAATAGTAC 1450
40  ACGGTGTTTC TTGGGACGCT AAATATGCCA CTTGGGATAA TTTCACCGGA 1500
    AAACCGGTTG ACGGTTATGA AGTAAATCGC ATTGTAGGGA CATACGAGTT 1550
    GGCTGAATCG CTTTTGAAGG CAAAAGAACT GGCTGCTACC CAAGGGTACG 1600
    GATTGCTTCT ATGGGACGGT TACCGTCCTA AGCGTGCTGT AAAGTTATTA 1650
    ATGCAATGGG CTGCACAGCC GGAAAATAAC CTGACAAAGG AAAGTTATTA 1700
45  TCCAATATT GACCGAACTG AGATGATTTT AAAAGGATAC GTGGCTTCAA 1750
    AATCAAGCCA TAGCCCGC 1768

```

50 2) INFORMATION FOR SEQ ID NO: 1140

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*
 (C) ACCESSION NUMBER: L29638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140

```

5   GTAAGAATCG GAAAAGCGGA AGGAAGAAAA ACATGAAAAA AATCGCCATT      50
    ATTTTGGGAG GCAATTCACC GGAATACACC GTTCTTTAG CTTCAGCAAC      100
    TAGCGCAATC GAAGCACTCC AATCATCTCC CTATGACTAC GACCTCTCTT      150
    TGATCGGGAT CGCCCCAGAT GCTATGGATT GGTACTTGTA TACAGGAGAA      200
10  CTGGAAAACA TCCGACAAGA CACGTGGTTG TTGGATACGA AACATAAACA      250
    GAAAATACAG CCGCTATTCTG AAGGAAACGG CTTTGGCTA AGTGAAGAGC      300
    AGCAAACGTT GGTACCTGAT GTTTTATTTT CCATTATGCA TGGCAAATAC      350
    GGGGAAGATG GCAGTATCCA AGGATTGTTT GAATTGATGA AGCTGCCTTA      400
    TGTAGGCTGC GGGGTGGCAG GTTCTGCCTT ATGTATGAAC AAATGGCTGC      450
15  TGCATCAAGC TGCAGCAGCC ATTGGCGTAC AAAGTGCTCC TACGATTCTC      500
    TTGACAAATC AAGCCAACCA GCAAGAACAA ATCGAAGCTT TTATCCAGAC      550
    CCATGGCTTC CCAGTTTCT TTAAGCCTAA TGAAGCGGGC TCCTCAAAG      600
    GGATCACTAA AGTCACCTGC GTTGAAGAAA TCGCTTCTGC CTTAAAAGAA      650
    GCCTTTACTT ATTGTTCCGC AGTGCTCCTA CAAAAAATA TTGCCGGTGT      700
20  TGAGATCGGT TCGGGTATTT TGGGCAACGA CTCCTTGACT GTCGGTGCTT      750
    GTGACGCCAT TTCATTAGTA GACGGCTTTT TCGATTTTGA AGAAAAGTAC      800
    CAGCTGATCA GCGCCAAAAT CACCGTCCCT GCGCCATTGC CTGAAACGAT      850
    TGAAACCAAG GTCAAAGAAC AAGCTCAGCT GCTCTATCGT AGTCTTGGTC      900
    TTAAAGGTCT TGCTCGCATC GACTTTTTTG TCACGGAGCG AGGAGAACTA      950
25  TACTTGAATG AAATCAATAC TATGCCGGGC TTTACGAGTC ACTCCCGCTA      1000
    TCCTGCCATG ATGGCAGCGG TCGGCTTATC CTATCAAGAA CTACTACAAA      1050
    AACTGCTTGT CTTAGCAAAG GAGGAAGTCA AATGAG                      1086
  
```

30 2) INFORMATION FOR SEQ ID NO: 1141

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3946 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: BM4147
 (C) ACCESSION NUMBER: extracted from M97297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141

```

    ATGAATAACA TCGGCATTAC TGTTTATGGA TGTGAGCAGG ATGAGGCAGA      50
    TGCATTCCAT GCTCTTTCGC CTCGCTTTGG CGTTATGGCA ACGATAATTA      100
    ACGCCAACGT GTCGGAATCC AACGCCAAAT CCGCGCCTTT CAATCAATGT      150
50  ATCAGTGTGG GACATAAATC AGAGATTTC GCCTCTATTC TTCTTGCGCT      200
    GAAGAGAGCC GGTGTGAAAT ATATTTCTAC CCGAAGCATC GGCTGCAATC      250
    ATATAGATAC AACTGCTGCT AAGAGAATGG GCATCACTGT CGACAATGTG      300
    GCGTACTCGC CGGATAGCGT TGCCGATTAT ACTATGATGC TAATTCTTAT      350
    TGCAGTACGC AACGTAAAAT CGATTGTGCG CTCTGTGGAA AAACATGATT      400
55  GCGAGTTGGA CAGCGACCGT GGCAAGGTAC TCAGCGACAT GACAGTTGGT      450
    GTGGTGGGAA CGGGCCAGAT AGGCAAAGCG GTTATTGAGC GGCTGCGAGG      500
    ATTTGGATGT AAAGTGTTGG CTTATAGTCG CAGCCGAAGT ATAGAGGTAA      550
    ACTATGTACC GTTTGATGAG TTGCTGCAAA ATAGCGATAT CGTTACGCTT      600
    CATGTGCCGC TCAATACGGA TACGCACTAT ATTATCAGCC ACGAACAAAT      650
60  ACAGAGAATG AAGCAAGGAG CATTTCTTAT CAATACTGGG CGCGGTCCAC      700
  
```

	TTGTAGATAC	CTATGAGTTG	GTTAAAGCAT	TAGAAAACGG	GAAACTGGGC	750
	GGTGCCGCAT	TGGATGTATT	GGAAGGAGAG	GAAGAGTTTT	TCTACTCTGA	800
	TTGCACCCAA	AAACCAATTG	ATAATCAATT	TTTACTTAAA	CTTCAAAGAA	850
	TGCCTAACGT	GATAATCACA	CCGCATACGG	CCTATTATAC	CGAGCAAGCG	900
5	TTGCGTGATA	CCGTTGAAAA	AACCATTAAA	AACTGTTTGG	ATTTTGAAAG	950
	GAGACAGGAG	CATGAATAGA	ATAAAAGTTG	CAATACTGTT	TGGGGGTTGC	1000
	TCAGAGGAGC	ATGACGTATC	GGTAAAATCT	GCAATAGAGA	TAGCCGCTAA	1050
	CATTAATAAA	GAAAAATACG	AGCCGTTATA	CATTGGAATT	ACGAAATCTG	1100
	GTGTATGGAA	AATGTGCGAA	AAACCTTGCG	CGGAATGGGA	AAACGACAAT	1150
10	TGCTATTTCAG	CTGTACTCTC	GCCGGATAAA	AAAATGCACG	GATTACTTGT	1200
	TAAAAAGAAC	CATGAATATG	AAATCAACCA	TGTTGATGTA	GCATTTTCAG	1250
	CTTTGCGATG	CAAGTCAGGT	GAAGATGGAT	CCATACAAGG	TCTGTTTGAA	1300
	TTGTCCGGTA	TCCCTTTTGT	AGGCTGCGAT	ATTCAAAGCT	CAGCAATTTG	1350
	TATGGACAAA	TCGTTGACAT	ACATCGTTGC	GAAAAATGCT	GGGATAGCTA	1400
15	CTCCCGCCTT	TTGGGTTATT	AATAAAGATG	ATAGGCCGGT	GGCAGCTACG	1450
	TTTACCTATC	CTGTTTTTGT	TAAGCCGGCG	CGTTCAGGCT	CATCCTTCGG	1500
	TGTGAAAAAA	GTCAATAGCG	CGGACGAATT	GGACTACGCA	ATTGAATCGG	1550
	CAAGACAATA	TGACAGCAAA	ATCTTAATTG	AGCAGGCTGT	TTCGGGCTGT	1600
	GAGGTCGGTT	GTGCGGTATT	GGGAAACAGT	GCCGCGTTAG	TTGTTGGCGA	1650
20	GGTGGACCAA	ATCAGGCTGC	AGTACGGAAT	CTTTCGTATT	CATCAGGAAG	1700
	TCGAGCCGGA	AAAAGGCTCT	GAAAACGCAG	TTATAACCGT	TCCCGCAGAC	1750
	CTTTCAGCAG	AGGAGCGAGG	ACGGATACAG	GAAACGGCAA	AAAAAATATA	1800
	TAAAGCGCTC	GGCTGTAGAG	GTCTAGCCCG	TGTGGATATG	TTTTTACAAG	1850
	ATAACGCCCG	CATTGTACTG	AACGAAGTCA	ATACTCTGCC	CGGTTTCACG	1900
25	TCATACAGTC	GTTATCCCCG	TATGATGGCC	GCTGCAGGTA	TTGCACTTCC	1950
	CGAACTGATT	GACCGCTTGA	TCGTATTAGC	GTTAAAGGGG	TGATAAGCAT	2000
	GGAAATAGGA	TTTACTTTTT	TAGATGAAAT	AGTACACGGT	GTTTCGTTGGG	2050
	ACGCTAAATA	TGCCACTTGG	GATAATTTCA	CCGGAAAACC	GGTTGACGGT	2100
	TATGAAGTAA	ATCGCATTTG	AGGGACATAC	GAGTTGGCTG	AATCGCTTTT	2150
30	GAAGGCAAAA	GAACCTGGCTG	CTACCCAAGG	GTACGGATTG	CTTCTATGGG	2200
	ACGGTTACCG	TCCTAAGCGT	GCTGTAAAGT	GTTTTATGCA	ATGGGCTGCA	2250
	CAGCCGGAAA	ATAACCTGAC	AAAGGAAAGT	TATTATCCCA	ATATTGACCG	2300
	AACTGAGATG	ATTTCAAAG	GATACGTGGC	TTCAAATCA	AGCCATAGCC	2350
	GCGGCAGTGC	CATTGATCTT	ACGCTTTTATC	GATTAGACAC	GGGTGAGCTT	2400
35	GTACCAATGG	GGAGCCGATT	TGATTTTATG	GATGAACGCT	CTCATCATGC	2450
	GGCAAATGGA	ATATCATGCA	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	2500
	CCATCATGGA	AAACAGTGGG	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	2550
	TATGTATTAA	GAGACGAACC	ATACCCCAAT	AGCTATTTTG	ATTTCCCCGT	2600
	TAAATAAACT	TTTAACCGTT	GCACGGACAA	ACTATATAAG	CTAACTCTTT	2650
40	CGGCAGGAAA	CCCGACGTAT	GTAACCTGGT	CTTAGGGAAT	TTATATATAG	2700
	TAGATAGTAT	TGAAGATGTA	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	2750
	GTGCGCTGCG	GCAAGATAGC	CTGATAATAA	GACTGATCGC	ATAGAGGGGT	2800
	GGTATTTTAC	ACCGCCCATT	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	2850
	AGCATGGGTA	TCACTTATGA	AAATTTCATCT	ACATTGGTGA	TAATAGTAAA	2900
45	TCCAGTAGGG	CGAAATAATT	GACTGTAATT	TACGGGGCAA	AACGGCACAA	2950
	TCTCAAACGA	GATTGTGCCG	TTTAAGGGGA	AGATTCTAGA	AATATTTTCAT	3000
	ACTTCCAAC	ATATAGTTAA	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	3050
	TTTTATTGTT	ATTGTTATTC	TTAATATACT	TAGGTTATGA	CTACGTTAAT	3100
	GAAGCACTGT	TTTCTCAGGA	AAAAGTCGAA	TTTCAAAATT	ATGATCAAAA	3150
50	TCCCAAAGAA	CATTTAGAAA	ATAGTGGGAC	TTCTGAAAAT	ACCCAAGAGA	3200
	AAACAATTAC	AGAAGAACAG	GTTTATCAAG	GAAATCTGCT	ATTAATCAAT	3250
	AGTAAATATC	CTGTTGCGCA	AGAAAGTGTG	AAGTCAGATA	TCGTGAATTT	3300
	ATCTAAACAT	GACGAATTAA	TAAATGGATA	CGGGTTGCTT	GATAGTAATA	3350
	TTTATATGTC	AAAAGAAATA	GCACAAAAAT	TTTCAGAGAT	GGTCAATGAT	3400
55	GCTGTAAAGG	GTGGCGTTAG	TCATTTTATT	ATTAATAGTG	GCTATCGAGA	3450
	CTTTGATGAG	CAAAGTGTGC	TTTACCAAGA	AATGGGGGCT	GAGTATGCCT	3500
	TACCAGCAGG	TTATAGTGAG	CATAATTTCAG	GTTTATCACT	AGATGTAGGA	3550
	TCAAGCTTGA	CGAAAATGGA	ACGAGCCCCC	GAAGGAAAGT	GGATAGAAGA	3600
	AAATGCTTGG	AAATACGGGT	TCATTTTACG	TTATCCAGAG	GACAAAACAG	3650
60	AGTTAACAGG	AATTCAATAT	GAACCATGGC	ATATTGCTA	TGTTGGTTTA	3700

	CCACATAGTG	CGATTATGAA	AGAAAAGAAT	TTCGTTCTCG	AGGAATATAT	3750
	GGATTACCTA	AAAGAAGAAA	AAACCATTTT	TGTTAGTGTA	AATGGGGAAA	3800
	AATATGAGAT	CTTTTATTAT	CCTGTTACTA	AAAATACCAC	CATTCATGTG	3850
	CCGACTAATC	TTCGTTATGA	GATATCAGGA	AACAATATAG	ACGGTGTAAT	3900
5	TGTGACAGTG	TTTCCCGGAT	CAACACATAC	TAATTCAAGG	AGGTAA	3946

2) INFORMATION FOR SEQ ID NO: 1142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142

GATCCTCTAA ATGATTCTCA GGTGG

25

2) INFORMATION FOR SEQ ID NO: 1143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143

CAATTAGCTT AGCAATAGGT GTTGG

25

2) INFORMATION FOR SEQ ID NO: 1144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144

TGTYTTCCAA GGTTCAGCTC

20

2) INFORMATION FOR SEQ ID NO: 1145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145

10 AACATATTKG GTTGATAGGT

20

2) INFORMATION FOR SEQ ID NO: 1146

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146

25

GGGATTACCT ATGCCAATATGAT

23

30 2) INFORMATION FOR SEQ ID NO: 1147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147

40

AGCTGTGTTA GCVCGAACAT CTTG

24

45

2) INFORMATION FOR SEQ ID NO: 1148

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148

GACTTTGTTT GCGTGATAT

20

2) INFORMATION FOR SEQ ID NO: 1149

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149
15 TCCYACWATT TCTTTTGWG 20

2) INFORMATION FOR SEQ ID NO: 1150

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150
30 TGATAATCAC ACCGCATACG 20

35 2) INFORMATION FOR SEQ ID NO: 1151

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151
TGCTGTCATA TTGTCTTGCC 20

50 2) INFORMATION FOR SEQ ID NO: 1152

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152

ATAAAGATGA TAGGCCGGTG

20

5

2) INFORMATION FOR SEQ ID NO: 1153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153

CTCGTATGTC CCTACAATGC

20

20

2) INFORMATION FOR SEQ ID NO: 1154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154

GTTTGAAGCA TATAGCCTCG

20

35

2) INFORMATION FOR SEQ ID NO: 1155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155

CAGTGCTTCA TTAACGTAGT C

21

50

2) INFORMATION FOR SEQ ID NO: 1156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases

55

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156

GTTGAAATGC ATCACGAACA ATT

23

10

2) INFORMATION FOR SEQ ID NO: 1157

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157

25 AAGAACGTTT CAGTTAAGGA AAT

23

2) INFORMATION FOR SEQ ID NO: 1158

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158

40

AAGAGGTAAT GTCTGTGGT

19

45 2) INFORMATION FOR SEQ ID NO: 1159

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159

TGAAGGTTTG CCAGGTGA

18

2) INFORMATION FOR SEQ ID NO: 1160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1160

CGTTTCTGTT AAAGAAATTA GAAG

24

2) INFORMATION FOR SEQ ID NO: 1161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161

TCCAGGTGAT AACGTTGG

18

2) INFORMATION FOR SEQ ID NO: 1162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162

CAAGTCCGTG GAAATGCA

18

2) INFORMATION FOR SEQ ID NO: 1163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1163

GTTGGTTTCA ACGTTAAGAA C

21

5

2) INFORMATION FOR SEQ ID NO: 1164

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164

GGTTTCAACG TCAAGAAC

18

20

2) INFORMATION FOR SEQ ID NO: 1165

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165

35 GGTTTCAACG TGAAGAAC

18

2) INFORMATION FOR SEQ ID NO: 1166

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166

50

ACGTTAAGAA TGTTTCTGTC AA

22

55 2) INFORMATION FOR SEQ ID NO: 1167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 bases
(B) TYPE: Nucleic acid

842

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167

GTTGGTTTCA ACGT

14

10

2) INFORMATION FOR SEQ ID NO: 1168

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168

GAACAATTGG TTGAAGGTGT

20

25

2) INFORMATION FOR SEQ ID NO: 1169

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 2160 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: SP-665
(C) ACCESSION NUMBER: AF139883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169

45	ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
	CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
	ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
	ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
	TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
50	TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
	ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
	TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
	ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
	GCTTGGTTAG	CGATTTCAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
55	GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
	AGACAGCAGC	TCAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
	CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
	CCCCTATTCA	CATCCAGAAG	CATCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
	CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
60	GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800

TTACCCTGCT TACATGGATA ATTACCTCAA GGAGGTCATC AATCAAGTAG 850
 AACAAAGAAAC TGGCTATAAC CTTCTAACTA CTGGGATGGA TGTTTACACA 900
 AATGTAGACC AAGAAGCTCA AAAACATCTG TGGGATATCT ACAACTCCGA 950
 TCAATACGTC TCTTACCCTG ACGATGATTT GCAAGTCGCA TCTACGGTCG 1000
 5 TAGATGTTTC AAATGGTAAA GTCATCGCCC AACTTGGAGC TCGTCACCAA 1050
 GCAAGTAACG TTTCATTTGG TACCAACCAA GCTGTGGAAA CCAATCGTGA 1100
 CTGGGGTTCT GCTATGAAAC CAATCACCGA TTATGCACCT GCCATAGAAT 1150
 ACGGTGTTTA TGATTCCACT GCAACTATGG TTAATGATAT TCCTTATAAC 1200
 TATCCGGGAA CAAGCACACC TGTCTACAAC TGGGATAGAG CATATTTTCGG 1250
 10 TAATATTACT CTGCAATATG CTCTTCAACA ATCACGAAAT GTCACAGCCG 1300
 TTGAGACTTT GAATAAGGTC GGTCTAGATA GAGCTAAAAC CTTCTTAAAT 1350
 GGTCTTGGTA TCGACTATCC AAGCATGCAT TATGCAAACG CCATTTCAAG 1400
 TAATACAACA GAATCTAATA AACAATACGG AGCAAGTAGT GAAAAAATGG 1450
 CTGCTGCTTA TGCTGCCTTT GCAAATGGTG GCACTTACTA TAAACCAATG 1500
 15 TATATCCATA AAGTCGTCTT CAGTGATGGA AGTAAAAAAG AGTTCTCTAA 1550
 TGTCGGAACG CGTGCCATGA AGGAAACGAC TGGGATATG ATGACCGACA 1600
 TGATGAAAAC AGTCTTGACT TATGGAACG GCGGTGGAGC CTATCTTCCT 1650
 TGGCTTCCCTC AAGCTGGTAA AACAGGAACC TCTAACTATA CAGATGAGGA 1700
 AGTTGAAAAC CACATCAAGA ACACTGGCTA TGTAAGCTCCA GATGAAATGT 1750
 20 TTGTTGGTTA TACTCGTAAG TATTCTATGG CTGTATGGAC AGGTTATTCG 1800
 AATCGTTTAA CTCCTATCGT TGGAGATGGT TTCCTAGTTG CAGCTAAAGT 1850
 TTATCGCTCA ATGATAACGT ATCTATCAGA AGATACTCAT CCAGAAGACT 1900
 GGACGATGCC AGACGGACTT TTCAGAAACG GGAATTTTGT ATTCAAAAAT 1950
 GGAGCTCGCC CAATATGGAC TGAACCCCTCT ACTCAACAAT CCTCAACAGC 2000
 25 TGAAAGTTCA AGCTCATCAT CAGATAGTTC AACTTCACAG TCTAGCTCAA 2050
 CCACTCCAAG CACAAATAAT AGTACGACTA CCAATCCTAA CAATAATACG 2100
 CAACAATCAA ATACAACCCC TGATCAACAA AATCAGAATC CTCAACCAGC 2150
 ACAACCATAA 2160

30

2) INFORMATION FOR SEQ ID NO: 1170

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 40 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170

45 ACGAATTGGA CTACGCAATT

20

2) INFORMATION FOR SEQ ID NO: 1171

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 55 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171

60 ACGAGGATGA TTTGATTGTC

20

2) INFORMATION FOR SEQ ID NO: 1172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: 64147
 (C) ACCESSION NUMBER: X13136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172

20	GATCCTCTAA	ATGATTCTCA	GGTGGCTGTT	ATTGCCTCTA	TTTCAAAGGA	50
	GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	GGATAGAAAG	GTTTGGGAAA	100
	CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	CCAGTGAAAA	AGCTGGTCTC	150
	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	AAAGGCTATT	CTCTAAATGA	200
25	CCGTGTAGGA	ACCTCCTATT	TGGAAAAGCA	ATATGAAGAG	ACCTTACAAG	250
	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	ACAAATATGG	CAACATGGAA	300
	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	GGAAACAATA	TCAAGCTGAC	350
	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	TGCTTTGCTG	AAAAGTTATT	400
	TCAATTCAGA	GTTGGGAAAT	GGTGGAGCCA	AGTATTCTGA	AGGTGTCTAT	450
30	GCAGTCGCCC	TTAACCCAAA	AACAGGTGCT	GTTTTGTCTA	TGTCAGGAAT	500
	TAAACATGAC	TTGAAAACAG	GAGAGTTGAC	GCCGGATTCC	TTGGGAACGG	550
	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	TCAAAGCAGC	GACCATCAGC	600
	TCTGGTTGGG	AAAATGGAGT	CTTGTCAGGA	AATCAGACCT	TGACAGACCA	650
	GTCCATTGTC	TTTCAAGGTT	CAGCTCCAAT	TAATTCCTTG	TATCCTGCCT	700
35	TTTCTAGACC	AATGCCGATT	ACGGCGGTTT	AGGCTCTAGA	GTATTCATCC	750
	AATGCTTATA	TGGTCCAAAC	AGCCCTAGGT	CTTATGGGGC	AGACCTATCA	800
	ACCCAATATG	TTTGTCGGCA	CCAGCAATCT	AGAGTCTGCT	ATGGGGAAAT	850
	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	GTTCTGCGAC	CGGAATTGAC	900
	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	AAAGAGTATA	GCTTTGCTAA	950
40	TTTCATTACC	AATGCCTTTG	GGCAGTTTGA	TAACTATACG	CCGATGCAGT	1000
	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	ATGGTGTTTC	TGTGGCTCCT	1050
	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	GATAAGGGAG	GACTGGGTGA	1100
	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	GAATAAGGTC	AATATATCCG	1150
	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	TTTATCAGGT	TGCCCATGGT	1200
45	ACTAGTGAAT	TGACAACTGG	ACGTGCCTTT	TCAAATGGCG	CCTTGGTATC	1250
	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	CTATGTGGCA	GATGGTCAGC	1300
	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	CCCCATCTGA	TAATCCCCAA	1350
	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	ACCAACCTTA	CAAATGGTGT	1400
	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	CCTCTATAAC	CAACATCATC	1450
50	CAATGAATTA	GAAAGGAACA	TATGCTTTAT	CCAACACCTA	TTGCTAAGCT	1500
	AATTGACAGT	TATTCGAAGT	TACCGGGTAT	CGGGATTAAG	ACGGCTACCC	1550
	GTTTGGCCTT					1560

2) INFORMATION FOR SEQ ID NO: 1173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: CS109
(C) ACCESSION NUMBER: Z49096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173

	GAGTCCCGAT	TGCTGAGGAT	GCAACCTCCT	ATAATGTCTA	TGCGGTCATT	50
	GATGAGAACT	ATAAGTCAGC	AACGGGTAAG	ATTCTTTACG	TAGAAAAAAC	100
15	ACAATTTAAC	AAGGTTGCAG	AGGTCTTTCA	TAAGTATCTG	GACATGGAAG	150
	AATCCTATGT	AAGAGAGCAA	CTCTCGCAAC	CTAATCTCAA	GCAAGTTTCC	200
	TTTGGAGCAA	AGGGAAATGG	GATTACCTAT	GCCAATATGA	TGACTATCAA	250
	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	300
	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGTCTA	350
20	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTGC	TGGGAACTTC	400
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGCATTG	450
	TTACCTATGA	AAAGGATCGT	CTGGGCAATA	TTGTACCCGG	AACAGAACTG	500
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	550
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	600
25	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	650
	ATTCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	700
	AATCACTGAG	GACTTTGTTC	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	750
	AACCAGGATC	AGCCTTTAAG	GTCATGATGT	TAGCTTCTTC	TATTGATAAT	800
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAAATAGC	850
30	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAGGGTTTG	ACTACTGGTG	900
	GGATGATGAC	TTTCTCACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAACG	950
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	1000
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	1050
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	1100
35	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	1150
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	1200
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1250
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1300
	AGTTGGGACG	GACCCCTCTAT	ATGGAACATAT	GTATAATCAC	TACACAGGAA	1350
40	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCCGTACG	1400
	GCTCAAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1450
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1500
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1550
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1600
45	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1650
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1700
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1750
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1800
	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1850
50	AGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1900
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTGT	TCAGAAGCAA	GATGTTTCGGA	1950
	CTAATACAGC	TATCAAAAAC	ATTAAAAAAA	TTAAATTAAC	TTTAGGAGAC	2000
	TAATATG					2007

2) INFORMATION FOR SEQ ID NO: 1174

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174

GAACGTGGTG AAGTTCGC

18

10

2) INFORMATION FOR SEQ ID NO: 1175

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175

25 GTTACTGGTG TAGAAATGTT C

21

2) INFORMATION FOR SEQ ID NO: 1176

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176

40

TACTGGTGTA GAAATGTTC

19

2) INFORMATION FOR SEQ ID NO: 1177

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177

55

GCTCAACAAG TTCCAGATTA

20

60

2) INFORMATION FOR SEQ ID NO: 1178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: NCTC8325
 (C) ACCESSION NUMBER: X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178

	ATGAACTGAT	TATACTTAAC	ATTAAAAAAG	ATGATAACAC	CTTCTACACC	50
	TCCATATCAC	AAAAAATTAT	AACATTATTT	TGACATAAAT	ACTACATTTG	100
20	TAATATACTA	CAAATGTAGT	CTTATATAAG	GAGGATATTG	ATGAAAAAGA	150
	TAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	GTTTGGTATA	200
	TATTTTATG	CTTCAAAAGA	TAAAGAAATT	AATAATACTA	TTGATGCAAT	250
	TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	TATATTTCTA	300
	AAAGCGATAA	TGGTGAAGTA	GAAATGACTG	AACGTCCGAT	AAAAATATAT	350
25	AATAGTTTAG	GCGTTAAAGA	TATAACATT	CAGGATCGTA	AAATAAAAAA	400
	AGTATCTAAA	AAATAAAAAAC	GAGTAGATGC	TCAATATAAA	ATTAAAACAA	450
	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTTTGT	TAAAGAAGAT	500
	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	CAGGAATGCA	550
	GAAAGACCAA	AGCATACATA	TTGAAAATTT	AAAATCAGAA	CGTGGTAAAA	600
30	TTTTAGACCG	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	ACATATGAGA	650
	TTAGGCATCG	TTCCAAGAA	TGTATCTAAA	AAAGATTATA	AAGCAATCGC	700
	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAACAACAAA	TGGATCAAAA	750
	TTGGGTACAA	GATGATACCT	TCGTTCCACT	TTAAAACCGT	TAAAAAAATG	800
	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	CAACTAATGA	850
35	AACAGAAAGT	CGTAACTATC	CTCTAGAAAA	AGCGACTTCA	CATCTATTAG	900
	GTTATGTTGG	TCCCATTAAC	TCTGAAGAAT	TAAAACAAAA	AGAATATAAA	950
	GGCTATAAAG	ATGATGTCAGT	TATTGGTAAA	AAGGGACTCG	AAAAACTTTA	1000
	CGATAAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	ATCGTTGACG	1050
	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	GAAAAAAGAT	1100
40	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	AGAGTATTTA	1150
	TAACAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	CACCC'TCAAA	1200
	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	CGTCTATCCA	1250
	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	AATAAATTAA	CCGAAGATAA	1300
	AAAAGAACCT	CTGCTCAACA	AGTTCCAGAT	TACAAC'TTCA	CCAGGTTCAA	1350
45	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAAATAACAA	AACATTAGAC	1400
	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	AAGATAAATC	1450
	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	GGTAATATCG	1500
	ACTTAAACAA	AGCAATAGAA	TCATCAGATA	ACATTTTCTT	TGCTAGAGTA	1550
	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	AAAGGCATGA	AAAAACTAGG	1600
50	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	GCTCAAATTT	1650
	CAAACAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATTG	AGGTTACGGA	1700
	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTTTCAA	TCTATAGCGC	1750
	ATTAGAAAAAT	AATGGCAATA	TTAACGCACC	TCAC'TTATTA	AAAGACACGA	1800
	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	CCAAAGAAAA	TATCAATCTA	1850
55	TTAAATGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	AAGAAGATAT	1900
	TTATAGATCT	TATGCAAACCT	TAATTTGGCAA	ATCCGGTACT	GCAGAACTCA	1950
	AAATGAAACA	AGGAGAAAAGT	GGCAGACAAA	TTGGGTGGTT	TATATCATAT	2000
	GATAAAGATA	ATCCAACACAT	GATGATGGCT	ATTAATGTTA	AAGATGTACA	2050
	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	AAAGTGTATG	2100
60	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	ACGATATAGA	TGAATAACAA	2150

	AACAGTGAAG	CAATCCGTAA	CGATGGTTGC	TTCACTGTTT	TATTATGAAT	2200
	TATTAATAAG	TGCTGTTACT	TCTCCCTTAA	ATACAATTTC	TTCATTTTCA	2250
	TTGTATGTTG	AAAGTGACAC	TGTAACGAGT	CCATTTTCTT	TTTTTATGGA	2300
	TTTCTTATTT	GTAATTTTCAG	CGATAACGTA	CAATGTATTA	CCTGGTATAC	2350
5	AGTTTAATAA	ATTTAACGTT	ATTCATTTGT	GTTCTGCTA	CAACTTCTTC	2400
	TCCGTATTTA	CCTTCTTCTA	CCCATAATTT	AAATGATATT	GAAAGTGTAT	2450
	GCATGC					2456

10

2) INFORMATION FOR SEQ ID NO: 1179

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179

ATTTGGTGAC GGGTGACTTT

20

25

2) INFORMATION FOR SEQ ID NO: 1180

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180

TCCACCGTTG CCAATCGCA

19

40

2) INFORMATION FOR SEQ ID NO: 1181

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181

55 AGCAGCTTAC TAGATGCCGT

20

60

2) INFORMATION FOR SEQ ID NO: 1182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182

AACTGCAAGA GATCCTTTGG

20

2) INFORMATION FOR SEQ ID NO: 1183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2535 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: 175
 (C) ACCESSION NUMBER: M18729

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1183

	ATGGCGATAG	AAAAGCTATC	ACCCGGCATG	CAACAGTATG	TGGATATTAA	50
	AAAGCAATAT	CCAGATGCTT	TTTTGCTCTT	TCGGATGGGT	GATTTTTATG	100
35	AATTATTTTA	TGAGGATGCG	GTCAATGCTG	CGCAGATTCT	GGAAATTTCC	150
	TTAACGAGTC	GCAACAAGAA	TGCCGACAAT	CCGATCCCTA	TGGCGGGTGT	200
	TCCCTATCAT	TCTGCCCAAC	AGTATATCGA	TGTCTTGATT	GAGCAGGGTT	250
	ATAAGGTGGC	TATCGCAGAG	CAGATGGAAG	ATCCTAAACA	AGCAGTTGGG	300
	GTTGTTAAAC	GAGAGGTTGT	TCAGGTCATT	ACGCCAGGGA	CAGTGGTCGA	350
40	TAGCAGTAAG	CCGGACAGTC	AGAATAATTT	TTTGGTTTCC	ATAGACCGCG	400
	AAGGCAATCA	ATTTGGCCTA	GCTTATATGG	ATTTGGTGAC	GGGTGACTTT	450
	TATGTGACAG	GTCTTTTGGA	TTTCACGCTG	GTTTGTGGGG	AAATCCGTAA	500
	CCTCAAGGCT	CGAGAAGTGG	TGTTGGGTTA	TGACTTGTCT	GAGGAAGAAG	550
	AACAAATCCT	CAGCCGCCAG	ATGAATCTGG	TACTCTCTTA	TGAAAAAGAA	600
45	AGCTTTGAAG	ACCTTCATTT	ATTGGATTTG	CGATTGGCAA	CGGTGGAGCA	650
	AACGGCATCT	AGTAAGCTGC	TCCAGTATGT	TCATCGGACT	CAGATGAGGG	700
	AATTGAACCA	CCTCAAACCT	GTTATCCGCT	ACGAAATTAA	GGATTTCTTG	750
	CAGATGGATT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	AGAATGCTCG	800
	CTCAGGTAAG	AAACAAGGCA	GTCTTTTCTG	GCTTTTGGAT	GAAACCAAAA	850
50	CGGCTATGGG	GATGCGTCTC	TTGCGTTCCT	GGATTCATCG	CCCCTTGATT	900
	GATAAGGAAC	GAATCGTCCA	ACGTCAAGAA	GTAGTGCAGG	TCTTTCTCGA	950
	CCATTTCTTT	GAGCGTAGTG	ACTTGACAGA	CAGTCTCAAG	GGTGTTTATG	1000
	ACATTGAGCG	CTTGGCTAGT	CGTGTTTCTT	TTGGCAAAAC	CAATCCAAAG	1050
	GATCTCTTGC	AGTTGGCGAC	TACCTTGTCT	AGTGTGCCAC	GGATTCGTGC	1100
55	GATTTTAGAA	GGGATGGAGC	AACCTACTCT	AGCCTATCTC	ATCGCACAAAC	1150
	TGGATGCAAT	CCCTGAGTTG	GAGAGTTTGA	TTAGCGCAGC	GATTGCTCCT	1200
	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	ATTATCCGGA	CTGGATTTGA	1250
	TGAGACTTTA	GACAAGTATC	GTTGCGTTCT	CAGAGAAGGG	ACTAGCTGGA	1300
	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	ACTCTGGTAT	CAGCACGCTC	1350
60	AAGATTGACT	ACAATAAAAA	GGATGGCTAC	TATTTTCATG	TGACCAATTC	1400

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME 3 DE 4

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME

THIS IS VOLUME 3 OF 4

NOTE: For additional volumes please contact the Canadian Patent Office

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME 4 DE 4

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

**THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME**

THIS IS VOLUME 4 OF 4

NOTE: For additional volumes please contact the Canadian Patent Office

```

GCAACTGGGA AATGTGCCAG CCCACTTTTT CCGCAAGGCG ACGCTGAAAA 1450
ACTCAGAACG CTTTGGAACC GAAGAATTAG CCCGTATCGA GGGAGATATG 1500
CTTGAGGCGC GTGAGAAGTC AGCCAACCTC GAATACGAAA TATTTATGCG 1550
CATTCGTGAA GAGGTCGGCA AGTACATCCA GCGTTTACAA GCTCTAGCCC 1600
5 AAGGAATTGC GACGGTTGAT GTCTTACAGA GTCTGGCGGT TGTGGCTGAA 1650
ACCCAGCATT TGATTCGACC TGAGTTTGGT GACGATTCAC AAATTGATAT 1700
CCGGAAAGGG CGCCATGCTG TCGTTGAAAA GGTATGGGG GCTCAGACCT 1750
ATATTCCAAA TACGATTCAG ATGGCAGAAG ATACCAGTAT TCAATTGGTT 1800
ACAGGGCCAA ACATGAGTGG GAAGTCTACC TATATGCGTC AGTTAGCCAT 1850
10 GACGGCGGTT ATGGCCCAGC TGGGTTCCTA TGTTCTTGCT GAAAGCGCCC 1900
ATTTACCGAT TTTTGATGCG ATTTTACCC GTATCGGAGC AGCAGATGAC 1950
TTGGTTTCGG GTCAGTCAAC CTTTATGGTG GAGATGATGG AGGCCAATAA 2000
TGCCATTTTCG CATGCGACCA AGAAGTCTCT CATTCTCTTT GATGAATTGG 2050
GACGTGGAAC TGCAACTTAT GACGGGATGG CTCTTGCTCA GTCCATCATC 2100
15 GAATATATCC ATGAGCACAT CGGAGCTAAG ACCCTCTTTG CGACCCACTA 2150
CCATGAGTTG ACTAGTCTGG AGTCTAGTTT ACAACACTTG GTCAATGTCC 2200
ACGTGGCAAC TTTGGAGCAG GATGGGCAGG TCACCTTCCT TCACAAGATT 2250
GAACCGGGAC CAGCTGATAA ATCCTACGGT ATCCATGTTG CCAAGATTGC 2300
TGGCTTGCCA GCAGACCTTT TAGCAAGGGC GGATAAGATT TTGACTCAGC 2350
20 TAGAGAATCA AGGAACAGAG AGTCCCTCCT CCATGAGACA AACTAGTGCT 2400
GTCACTGAAC AGATTTCAT CTTTGATAGG GCAGAAGAGC ATCCTATCCT 2450
AGCAGAATTA GCTAAACTGG ATGTGATATA TATGACACCT ATGCAGGTTA 2500
TGAATGTCTT AGTAGAGTTA AAACAGAAAC TATAA 2535

```

25

2) INFORMATION FOR SEQ ID NO: 1184

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 623 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Streptococcus pneumoniae
(B) STRAIN: StrR-05

```

40 (xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1184

```

TGACGGGTGA CTTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
GGGGAAATCC GTAACCTCAA GGCTCGAGAA TGGGTGTTGG GTTATGACTT 100
GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
45 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCAGT ATGTTTCATC 250
GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGATACGAAA 300
TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTTG 350
GTTGAGAATG CTCGCTCAGG TAAGAAACAA GGCAGTCTTT TCTGGCTTTT 400
50 GGATGAAACC AAAACGGCTA TGGGGATGCG TCTCTTGCGT TCTTGATTTC 450
ATCGCCCTTT GATTGATAAG GAACGAATCG TCCAACGTCA AGAAGTAGTG 500
CAGGTCTTTC TCGACCATTT CTTTGAGCGT AGTGACTTGA CAGACAGTCT 550
CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
AAACCAATCC AAAGGATCTC TTG 623

```

55

2) INFORMATION FOR SEQ ID NO: 1185

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1185

15	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
20	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTG	350
	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGATTTC	450
	ATCGCCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
25	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
	AAACCAATCC	AAAGGATCTC	T			621

30 2) INFORMATION FOR SEQ ID NO: 1186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1186

45	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
50	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGCTACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTG	350
	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGATTTC	450
55	ATCGCCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
	AAACCAATCC	AAAGGATCTC	TT			622

2) INFORMATION FOR SEQ ID NO: 1187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1187

	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
20	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCGGT	ATGTTTCATCG	250
	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGCTACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
25	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
30	AAACCAATCC	AAAGGATCTC	TT			622

2) INFORMATION FOR SEQ ID NO: 1188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1188

50	GGGTGACTTT	TATGTAACGG	GGCTATTGGA	TTTCACGTTG	GTTTGTGGGG	50
	AAATTCGCAA	TCTCAAGGCT	AGAGAAGTGG	TGCTGGGTTA	TGACTTGTCT	100
	GAGGAAGAAG	AACAAATCCT	CAGTCGTCAG	ATGAATCTGG	TGCTTTCTTA	150
	TGAGAAGGAA	GGCTTTGAGG	ACCTTCATTT	ACTGGATCCA	CGACTGGCAG	200
	CTGTGGAGCA	AGCGGCAGCT	AGTAAGCTCC	TCCAGTATGT	TCACCGGACC	250
55	CAGATGCGGG	AATTGAACCA	CCTCAAACCA	GTTATCCGCT	ATGAAATCAA	300
	AGATTTCTTA	CAGATGGACT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	350
	AGAA TGCCCG	TTCAGGCAAG	AAGCAAGGCA	GTCTTTTCTG	GCTTTTAGAT	400
	GAAACCAAGA	CGGCTATGGG	AATGCGTCTC	TTGCGTTCTT	GGATTTCATCG	450
	TCCTTTGATT	GATAAGGAGC	GAATCGTCCA	GCGTCAAGAG	GTGGTGCAGG	500
60	TCTTTCTTGA	CCACTTCTTT	GAGCGTAGTG	ATTTAACGGA	CAGTCTTAAG	550

GGTGTATTATG ATATCGAACG CTTGGCTAGT CGGGTTTCTT TTGGCAAGA

599

5 2) INFORMATION FOR SEQ ID NO: 1189

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 624 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(x) SEQUENCE DESCRIPTION: SEQ ID NO: 1189

20 GGTGACGGGT GACTTTTATG TGACAGGTCT TTTGGATTTT ACGCTGGTTT 50
 GTGGGGAAAT CCGCAATCTC AAGGCTCGAG AAGTGGTGCT GGGTTATGAC 100
 TTGTCTGAGG AAGAAGAACA GATCCTTAGT CGTCAGATGA ATCTGGTACT 150
 TTCCTATGAA AAAGAAGGCT TTGAAGACCT TCATTTACTG GATTCACGAT 200
 25 TGGCAGCTGT GGAGCAAGCG GCATCTAGTA AACTGCTTCA GTATGTTTCA 250
 CGGACTCAGA TGAGGGAATT GAACCACCTC AAGCCTGTTA TCCGCTATGA 300
 AATCAAAGAT TTTTTCGAGA TGGATTATGC GACCAAGGCT AGTCTGGATT 350
 TGGTTGAGAA TGCCCGTTCA GGCAAGAAGC AAGGTAGTCT TTTTGGCTT 400
 TTGGATGAAA CCAAACAGC TATGGGAATG CGTCTCTTGC GGTCTTGGAT 450
 30 TCATCGCCCC CTGATTGATA AGGAACGAAT TGTCCAACGC CAAGAAGTTG 500
 TGCAGGTCTT TCTCGACCAT TTCTTTGAGC GTAGTGATTT GACAGACAGT 550
 CTCAAGGGTG TTTATGACAT TGAGCGCTTG GCTAGTCGTG TTTCTTTTGG 600
 CAAAACCAAT CCAAAGGATC TCTT 624

35

2) INFORMATION FOR SEQ ID NO: 1190

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190

55 TGACGGGTGA CTTTCAGGTG ACTAGTTTAG AGGACTTTGT CTTGGTCTGC 50
 GGGGAAATCC GCAATTGAA AGCTAGGGAA GTGGTGCTGG GCTATGCCTT 100
 GCCAGAAGCT GAGGAGCAGG TTTTGGCTGG ACAGATGAAC CTTTACTGT 150
 CCTATGTGGA GAAGGTTTGG GAGGATGTTT AGCTGCTGGG CGAGGAGCTG 200
 TCTCCTATGG AGCGTCAGGC AGCAGGGAAA CTGCTGGAGT ATGTGCACCG 250
 GACCCAGATG AGGGAGCTCA GCCATTTGAA GAAGGCTCAG CATTATGAAA 300
 TCAAGGACTT CCTGCAAATG GACTATGCCA CCAAGGCGAG TCTGGATTTG 350
 60 ACAGAAAATG CTCGCTCGGG CAAGAAGCAC GGCAGTCTTT ATTGGCTGAT 400

GGACGAGACT	AAGACGGCCA	TGGGCGGCCG	CATGCTGCGC	TCTTGGATCC	450
AGCGTCCGCT	GATTGATGAA	GCGCGAATTA	GCCAGCGACA	GAATGTCGTT	500
GAGGTTTTTC	TGGATCATTT	CTTTGAGCGG	AGTGATTTGA	CGGAGAGCCT	550
CAAGGGGGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGC	599

5

2) INFORMATION FOR SEQ ID NO: 1191

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903
- 20 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1191

25	TGACGGGTGA	CTTTCAGGTG	ACTAGTTTAG	AGGACTTTGC	CCTGGTCTGC	50
	GGGGAAATCC	GTAATTTGAA	GGCTAGGGAA	GTGGTGCTGG	GCTATGCTTT	100
	GCCAGAAGCT	GAGGAGCAGG	TCTTGGCTGG	ACAGATGAAT	CTTTTGCTGT	150
	CCTATGTACA	GACGGCCTTG	GACGATGTCC	AGCTGCTGGG	CGAGGAACTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCGGGGAAA	TTGCTAGAGT	ATGTGCACCG	250
	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCCCCAG	CATTATGAAA	300
30	TCAAGGACTT	TCTGCAAATG	GATTATGCTA	CCAAGGCGAG	TCTGGATTTG	350
	ACAGAAAATG	CTCGCTCGGG	TAAGAAACAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACC	AAGACGGCCA	TGGGCGGCCG	TATGCTGCGC	TCTTGGATCC	450
	AGCGTCCGTT	GATTGATGAA	GTGCGAATTA	GCCAGCGGCA	GAATGTCGTC	500
	GAGGTTTTTC	TGGAACATTT	CTTTGAGCGG	AGTGATTTGA	CGGAGAGCCT	550
35	CAAGGGAGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGCA	600
	AGACCAATCC	AAAGGATCTC	TT			622

40 2) INFORMATION FOR SEQ ID NO: 1192

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192

GGTAAAACAG GAACCTCTAA CT

22

55

2) INFORMATION FOR SEQ ID NO: 1193

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid

60

855

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193

GGTAAGACAG GTACTTCTAA CT

22

10

2) INFORMATION FOR SEQ ID NO: 1194

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194

25 CATTTC AAGT AATACAACAG AATC

24

30

2) INFORMATION FOR SEQ ID NO: 1195

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195

40

CATTTC AAGT AACACA ACTG AATC

24

45 2) INFORMATION FOR SEQ ID NO: 1196

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196

GCCATTTC AA GTAATACAAC AGAA

24

60

2) INFORMATION FOR SEQ ID NO: 1197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197

CAAACGCCAT TTCAAGTAAT ACAAC

25

2) INFORMATION FOR SEQ ID NO: 1198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
- (B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198

AACGGGCGTC	TCGATAGAAA	AACACGTGAA	AATCCCAATG	ATTATAAACA	50
ATCAATATAC	GATTTTGCTG	AAGCTGTAAC	AAAAGGTATT	AAGGAACAAA	100
CAAATAAAAA	TTAATAGGCA	ACTTAACCG	AATCGTTAAA	ACTATATGAC	150
GATTCTGGTT	TTTTAAATTC	AAAAAGTTTT	CTAAAAAATT	TACTTGCTTC	200
TTTAAAGTAT	AGGTATGAAA	TACAATTGAT	TAAAATAGTA	AAGGAAATGA	250
ATCATGAAAC	AATTAACATA	GCCTTTATAC	TTTACCTAT	TACTTTTAT	300
TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTTGCCA	ATCACAKGTA	350
AACATCCTAT	TGATTTTGTG	GACGCCCGTT	A		381

2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199

GTATTAAAGA AGATATCCAA AAAGC

25

2) INFORMATION FOR SEQ ID NO: 1200

857

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200
TCAAAGAAGA AACTAAAAA GCTGT

2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201
AACGTAGGTG TCCTTCTTC

2) INFORMATION FOR SEQ ID NO: 1202

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202
GTGTTGAAAT GTTCCGTAAA CA

2) INFORMATION FOR SEQ ID NO: 1203

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203
GGIGARMGIG GIAAYGARAT G

2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1204

GCIAAYAACI TCIWMYATGC C

21

2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205

AAYACITCIA WYATGCCIGT

20

2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206

CKISRIGTIG ARTCIGCCA

19

2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207

CCITCITCWC CIGGCATYTC

20

5

2) INFORMATION FOR SEQ ID NO: 1208

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208

20 TCAAAAAGTT TTCTAAAAAA TTTAC

25

2) INFORMATION FOR SEQ ID NO: 1209

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209

35 ACGGGCGTCC ACAAATCAA TAGGA

25

40 2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210

ACCAGCTTGC CCAATACAAA GG

22

55

2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
60 (B) TYPE: Nucleic acid

860

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211

ATTCTTGTA CAGGCTTTGA TCCC

24

2) INFORMATION FOR SEQ ID NO: 1212

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212

CCICCCIRGIG GIGAIACIGC WCC

23

2) INFORMATION FOR SEQ ID NO: 1213

(i) SEQUENCE CHARACTERISTICS:

~~(A) LENGTH: 26 bases~~
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213

AARGGIGGIA CIGCIGCIAT HCCIGG

26

2) INFORMATION FOR SEQ ID NO: 1214

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214

GGTAAAACAG GTACCTCTAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1215

861

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (B) STRAIN: D471
 (C) ACCESSION NUMBER: X65717

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1215

AACAAAATAA AAGAACTTAC CTATTTTCCA TCCAAAATGT TTAGCAATCA 50
 TCATCTGCAA GGCAACGTAT TGCATGGCAT TGATGTGATG AGCAACTAAT 100
 ATGTCATTAG AACGTTGCGT CAAACTAGCA TCTAAATAAA GATCGAAATG 150
 CAGTTATCAA AAATGCAAGC TCCTATCGGC CCTTGTTTTA ATTATTACTC 200
 ACATTGCCTT AATGTATTTA CTTGCTTATT ATTAACCTTT TTGCTAAGTT 250
 AGTAGCGTCA GTTATTCATT GAAAGGACAT TATTATGAAA ATTCTTGTA 300
 CAGGCTTTGA TCCCTTTGGC GGCGAAGCTA TTAATCCTGC CCTTGAAGCT 350
 ATCAAGAAAT TGCCAGCAAC CATTCATGGA GCAGAAATCA AATGTATTGA 400
 AGTTCCAACG GTTTTTCAAA AATCTGCCGA TGTGCTCCAG CAGCATATCG 450
 AAAGCTTTCA ACCTGATGCA GTCCTTTGTA TTGGGCAAGC TGGTGGCCGG 500
 ACTGGACTAA CGCCAGAACG CGTTGCCATT AATCAAGACG ATGCTCGCAT 550
 TCCTGATAAC GAAGGGAATC AGCCTATTGA TACACCTATT CGTGCAGATG 600
 GTAAAGCAGC TTATTTTTCA ACCTTGCCAA TCAAAGCGAT GGTGCTGCC 650
 ATTCATCAGG CTGGGCTTCC TGCTTCTGTT TCTAATACAG CTGGTACCTT 700
 TGTTTGCAAT CATTGATGT ATCAAGCCCT TTACTTAGTG GATAAATATT 750
 GTCCAATGC CAAAGCTGGG TTTATGCATA TTCCCTTTAT GATGGAACAG 800
 GTGTTGATA AACCTAATAC AGCTGCCATG AACCTCGATG ATATTACAAG 850
 AGGAATTGAG GCTGCTATTT TTGCCATTGT CGATTTCAAA GATCGTTCCG 900
 ATTTAAAACG TGTAGGGGGC GCTACTCACT GACTGTGACG CTACTAAACC 950
 TATTTTAAAA AAACAGAGAT ATGAACTAAC TCTGTTTTTT TTGTGCTAAA 1000
 AATGAAAGAC CTAGGGAAAC TTTTCATCGG TCTTTCTCAA TTGTCATCTT 1050
 AATCTAATAC TACTTCTAAC ATCAGCGGGT ATAGTTTGCC AGTAATTAAG 1100
 AAACGTTGTT GATCTAAATG AGCAATCCCA TTCAAACAT TAAGGTCAGG 1150
 GTAATGGGAC TTATCAAGAT TTAAGGCTTT TAACAAAGGA CTAATATCAT 1200
 AGGTGGCTAC CACCTTTCCA GAATCAGGTT GGAGTTTGAC AATAGTATTG 1250
 GTTTGCCAAA TATTGGCATA GAGATAACCA TCTACATACT CTAATTCGTT 1300
 AAGCATTGAG ATAGGGACAC TTTCTATAGC AACTAGT 1337

2) INFORMATION FOR SEQ ID NO: 1216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216

GGTAAGACTG GTACATCAAA CTA

2) INFORMATION FOR SEQ ID NO: 1217

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217
15 CAAATGCCAT TTCAAGTAAC ACAAC 25

2) INFORMATION FOR SEQ ID NO: 1218

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218
30 CAAACGCCAT TTCAAGTAAC ACAAC 25

2) INFORMATION FOR SEQ ID NO: 1219

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219
CAAATGCTAT TTCAAGTAAT ACAAC 25

2) INFORMATION FOR SEQ ID NO: 1220

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220

CAAACGC CATTTCAAGT AATACGAC

25

5

2) INFORMATION FOR SEQ ID NO: 1221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221

GAYACICCG GICAYGTIGA YTT

23

20

2) INFORMATION FOR SEQ ID NO: 1222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222

ATYGAYACIC CIGGICAYGT IGAYTT

26

35

2) INFORMATION FOR SEQ ID NO: 1223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223

50

AYITCIARRT GIARYTCRCC CATICC

26

2) INFORMATION FOR SEQ ID NO: 1224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224
CCIGYIHTIY TIGARCCIAT IATG

24

10

2) INFORMATION FOR SEQ ID NO: 1225

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225

TAICCRAACA TYTCISMIAR IGGIAC

26

25

2) INFORMATION FOR SEQ ID NO: 1226

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226

40 GTIRMRTAIC CRAACATYTC

20

2) INFORMATION FOR SEQ ID NO: 1227

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227

55 GTICCIYTIK CIGARATGTT YGGITA

26

60

2) INFORMATION FOR SEQ ID NO: 1228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228

GTICCIYTIK CIGARATGTT YGGITAYGC

29

2) INFORMATION FOR SEQ ID NO: 1229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229

TCCATYTGIG CIGCICCI GT IATCAT

26

2) INFORMATION FOR SEQ ID NO: 1230

~~(i) SEQUENCE CHARACTERISTICS:~~

- (A) LENGTH: 2145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (D) ACCESSION NUMBER: X00415

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1230

45	TGAACGCCTA AAAGATAAAC GAGGAAACAA ATGGCTCGTA CAACACCCAT	50
	CGCACGCTAC CGTAACATCG GTATCAGTGC GCACATCGAC GCCGGTAAAA	100
	CCACTACTAC CGAACGTATT CTGTTCTACA CCGGTGTAAA CCATAAAATC	150
	GGTGAAGTTC ATGACGGCGC TGCAACCATG GACTGGATGG AGCAGGAGCA	200
	GGAACGTGGT ATTACCATCA CTTCCGCTGC GACTACTGCA TTCTGGTCTG	250
50	GTATGGCTAA GCAGTATGAG CCGCATCGCA TCAACATCAT CGACACCCCG	300
	GGGCACGTTG ACTTCACAAT CGAAGTAGAA CGTTCCATGC GTGTTCTCGA	350
	TGGTGCGGTA ATGGTTTACT GCGCAGTTGG TGGTGTTTCAG CCGCAGTCTG	400
	AAACCGTATG GCGTCAGGCA AACAAATATA AAGTTCCGCG CATTGCGTTC	450
	GTTAACAAAA TGGACCGCAT GGGTGCGAAC TTCTTGAAAG TTGTTAACCA	500
55	GATCAAAACC CGTCTGGGCG CGAACCCGGT TCCGCTGCAG CTGGCGATTG	550
	GTGCTGAAGA ACATTTACAC GTTGTTGTTG ACCTGGTGAA AATGAAAGCT	600
	ATCAACTGGA ACGACGCTGA CCAGGGCGTA ACCTTCGAAT ACGAAGATAT	650
	CCCGGCAGAC ATGGTTGAAC TGGCTAACGA ATGGCACCAG AACCTGATCG	700
	AATCCGCAGC TGAAGCTTCT GAAGAGCTGA TGGAAAAATA CCTGGGTGGT	750
60	GAAGAACTGA CTGAAGCAGA AATCAAAGGT GCTCTGCGTC AGCGCGTTCT	800

	GAACAACGAA	ATCATCCTGG	TAACCTGTGG	TTCTGCGTTC	AAGAACAAAG	850
	GTGTTTCAGGC	GATGCTGGAT	GCGGTAATTG	ATTACCTGCC	ATCCCCGGTT	900
	GACGTACCTG	CGATCAACGG	TATCCTGGAC	GACGGTAAAG	ACACTCCGGC	950
5	TGAACGTCAC	GCAAGTGATG	ACGAGCCGTT	CTCTGCACTG	GCGTTCAAAA	1000
	TCGCTACCGA	CCCGTTTGTT	GGTAACCTGA	CCTTCTTCCG	TGTTTACTCC	1050
	GGTGTGGTTA	ACTCTGGTGA	TACCGTACTG	AACTCCGTGA	AAGCTGCACG	1100
	TGAGCGTTTC	GGTCGTATCG	TTCAGATGCA	CGCTAACAAA	CGTGAAGAGA	1150
	TCAAAGAAGT	TCGCGCGGGC	GACATCGCTG	CTGCTATCGG	TCTGAAAGAC	1200
10	GTAACCACTG	GTGACACCCT	GTGTGACCCG	GATGCGCCGA	TCATTCTGGA	1250
	ACGTATGGAA	TTCCCTGAGC	CGGTAATCTC	CATCGCAGTT	GAACCGAAAA	1300
	CCAAAGCTGA	CCAGGAAAAA	ATGGGTCTGG	CTCTGGGCCG	TCTGGCTAAA	1350
	GAAGACCCGT	CTTTCCTGT	ATGGACTGAC	GAAGAATCTA	ACCAGACCAT	1400
	CATCGCGGGT	ATGGGCGAAC	TGCACCTCGA	CATCATCGTT	GACCGTATGA	1450
	AGCGTGAATT	CAACGTTGAA	GCGAACGTAG	GTAAACCGCA	GGTTGCTTAC	1500
15	CGTGAAACTA	TCCGCCAGAA	AGTTACCGAT	GTTGAAGGTA	AACACGCGAA	1550
	ACAGTCTGGT	GGTCGTGGTC	AGTATGGTCA	TGTTGTTATC	GACATGTACC	1600
	CGCTGGAGCC	GGGTTCAAAC	CCGAAAGGCT	ACGAGTTCAT	CAACGACATT	1650
	AAAGGTGGTG	TAATCCCTGG	CGAATACATC	CCGGCCGTTG	ATAAAGGTAT	1700
	CCAGGAACAG	CTGAAAGCAG	GTCCGCTGGC	AGGCTACCCG	GTAGTAGACA	1750
20	TGGGTATTTCG	TCTGCACTTC	GGTTCTTACC	ATGACGTTGA	CTCCTCTGAA	1800
	CTGGCGTTTA	AACTGGCTGC	TTCTATCGCC	TTTAAAGAAG	GCTTTAAGAA	1850
	AGCGAAACCA	GTTCTGCTTG	AGCCGATCAT	GAAGGTTGAA	GTAGAAACTC	1900
	CGGAAGAGAA	CACCGGTGAC	GTTATCGGTG	ACTTGAGCCG	TCGTCTGGT	1950
	ATGCTCAAAG	GTCAGGAATC	TGAAGTTACT	GGCGTTAAGA	TCCACGCTGA	2000
25	AGTACCGCTG	TCTGAAATGT	TCGGATACGC	AACTCAGCTG	CGTTCTCTGA	2050
	CCAAAGGTCG	TGCATCATAC	ACTATGGAAT	TCCTGAAGTA	TGATGAAGCG	2100
	CCGAGTAACG	TTGCTCAGGC	CGTAATTGAA	GCCCGTGGTA	AATAA	2145

30

2) INFORMATION FOR SEQ ID NO: 1231

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231

GCGAGCCCGA AGATAAAAAA GAACCTCTGC TGCTCGC

37

45

2) INFORMATION FOR SEQ ID NO: 1232

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232

GGAGCCGCGC GATTTTATAA ATGAATGTTG ATAACCGGCT CC

60

42

2) INFORMATION FOR SEQ ID NO: 1233

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233
15 GCGAGCGTTA CTGGTGTAGA AATGTTCCGG CTCGC 35

2) INFORMATION FOR SEQ ID NO: 1234

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:
30 ACTAAATAAA CGCTCATTCG 20

2) INFORMATION FOR SEQ ID NO: 1235

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235
GCGAGCCGAA GTTGAAGTTG TTGGTATTGC TGGCTCGC 38

2) INFORMATION FOR SEQ ID NO: 1236

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236

GCGAGCCGTG GTGAAGTTCG CGTTGGTGGC TCGC

34

5

2) INFORMATION FOR SEQ ID NO: 1237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237

GCGAGCCGCG AAATCGAAGT TGCTGTATTA GGGCTCGC

38

20

2) INFORMATION FOR SEQ ID NO: 1238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238

GCGAGCGGCG TTAATTTTGG CACCGAAGAA GAGCTCGC

38

35

2) INFORMATION FOR SEQ ID NO: 1239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239

GCGAGCGCAG ACCTTTCAGC AGAGGAGGCT CGC

33

40

45

50

2) INFORMATION FOR SEQ ID NO: 1240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240

GCGAGCCGGC AAGACAATAT GACAGCAAAA TCGCTCGC

38

10

2) INFORMATION FOR SEQ ID NO: 1241

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241

GCGAGCGGGG AACGAGGATG ATTTGATTGG CTCGC

35

25

2) INFORMATION FOR SEQ ID NO: 1242

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 600 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
(E) STRAIN: BM4147-1
40 (F) ACCESSION NUMBER: U39790

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1242

45	TTCTTAGAGA CATTGAATAT GCCTTATGTC GCGCGAGGCG TATTGACCAG	50
	TGCATGTGCC ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG	100
	GTGTGCCGCA AGTTCCTTAT GTACCAGTAC TTAAGAATCA ATGGAAAAGAA	150
	AATCCTAAAA AAGTATTTGA TCAATGTGAA GGTTCCTTGC TTTATCCGAT	200
	GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT ACAAAGGCAG	250
	AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT	300
50	TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC	350
	TGTATTAGGA AATGAAGATG TTCGGACGAC TTTGCCTGGC GAAGTCGTAA	400
	AAGACGTAGC ATTCTATGAT TATGAAGCCA AATATATCAA TAATAAAATC	450
	GAAATGCAGA TTCCAGCCGA AGTGCCGGAA GAAGTTTATC AAAAAGCGCA	500
	AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC GGATTGAGCC	550
55	GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA	600

2) INFORMATION FOR SEQ ID NO: 1243

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2275 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (C) ACCESSION NUMBER: M38386

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1243

15	GGTACCAAAG	AAAAAAACGA	ACGCCACAAC	CAACAGCCTC	TAAAGCAACA	50
	CCTGCTTCTG	AAATTGAGGG	AGATTTAGCA	AATGTCAATG	AGATTCTTTT	100
	GGTTCACGAT	GATCGTGTCTG	GGTCAGCAAC	GATGGGAATG	AAAGTCTTAG	150
	AAGAAATTTT	AGATAAAGAG	AAAAATTTCAA	TGCCGATTCTG	AAAAATTAAT	200
	ATTAATGAAT	TAACCAACA	AACACAGGCT	TTAATTGTCA	CAAAAGCTGA	250
20	ACTAACGGAA	CAAGCACGTA	AAAAAGCACC	GAAAGCGACA	CACTTATCAG	300
	TAAAAAGTTA	TGGTTAATCC	CCAAAAATAT	GAAACAGTGG	GTTTCGCTCT	350
	TAAAAGAAAG	TGCCTAGAGA	GGAAGAAAAC	AATGGAAAAT	CTTACGAATA	400
	TTTCAATTGA	ATTAAATCAA	CAGTTTAATA	CAAAAGAAGA	AGCTATTTCGC	450
	TTTTCCGGCC	AGAACTAGT	CGAGGCAGGC	TGTGTTGAGC	CCGCTTATAT	500
25	CGAAGCAATG	ATTGAAAGAG	ACCAATTGCT	ATCTGCCCAT	ATGGGGAATT	550
	TTATTGCCAT	TCCTCATGGA	ACAGAAGAAG	CCAAAAAATT	AGTGAAAAAA	600
	TCAGGAATCT	GTGTAGTGCA	AGTCCCAGAG	GGCGTTAATT	TTGGCACCGA	650
	AGAAGATGAA	AAAATTGCTA	CCGTATTATT	TGGGATTGCC	GGAGTCGGTG	700
	AAGAACATTT	GCAATTAGTC	CAACAAATTG	CACTTTATTG	TAGTGATATG	750
30	GATAACGTGG	TGCAACTTGC	CGATGCATTA	AGTAAAGAAG	AAATAACAGA	800
	AAATTTAGCC	ATTGCTTAAA	GGAGAGAATA	AGAATGAACG	CAGTACATTT	850
	TGGAGCAGGA	AATATTGGAC	GCGGCTTTAT	TGGCGAAATT	TTAGCTAAAA	900
	CGGGTTTCAT	ATTACCGTTT	GTGGATGTTA	ATGGAAACCA	TCATCAAGCG	950
	TTAAAAGAAC	GTAAAAGTTA	TACAATTGAA	TTGGCCGATG	CCTCACATCA	1000
35	ACAAATTAAC	GTTGAAAATG	TGACCGGGTT	AAATAACATG	ACAGAACCAG	1050
	AAAAAGTAGT	AGAAGCAATT	GCGGAAGCCG	ATTTAGTCAC	GACGGCAATT	1100
	GGTCCTAATA	TTTTACCAAG	AATTGCTGAA	TTAATTGCTC	AAGGAATTGA	1150
	TGCACGTGCC	GAAGCAAATT	GTCAAAACGG	CCCGCTGGAT	ATTATCGCTT	1200
	GTGAAAATAT	GATTGGTGGT	TCAACCTTTT	TAGCAGAAGA	AGTGGCCATA	1250
40	ATATTTGAAA	AACCCAGCTT	ATCTGAACAA	TGGATTGGTT	TTCTTGATGC	1300
	GGCAGTTGAT	CGGATTGTTT	CATTACAAAA	ACATAAAGAT	CCACTTTTTG	1350
	TTCAAGTTGA	GCCTTTTTTG	GAATGGGTCA	TTGATGATAC	CAACCGAAAA	1400
	GCCAAAGAGA	TTCAAGTTAG	AGGCGTCATT	ACTTGTCGAT	TAGAGCCGTA	1450
	TATTGAACGA	AAATTATTTA	GTGTAACCAG	TGGCCATGCT	ACAGTTGCCT	1500
45	ATACAGGGGC	GTTGTTAGGC	TATCAAACCA	TTGACGAAGC	GATGCAGGAC	1550
	GCCTTAGTGG	TAGCGCAACT	CAAATCAGTT	TTGCAGGAAA	CCGGTAAACT	1600
	TTTAGTGGCC	AAATGGAATT	TTGATGAACA	AGAACATGCA	GCCTATATTG	1650
	AAAAAATTAT	CAACCGTTTC	CAAAATAAAT	ATATTTTCAGA	TGCTATTACA	1700
	CGTGTAGCAC	GGACACCAAT	CAGAAAATTA	GGTGCGCAAG	AACGGTTTAT	1750
50	TCGACCAATC	CGTGAATTAC	AGGAACGCAA	TCTAGTGTCTG	GCCGCATTTA	1800
	TAGCAATGAT	TGGTATTGTC	TTTAATTATC	ATGATCCAGA	AGATGAACAA	1850
	AGCCGTCAAT	TACAGGAAAT	GCTTGACCAA	GAAAGTGTTG	ATACAGTGGA	1900
	TCGCTGAAGT	AACGGGCATT	GAAGATCCAG	AAACGGTTAA	AAATATTAAA	1950
	CAAAACGTAG	AACGCTATG	CGCGACCACA	AGTAGCATAA	TTAACAAAAT	2000
55	CCTTCTACCA	AGATACTTCA	CATTTCTTAA	TTAAAGAAAA	AACAACCGCG	2050
	CCTCACCTGA	GCCGACCCCC	AAAAGTTAGA	CCTAGAAATC	TAACCTTTTG	2100
	AGGTTTTTTT	GTATGGCAAA	ATACAGTTTT	GAAATTTAAA	CTTAAACTTG	2150
	TTCATGACTA	CTTATATGGT	CAAGGAGGTC	TAAGGTTTCT	CGCAAAGAAG	2200
	TATGGGTTTA	AAGATAGTCT	CAAATAAGCA	AATGGATAAA	TGCCTATAAA	2250
60	GAACCTGGTG	AAGAAGGGGG	GATCC			2275

2) INFORMATION FOR SEQ ID NO: 1244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
- (B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244

20	GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
	TTCGCGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
	AATCTCATTA	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
	CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
	CCAGCCAAAA	CGATATTTTT	ATAATCATTA	CGTGAAAAAG	GTTTCCCTTC	250
25	ATTATCACAC	AAATATTTTA	GCTTTTCAGT	TTCTATATCA	ACTGTAGCTT	300
	CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTTGC	350
	ACACCTTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
	ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME 4 DE 4

NOTE: Pour les tomes additionnels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME

THIS IS VOLUME 4 OF 4

NOTE: For additional volumes please contact the Canadian Patent Office